

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 31.1423 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-1  
Perfect score: 234  
Sequence: 1 ELKRLRLPLVLFSEER.....QGALDIAIRDEELSGESS 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	100.0	47	5	ABB80769 A. salmon
2	153	65.4	97	7	ABO81308 Pseudomon
3	68.5	29.3	4558	6	ABU49362 Protein e
4	68	29.1	365	3	AB14131 Bordetell
5	68	29.1	386	6	ABU22986 Protein e
6	68	29.1	395	9	ABU43018 Lawsonia
7	66.5	28.4	5206	9	AEA29369 Vibrio vu
8	66	28.2	445	9	AEB39774 L. pneumo
9	66	28.2	451	9	AEB36357 L. pneumo
10	65	27.8	2000	9	ADY15562 PRO polyp
11	65	27.8	5032	7	ADJ68220 Human hea
12	65	27.8	5038	8	ADQ18491 Human sof
13	65	27.8	5038	8	ADY19486 PRO polyp
14	65	27.8	5072	2	AAR11510 Rvancodine
15	65	27.8	5081	4	ABB11480 Human rva
16	65	27.8	5081	4	ABG04969 Novel hum
17	61.5	26.3	61	4	AAU43730 Propionib
18	61.5	26.3	61	6	ABM40249 Propionib
19	61	26.1	840	10	AEG11146 Human tra
20	60.5	25.9	385	7	ADM25471 Hyperther
21	59.5	25.4	993	9	AEB08385 c-Jun inh
22	59.5	25.4	1225	6	ABU04466 Human exp
23	59.5	25.4	1225	6	ABU04463 Human exp

ALIGNMENTS

RESULT 1

ABB80769	24	59.5	25.4	1225	7	ADJ68360	Human hea
ID ABB80769 standard; protein; 47 AA.	25	59.5	25.4	1233	6	ABU71102	Human adi
XX	26	59.5	25.4	1233	6	ABU04465	Human exp
AC ABB80769;	27	59.5	25.4	1233	6	ABU04467	Human exp
XX	28	59.5	25.4	1233	6	ABU04464	Human exp
DT 23-SEP-2002 (first entry)	29	59.5	25.4	1233	7	ADES5562	Human pro
XX	30	59.5	25.4	1233	7	ADES5558	Human pro
DE A. salmonicida type III secretion protein acr1 sequence.	31	59.5	25.4	1233	8	ABM82411	Tumour-as
XX	32	59.5	25.4	1233	9	ADZ09730	Human bre
XX	33	59.5	25.4	1233	9	AEB56526	Radiochem
XX	34	59	25.2	609	4	AAU35147	Enterococ
Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;	35	59	25.2	609	6	ABU29041	Protein e
acrV; acrH; antibiotic; vaccine; fish.	36	58.5	25.0	155	9	ABM92719	M. xanthu
XX	37	57.5	24.6	481	5	ABP27255	Streptoco
OS Aeromonas salmonicida.	38	57.5	24.6	481	6	ABU46483	Protein e
XX	39	57.5	24.6	1233	7	ADD47479	Rat Prote
PN WO200240514-A2.	40	57.5	24.6	1233	7	ADD47483	Rat Prote
XX	41	57.5	24.6	1233	7	ADES5556	Rat Prote
PD 23-MAY-2002.	42	57.5	24.6	1233	7	ADES5560	Rat Prote
PF 15-NOV-2001; 2001WO-CA001589.	43	57.5	24.6	5035	2	AAR25450	MH mutant
XX	44	57	24.4	221	4	AAV72759	Nicotiana
PR 15-NOV-2000; 2000US-0248864P.	45	57	24.4	518	6	ABR40775	Nicotiana
XX							
(FREY/) FREY J.							
(STUB/) STUBER K.							
(THOR/) THORNTON J C.							
(KUZ/) KUZIK M A.							
(BURI/) BURIAN J.							
Frey J; Stuber K, Thornton JC, Kuzik MA, Burian J;							
WPI: 2002-537338/57.							
N-PSDB; ABR86172.							
Novel protein from Aeromonas salmonicida and nucleic acid encoding the							
protein, useful for reducing susceptibility of fish to infection by a							
virulent strain of Aeromonas salmonicida.							
Claim 13; Page 26; 39pp; English.							
The invention relates to A. salmonicida type III secretion genes and							
encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.							
A.salmonicida type III secretion apparatus is useful for producing							
selected products, especially Aext. AcrV in vaccine, epitope or epitopic							
region of AcrV or any other protein of A. salmonicida type III secretion							
apparatus is useful for reducing the susceptibility of fish to infection							

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present  
CC sequence represents the *A. salmonicida* type III secretion protein acrl  
XX  
SQ Sequence 47 AA;

Query Match 100.0%; Score 234; DB 5; Length 47;  
Best Local Similarity 100.0%; Pred. No. 5.8e-24;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELKRLIRLLPVELFSEEEQRNLQCCGALDIAEREEDELSGSS 47  
DB 1 ELKRLIRLLPVELFSEEEQRNLQCCGALDIAEREEDELSGSS 47

RESULT 2  
ABO81308  
ID ABO81308 standard; protein; 97 AA.  
XX  
AC ABO81308;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #13483.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
PF 18-FEB-1999; 98US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
XX  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
PT WPI; 2003-615309/58.  
XX  
DR N-PSDB; ABD14879.  
XX

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 30054; 455pp; English.  
XX

The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO6782a-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 97 AA;

Query Match 65.4%; Score 153; DB 7; Length 97;  
Best Local Similarity 70.5%; Pred. No. 1.3e-12;  
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
OY 1 ELKRLIRLLPVELFSEEEQRNLQCCGALDIAEREEDELSG 44  
DB 52 ELKRLYLLPVEVFGDDEQRNLNACQMALDLAIEREEQOHG 95

RESULT 3  
ABU49362  
ID ABU49362 standard; protein; 4558 AA.  
XX

XX AC ABU49362;  
XX  
DT 19-JUN-2003 (first entry)  
XX

DE Protein encoded by Prokaryotic essential gene #34889.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX

OS Vibrio cholerae.  
XX

PN WO200277183-A2.  
XX

PD 03-OCT-2002.  
XX

PF 21-MAR-2002; 2002WO-US009107.  
XX

PR 21-MAR-2001; 2001US-00815242.  
XX

PR 06-SEP-2001; 2001US-00948993.  
XX

PR 25-OCT-2001; 2001US-0342923P.  
XX

PR 08-FEB-2002; 2002US-00072851.  
XX

PR 06-MAR-2002; 2002US-0362699P.  
XX

XX (ELIT-) ELITRA PHARM INC.  
XX

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsein KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX

XX WPI; 2003-029926/02.  
DR N-PSDB; ACA53232.  
XX

New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX

PS Claim 25; SEQ ID NO 77286; 1766pp; English.  
XX

The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC on a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational





CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 386 AA;

Query Match 29.1%; Score 68; DB 6; Length 386;  
Best Local Similarity 32.4%; Pred. No. 2.2;  
Matches 12; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 2 LKRLIRLLPVELFSEEEQRQNLQCCGALDIAIERE 38  
Db 348 VRQILKULPTQIYADMDVRATVLAQAQDALDAIAME 384

RESULT 6  
AEB43018  
ID AEB43018 standard; protein; 395 AA.

XX  
AC AEB43018;

XX  
DT 06-OCT-2005 (first entry)

XX  
DE Lawsonia intracellularis protein #6.

XX  
KW Vaccine; antigen; bacterial infection; infection; antibacterial.

XX  
OS Lawsonia intracellularis.

XX  
PN WO2005070958-A2.

XX  
PD 04-AUG-2005.

XX  
PF 18-JAN-2005; 2005WO-EP000562.

XX  
PR 22-JAN-2004; 2004EP-00100202.

XX  
PR 22-JAN-2004; 2004EP-00100203.

XX  
PR 22-JAN-2004; 2004EP-00100204.

XX  
PR 22-JAN-2004; 2004EP-00100205.

XX  
PR 22-JAN-2004; 2004EP-00100206.

XX  
PR 22-JAN-2004; 2004EP-00100208.

XX  
PR 22-JAN-2004; 2004EP-00100209.

XX  
PR 22-JAN-2004; 2004EP-00100210.

XX  
PR 22-JAN-2004; 2004EP-00100211.

XX  
PA (ALKU ) AKZO NOBEL NV.

XX  
PI Vermeij P;

XX  
DR WPI; 2005-533996/54.

XX  
DR N-PSDB; AEB43017.

XX  
PT New Lawsonia intracellularis nucleic acids and proteins, useful as

XX  
PT vaccines or for manufacturing vaccines for combating Lawsonia

XX  
PT intracellularis infections.

XX  
PS Claim 19; SEQ ID NO 12; 99pp; English.

XX  
CC The invention relates to a nucleic acid encoding a Lawsonia  
CC intracellularis protein or a part of the nucleic acid that encodes an  
CC immunogenic fragment of the protein. The invention also relates to a DNA  
CC fragment comprising the nucleic acid, a recombinant DNA molecule  
CC comprising the nucleic acid or the DNA fragment under the control of a  
CC functionally linked promoter, a vaccine for combating L. intracellularis  
CC infections comprising the nucleic acid, the DNA fragment, recombinant DNA  
CC molecule, live recombinant carrier, host cell, or protein and a  
CC pharmaceutical carrier, a vaccine for combating L. intracellularis  
CC infections comprising antibodies against the protein above, a method of  
CC preparing the vaccine and a diagnostic test for the detection of  
CC antibodies against L. intracellularis comprising the protein or its  
CC fragment or comprising antibodies against the protein or its fragment.  
CC The L. intracellularis nucleic acid and protein can be used in a vaccine  
CC or in the manufacture of a vaccine for combating L. intracellularis  
CC infections. They can also be used for detecting antibodies against L.

CC intracellularis. This sequence represents an L. intracellularis protein  
CC of the invention.  
XX  
SQ Sequence 395 AA;

Query Match 29.1%; Score 68; DB 9; Length 395;  
Best Local Similarity 31.0%; Pred. No. 2.3;  
Matches 13; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 LKRLIRLLPVELFSEEEQRQNLQCCGALDIAIEREDEL 42  
Db 336 EMLAAVRKFPIMVDNVRVGVQDVAVDVAREDEFL 377

RESULT 7  
AEA29369  
ID AEA29369 standard; protein; 5206 AA.

XX  
AC AEA29369;

XX  
DT 28-JUL-2005 (first entry)

XX  
DE Vibrio vulnificus RTX toxin rtxA protein SEQ ID NO:2.

XX  
KW vaccine; toxin; rtxA.

XX  
OS Vibrio vulnificus.

XX  
PN KR2004098202-A.

XX  
PD 20-NOV-2004.

XX  
PF 14-MAY-2003; 2003KR-00030495.

XX  
PR 14-MAY-2003; 2003KR-00030495.

XX  
PA (UYCH-) UNIV CHONNAM NAT.

XX  
PI Kim SY, Kim YR, Lee JH, Lee SE;

XX  
DR WPI; 2005-239015/25.

XX  
DR N-PSDB; AEA29368.

XX  
PT RTX toxin and related genes of vibrio vulnificus responsible for the

XX  
PT contact-cytotoxicity and lethality to animals.

XX  
PS Example 4; SEQ ID NO 2; 62pp; Korean.

XX  
CC The invention relates to the Vibrio vulnificus RTX toxin and related  
CC genes responsible for the contact-cytotoxicity and lethality to animals.  
CC Also described is a method for producing a mutant Vibrio vulnificus  
CC strain with attenuated cytotoxicity by deletion of the cytotoxicity  
CC related genes. The mutant strain with attenuated cytotoxicity is produced  
CC by deletion of one or more genes in the RTX operon of Vibrio vulnificus,  
CC selected from the rtxB2 gene of AEA29372, the rtxD gene of AEA29374, the  
CC rtxB1 gene of AEA29370, the ORF (open reading frame) between the rtxB1  
CC gene and rtxC gene of AEA29378, the rtxC gene of AEA29376 and the rtxA  
CC gene of AEA29368. An alive vaccine against Vibrio vulnificus is produced  
CC by using the RTX toxin production of the deficient mutant strain. The  
CC present sequence represents the Vibrio vulnificus rtxA protein, which is  
CC used in the exemplification of the present invention.

XX  
SQ Sequence 5206 AA;

Query Match 28.4%; Score 66.5; DB 9; Length 5206;  
Best Local Similarity 35.4%; Pred. No. 76;  
Matches 17; Conservative 10; Mismatches 18; Indels 3; Gaps 1;

QY 2 LKRLIRLLPVELFSEEEQRQNLQCCGALDIAIEREDEL--LSGES 46  
Db 2926 LSPFLTRFLNNELVGEKDARRKIGETITOTLDDHAVENGESQKVTLKGEA 2973

```
RESULT 8
AEB39774
ID AEB39774 standard; protein; 445 AA.
XX AC AEB39774;
XX
XX 08-SEP-2005 (first entry)
DT
XX L. pneumophila protein SEQ ID NO 4106.
DE
XX detection; infection; Antibacterial; Vaccine.
KW
XX Legionella pneumophila.
OS
XX WO2005049642-A2.
PN
XX 02-JUN-2005.
PD
XX 23-SEP-2004; 2004WO-IB003578.
PF
XX 21-NOV-2003; 2003FR-00013687.
PR
XX (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
PI
XX WPI; 2005-388305/40.
XX
XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
PT
XX Claim 3; SEQ ID NO 4106; 660pp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents the amino acid sequence of a
CC L. pneumophila protein.
XX
XX Sequence 445 AA;
SQ
Query Match 28.2%; Score 66; DB 9; Length 445;
Best Local Similarity 26.8%; Pred. No. 4.9;
Matches 22; Conservative 7; Mismatches 13; Indels 40; Gaps 2;

QY 2 LKRLIRLLPVELFSEEEQRQ-----NLQCCQ----- 28
DB 17 LKDLIRMTAEQFLSEKQVLLQKMRAPSGLEASRYESLCSVLVENLVNYCNQLPETAN 76
QY 29 -----GALDNAIEREDEL 43
DB 77 SYYSQPGGLVDHALNTEAALS 98

RESULT 9
AEB36357
ID AEB36357 standard; protein; 451 AA.
XX AC AEB36357;
XX
XX 05-MAY-2005 (first entry)
DT
XX PRO polypeptide SEQ ID NO 1368.
DE
XX
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```
XX 08-SEP-2005 (first entry)
XX L. pneumophila protein SEQ ID NO 689.
XX detection; infection; Antibacterial; Vaccine.
XX Legionella pneumophila.
XX WO2005049642-A2.
XX 02-JUN-2005.
XX 23-SEP-2004; 2004WO-IB003578.
XX 21-NOV-2003; 2003FR-00013687.
XX (INSP ) INST PASTEUR.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
XX Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
XX Jarraud S;
XX WPI; 2005-388305/40.
XX
XX New genome of Legionella pneumophila Paris strain and derived
XX polypeptides, useful for detection or identification of the strain and
XX for treatment and prevention of infections.
XX Claim 3; SEQ ID NO 689; 660pp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
XX from Legionella pneumophila Paris strain. (I), and their related
XX sequences or fragments, are useful as primers and probes for detection
XX and amplification, including differentiation between the Paris and
XX Philadelphia strains of Legionella pneumophila and to prepare recombinant
XX (hybrid) polypeptides (II). (II) are also useful for preparation of
XX specific antibodies (Ab), also used for detection/identification of
XX Legionella, and some (I), specifically those involved in synthesis of
XX surface proteins, are targets for identification of inhibitors. (II), or
XX vectors that contain (I), are useful as vaccines and immunogenic
XX compositions, for treatment and prevention of infections by L.
XX pneumophila. The present sequence represents the amino acid sequence of a
XX L. pneumophila protein.
XX
XX Sequence 451 AA;
XX
Query Match 28.2%; Score 66; DB 9; Length 451;
Best Local Similarity 26.8%; Pred. No. 5;
Matches 22; Conservative 7; Mismatches 13; Indels 40; Gaps 2;

QY 2 LKRLIRLLPVELFSEEEQRQ-----NLQCCQ----- 28
DB 23 LKDLIRMTAEQFLSEKQVLLQKMRAPSGLEASRYESLCSVLVENLVNYCNQLPETAN 82
QY 29 -----GALDNAIEREDEL 43
DB 83 SYYSQPGGLVDHALNTEAALS 104

RESULT 10
ADY15562
ID ADY15562 standard; protein; 2000 AA.
XX AC ADY15562;
XX
XX 05-MAY-2005 (first entry)
DT
XX PRO polypeptide SEQ ID NO 1368.
DE
XX
```



PT Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.

XX  
XX  
PS Example 2; SEQ ID NO 1310; 210pp; English.

XX  
CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytosstatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC protein of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX  
SQ Sequence 5038 AA;

Query Match 27.8%; Score 65; DB 8; Length 5038;  
Best Local Similarity 29.3%; Pred. No. 1.2e+02;  
Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;  
QY 1 ELKRLRLPVLFESEEQRLNCCGALDIAIEREED 41  
DB 1858 DVKQILKMEPVEFTTEEEDEE--EGEEDEEKEEDE 1896

RESULT 13

ADY19486  
ID ADY19486 standard; protein; 5038 AA.

AC ADY19486;

XX  
DT 05-MAY-2005 (first entry)

XX  
DE PRO polypeptide SEQ ID NO 5292.

XX  
KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotrophic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; diagnosis.

XX  
OS Homo sapiens.

XX  
PN WO2005016962-A2.

XX  
PD 24-FEB-2005.

XX  
PF 11-AUG-2004; 2004WO-US026249.

XX  
PR 11-AUG-2003; 2003US-0493546P.

XX  
PA (GETH ) GENENTECH INC.

XX  
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX  
DR WPI; 2005-182330/19.

XX  
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX  
PS Claim 8; SEQ ID NO 5292; 158pp; English.

XX  
CC The invention relates to an isolated nucleic acid encoding a PRO  
CC polypeptide. The polypeptide, agonist or an antagonist, antibody, or  
CC composition, and method are useful for diagnosing and treating an immune

CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
CC arthritis. The present sequence represents a PRO polypeptide.

XX  
SQ Sequence 5038 AA;

Query Match 27.8%; Score 65; DB 9; Length 5038;  
Best Local Similarity 29.3%; Pred. No. 1.2e+02;  
Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;

QY 1 ELKRLRLPVLFESEEQRLNCCGALDIAIEREED 41  
DB 1858 DVKQILKMEPVEFTTEEEDEE--EGEEDEEKEEDE 1896

RESULT 14

AAR11510

ID AAR11510 standard; protein; 5072 AA.

XX  
AC AAR11510;

XX  
DT 25-MAR-2003 (revised)

DT 17-JUN-1991 (first entry)

XX  
DE Ryanodine receptor deduced from cDNA clone.

XX  
KW Malignant hyperthermia; hypermetabolic syndrome; inhalation;  
KW anaesthetics; probe; calcium release channel; sarcoplasmic; reticulum.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT Peptide 1629..1632

FT Peptide 1742..1748

FT Peptide 3119..3130

FT Peptide 3196..3210

FT Active-site 3981..3985

FT /label= phosphorylation site

FT Active-site 4315..4318

FT /label= phosphorylation site

XX  
PN WO9104328-A.

XX  
PD 04-APR-1991.

XX  
PF 25-SEP-1989; 89CA-00612726.

XX  
PR 25-SEP-1989; 89CA-00612726.

XX  
PA (UTOR ) UNIV TORONTO INNOVA.

PA (HSCR-) HSC R&D LTD PARTNERSHIP.

PA (TORO-) TORONTO HOSPITAL.

XX  
PI Worton RG, MacLenna DH, Britt BA;

XX  
DR WPI; 1991-117517/16.

DR N-PSDB; AAQ11415.

XX  
PT Purified DNA specific for human ryanodine receptor - useful for diagnosis  
PT of malignant hyperthermia.

XX  
PS Claim 11; Fig 2; 49pp; English.

XX  
CC The sequence was obtd. from several overlapping clones isolated from a  
CC human skeletal muscle cDNA library in lambda gt10. The protein encodes  
CC the human ryanodine receptor (HRR), a calcium release channel which spans  
CC the gap between the transverse tubule and the sarcoplasmic reticulum (SR)  
CC in muscle. The sustained muscle contraction in malignant hyperthermia  
CC (MH) may be caused by the release of calcium into the muscle cell  
CC cytoplasm from the SR. This is due to a defect in the gene encoding HRR.  
CC Sequences from the gene can be used for diagnosis of MH using FRPL  
CC analysis. The protein sequence would give rise to several transmembrane  
CC passages in the C-terminal fifth of the molecule; the bulk would be hydro  
CC - philic. This matches well with the structure of known ryanodine

CC receptors. The peptides in the feature table were determined from the  
 CC purified receptor protein. (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 5072 AA;  
 SQ Sequence 5072 AA;  
 Query Match 27.8%; Score 65; DB 2; Length 5072;  
 Best Local Similarity 29.3%; Pred. No. 1.2e+02;  
 Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;  
 QY 1 ELKRLIRLLPVELFSEEEQRNLLQCCGALDNALIERDEE 41  
 DB 1857 DVKQILKMIPEVFTSEEEDEEE--EGEEDDEBEKDEE 1895  
 RESULT 15  
 ID ABB11480 standard; peptide; 5081 AA.  
 AC ABB11480;  
 XX  
 DT 11-JAN-2002 (first entry)  
 XX  
 DE Human ryanodine receptor homologue, SEQ ID NO:1850.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antischmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US003800.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-457740/49.  
 DR N-PSDB; ABA08724.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing, treating  
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.  
 XX  
 PS Claim 20; Page 197-200; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors, and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention  
 XX Sequence 5081 AA;  
 SQ

Query Match 27.8%; Score 65; DB 4; Length 5081;  
 Best Local Similarity 29.3%; Pred. No. 1.2e+02;  
 Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;

QY 1 ELKRLIRLLPVELFSEEEQRNLLQCCGALDNALIERDEE 41  
 DB 1901 DVKQILKMIPEVFTSEEEDEEE--EGEEDDEBEKDEE 1939

Search completed: June 16, 2006, 19:06:42  
 Job time : 33.1423 secs



Db 47 DLKRMFLPLGVFSDEEQRQLNQMCQAIDMAIESEEBELS 89

RESULT 3

T43587

Yop secretion and targeting control protein - Yersinia pestis plasmid pCD1

C:Species: Yersinia pestis

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T43587; T42882

R:Hu P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker J.; Bacteriol. 180, 5192-5202, 1998

A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.

A:Reference number: 222578; MUID:98422474; PMID:974654

A:Accession: T43587

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-92 <HUP>

A:Cross-references: UNIPROT:P16161; UNIPARC:UPI0000000BC6; EMBL:AF053946; NID:G2996222;

A:Experimental source: strain KIM

R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998

A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia P

A:Reference number: 222273; MUID:98427122; PMID:9746557

A:Accession: T42882

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-92 <PER>

A:Cross-references: UNIPARC:UPI0000000BC6; EMBL:AF074612; NID:G3822037; PIDN:AAC69793.1;

A:Experimental source: strain KIM5

C:Genetics:

A:Gene: tyeA

A:Genome: plasmid pCD1

Query Match 64.1%; Score 150; DB 2; Length 92;

Best Local Similarity 67.4%; Pred. No. 2.4e-11;

Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELKRLRLPLVELSEEBQRQLNQCCGALDNAIEREEDLS 43

Db 47 DLKRMFLPLGVFSDEEQRQLNQMCQAIDMAIESEEBELS 89

RESULT 4

S15321

hypothetical protein 1 - Yersinia pseudotuberculosis plasmid

C:Species: Yersinia pseudotuberculosis

C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004

C:Accession: S15321; S08670

R:Forsberg, A.; Viitanen, A.M.; Skurnik, M.; Wolf-Watz, H. Mol. Microbiol. 5, 977-986, 1991

A:Title: The surface-located yopN protein is involved in calcium signal transduction in

A:Reference number: S15320; MUID:91312137; PMID:1857212

A:Accession: S15321

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-92 <MOL>

A:Cross-references: UNIPROT:P16161; UNIPARC:UPI0000000BC6; EMBL:X51833; NID:G48633; PIDN

C:Genetics:

A:Genome: plasmid

Query Match 64.1%; Score 150; DB 2; Length 92;

Best Local Similarity 67.4%; Pred. No. 2.4e-11;

Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELKRLRLPLVELSEEBQRQLNQCCGALDNAIEREEDLS 43

Db 47 DLKRMFLPLGVFSDEEQRQLNQMCQAIDMAIESEEBELS 89

RESULT 5

C82199

RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: C82199

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82199

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4558 <HEI>

A:Cross-references: UNIPROT:Q9RS12; UNIPARC:UPI0000110215; GB:AE004223; GB:AE003852; NID

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1451

A:Map position: 1

Query Match 29.3%; Score 68.5; DB 2; Length 4558;

Best Local Similarity 35.4%; Pred. No. 12;

Matches 17; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

Qy 2 LKRLRLPLVELSEEBQRQLNQCCGALDNAIEREEDLS 46

Db 3123 LSPLTRENNELYGDKEARRKIGBITQTLLDHAVERGESQKITLQGEA 3170

RESULT 6

A35041

ryanodine receptor type 1, skeletal muscle - human

N:Alternate names: calcium release channel protein

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: A35041; I84622; S66630

R:Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meisner, G.; J. Biol. Chem. 265, 2244-2256, 1990

A:Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) release

A:Reference number: A35041; MUID:90130482; PMID:2298749

A:Accession: A35041

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-5032 <ZOR>

A:Cross-references: UNIPROT:P21817; UNIPARC:UPI0000055AFF; GB:J05200; NID:G337721; PIDN

R:Otsu, K.; Phillips, M.S.; Khanna, V.K.; de Leon, S.; MacLennan, D.H. Genomics 13, 835-837, 1992

A:Title: Refinement of diagnostic assays for a probable causal mutation for porcine and

A:Reference number: I46644; MUID:92347887; PMID:1639409

A:Accession: I84622

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 598-722 <RES>

A:Cross-references: UNIPARC:UPI000016AFDE; GB:M91455; NID:G337723; PIDN:AAA60295.1; PID

R:Lynn, S.; Morgan, J.M.; Lamb, H.K.; Meisner, G.; Gillespie, J.I. FEBS Lett. 372, 6-12, 1995

A:Title: Isolation and partial cloning of ryanodine-sensitive Ca(2+) release channel pro

A:Reference number: S66630; MUID:96032536; PMID:7556644

A:Accession: S66630

A:Molecule type: mRNA

A:Residues: 4690-4968 <LYN>

A:Cross-references: UNIPARC:UPI000001741C7

A:Experimental source: myometrial smooth muscle

C:Genetics:

A:Gene: GDB:RVR1

A:Cross-references: GDB:120359; OMIM:180901

A:Map position: 19q13.1-19q13.1

A:Introns: 642/2

C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog

C:Keywords: calcium channel; homotetramer; phosphoprotein; skeletal muscle; transmembran

F:1788-1984/Domain: transcription initiation factor sigma region 1 homology <SR1>

Query Match 27.8%; Score 65; DB 1; Length 5032;

Best Local Similarity 29.3%; Pred. No. 35;

Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;





RESULT 13  
EDBEF7  
immediate-early protein IE68 - equine herpesvirus 1 (strain Ab4p)  
N;Alternate names: in vitro host-range factor  
C;Species: equine herpesvirus 1  
A;Note: host Equus caballus (domestic horse)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: B36802  
R;RefId, E.A.R.: Watson, M.S.; McBride, K.; Davison, A.J.  
submitted to GenBank, March 1992  
A;Description: The DNA sequence of equine herpesvirus-1.  
A;Reference number: A36805  
A;Accession: B36902  
A;Molecule type: DNA  
A;Residues: 1-293 <TEL>  
A;Cross-references: UNIPROT:P28940; UNIPARC:UP1000012D221; GB:M86664; NID:G330791; PIDN:  
R;RefId, E.A.R.: Watson, M.S.; McBride, K.; Davison, A.J.  
Virology 189, 304-316, 1992  
A;Title: The DNA sequence of equine herpesvirus-1.  
A;Reference number: A41831; MUID:92295566; PMID:1318606  
A;Contents: annotation; possible protein-coding frames  
A;Note: neither amino acid nor nucleotide sequence is given  
C;Genetics:

submitted to the EMBL Data Library, November 1992



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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 36.9122 Seconds  
 (without alignments)  
 1177.815 Million cell updates/sec

Title: US-10-813-908A-1  
 Perfect score: 234  
 Sequence: 1 ELKRLIRLLPVELFSEERQ.....QGALDIAIERDELSGESS 47

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_prot.\*  
 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result #	No.	Score	Query Match	Length	ID	Description
1	234	100.0	93	2	Q8GA95_AERSA	Q8GA95 aeromonas s
2	225	96.2	93	2	Q5XL11_AERHY	Q5XL11 aeromonas h
3	225	96.2	93	2	Q6TLM9_AERHY	Q6TLM9 aeromonas h
4	224	95.7	93	2	Q699R7_AERHY	Q699R7 aeromonas h
5	178.5	76.3	95	2	Q84GZ2_PHOLU	Q84GZ2 photorhabdu
6	176.5	75.4	95	2	Q7N0W4_PHOLU	Q7N0W4 photorhabdu
7	153	65.4	46	2	Q30MX6_PSEAE	Q30MX6 pseudomonas
8	153	65.4	92	2	Q30532_PSEAE	Q30532 pseudomonas
9	150	64.1	92	1	TYEA_YEREN	P69967 versinia en
10	150	64.1	92	1	TYEA_YERPE	P69968 versinia pe
11	150	64.1	92	1	TYEA_YERPS	P69969 versinia ps
12	150	64.1	92	2	Q79NG7_YEREN	Q79NG7 versinia en
13	150	64.1	108	2	Q84GT7_YEREN	Q84GT7 versinia en
14	129	55.1	94	2	Q66PU2_PASPI	Q66PU2 pasteurella
15	129	55.1	94	2	Q6QVR5_VIBHA	Q6QVR5 vibrio harv
16	126	53.8	94	2	Q87P52_VIBPA	Q87P52 vibrio para
17	80	34.2	374	2	Q72W13_DESVH	Q72W13 desulfovibr
18	69.5	29.7	621	2	Q4D246_TRYCR	Q4D246 trypanosoma
19	68.5	29.3	4545	2	Q9X4W2_VIBCH	Q9X4W2 vibrio chol
20	68.5	29.3	4558	2	Q9XS12_VIBCH	Q9XS12 vibrio chol
21	68	29.1	365	2	Q9REZ4_BORBR	Q9REZ4 bordetella
22	68	29.1	365	2	Q7W8C0_BORBR	Q7W8C0 bordetella
23	68	29.1	365	2	Q7WLX7_BORBR	Q7WLX7 bordetella
24	68	29.1	365	2	Q84CS9_BORPE	Q84CS9 bordetella
25	66.5	28.4	5206	2	Q86P9_VIBVU	Q86P9 vibrio vuln
26	66	28.2	445	2	Q5X0V2_LEGPA	Q5X0V2 legionella
27	66	28.2	449	2	Q5ZRF5_LEGPA	Q5ZRF5 legionella
28	65.5	28.0	5206	2	Q7MDK6_VIBVY	Q7MDK6 vibrio vuln
29	65	27.8	5038	1	RYR1_HUMAN	P21817 homo sapien
30	64.5	27.6	644	2	Q4DW36_TRYCR	Q4DW36 trypanosoma
31	64.5	27.6	953	2	O85299_HAEIN	O85299 haemophilus

32 64.5 27.6 1233 1 SMC1A\_MOUSE  
 33 64.5 27.6 1378 2 Q4RMM9\_TETNG  
 34 64 27.4 377 2 Q2SH40\_9GAMM  
 35 63 26.9 358 2 Q9TXN9\_CAEEL  
 36 63 26.9 688 2 Q8W311\_ORYSA  
 37 62 26.5 158 2 Q46KH1\_PROMT  
 38 62 26.5 289 2 Q4HA57\_9DEIO  
 39 62 26.5 445 2 Q5WSM4\_LEGPL  
 40 62 26.5 1634 2 Q54W73\_DICDI  
 41 61 26.1 160 2 Q2QXD0\_ORYSA  
 42 61 26.1 517 2 Q3KI33\_PSEPF  
 43 61 26.1 539 1 TCPH\_PEAR7  
 44 61 26.1 555 2 Q4D9X9\_TRYCR  
 45 61 26.1 840 2 Q8IYY8\_HUMAN

## ALIGNMENTS

RESULT 1  
 Q8GA95\_AERSA  
 ID Q8GA95\_AERSA PRELIMINARY; PRT; 93 AA.  
 AC Q8GA95  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DE 07-FEB-2006, entry version 8.  
 DE Acr1 protein.  
 GN Name=acr1;  
 OS Aeromonas salmonicida subsp. salmonicida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
 OC Aeromonadaceae; Aeromonas.  
 OX NCBI\_TaxID=29491;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JF2267;  
 RX MEDLINE=226211; PubMed=12374830;  
 RX DOI=10.1128/JB.184.21.5966-5970.2002;  
 RA Burr S.E., Stuber K., Wahli T., Frey J.;  
 RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida."  
 RT subsp. salmonicida."  
 RL J. Bacteriol. 184:5966-5970(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JF2267;  
 RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;  
 RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model."  
 RT Microbiol. 151:2111-2118(2005).  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AJ458292; CAD30214.1; -; Genomic DNA.  
 DR EMBL; AJ616218; CAE93101.1; -; Genomic DNA.  
 SQ SEQUENCE 93 AA; 10609 MW; E90FB0E802B4B4BD CRC64;  
 Query Match 100.0%; Score 234; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ELKRLIRLLPVELFSEERQNLQCCQCGALDIAIERDELSGESS 47  
 Db 47 ELKRLIRLLPVELFSEERQNLQCCQCGALDIAIERDELSGESS 93  
 RESULT 2  
 Q5XL11\_AERHY  
 ID Q5XL11\_AERHY PRELIMINARY; PRT; 93 AA.  
 AC Q5XL11  
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.  
 DT 23-NOV-2004, sequence version 1.  
 DE 07-FEB-2006, entry version 7.  
 DE Acr1.

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GN Name=acrl;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RL Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY763611; AAV30226.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10560 MW; EB215E253BB31A39 CRC64;

Query Match 96.2%; Score 225; DB 2; Length 93;
Best Local Similarity 93.6%; Pred. No. 1.6e-19;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGSS 47
Db 47 ELKRLVRLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGDP 93

RESULT 3
Q6TLM9 AERHY
I.Q. Q6TLM9 AERHY PRELIMINARY; PRT; 93 AA.
AC Q6TLM9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Acrl.
GN Name=acrl;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
CC -----
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CC -----
DR EMBL; AY394563; AAR26332.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10590 MW; CD3D11726471CB52 CRC64;

Query Match 96.2%; Score 225; DB 2; Length 93;
Best Local Similarity 93.6%; Pred. No. 1.6e-19;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGSS 47
Db 47 ELKRLVRLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGDP 93

RESULT 4
Q699R7 AERHY
ID Q699R7 AERHY PRELIMINARY; PRT; 93 AA.
AC Q699R7;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
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DT 07-FEB-2006, entry version 8.
DE Acrl.
GN Name=acrl;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
CC -----
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CC -----
DR EMBL; AY528667; AAS91812.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10522 MW; 8BEFFBF64A3D71A CRC64;

Query Match 95.7%; Score 224; DB 2; Length 93;
Best Local Similarity 95.7%; Pred. No. 2.1e-19;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGSS 47
Db 47 ELKRLVRLPVLPFSEEQRONLLQCCOGALDNAIEREDELSSGSS 93

RESULT 5
Q84GZ2 PHOLU
ID Q84GZ2 PHOLU PRELIMINARY; PRT; 95 AA.
AC Q84GZ2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LsaA.
GN Name=LsaA;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
CC -----
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CC -----
DR EMBL; AY144116; AAO18046.1; -; Genomic DNA.
SQ SEQUENCE 95 AA; 10859 MW; F12B5D44A35E808F CRC64;

Query Match 76.3%; Score 178.5; DB 2; Length 95;
Best Local Similarity 79.2%; Pred. No. 8.2e-14;
Matches 38; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 ELKRLIRLLPVLPFSEEQRONLLQCCOGALDNAIEREDEL-SGESS 47
Db 47 ELKRLVRLPVLPFSEEQRONLLQCCOGALDNAIEREDELWSGEGA 94

RESULT 6
Q7NOW4 PHOLL
ID Q7NOW4 PHOLL PRELIMINARY; PRT; 95 AA.
AC Q7NOW4;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
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[3]
RN STRAIN=CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RX Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feitwell T., Hamlin N., Holroyd S.J., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Bartell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=91001 / Biovar Mediaevalis;
RC PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RX Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans.";
RL Data Res. 11:179-197(2004).
CC -|- FUNCTION: Involved in the control of Yop release (By similarity) .
CC -|- SUBUNIT: Interacts with the translocator YopD and with residues 242-293 of YopN (By similarity) .
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DR EMBL: AF074612; AAC69793.1; - ; Genomic_DNA.
DR ENBL: AF053946; AAC62566.1; - ; Genomic_DNA.
DR ENBL: AL117189; CAB54315.1; - ; Genomic_DNA.
DR EMBL: AE017043; AAS58564.1; - ; Genomic_DNA.
DR PIR: T43587; T43587.
DR PD8; 1XL3; X-ray; C/D=1-92.
DR SMR; P69968; 2-86.
DR GenomeReviews; AE017043 GR; pCD45.
DR GenomeReviews; AL117189 GR; YPCD1_38C.
KW 3D-structure; Complete proteome; Plasmid.
FT CHAIN 1 92
FT FTID=PRO_0000065703.
SQ SEQUENCE 92 AA; 10753 MW; E5046EDD93D9F29 CRC64;
Query Match 64.1%; Score 150; DB 1; Length 92;
Best Local Similarity 67.4%; Pred.No. 2.4e-10;
Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELKRLIRLPVLVFSBEQRQNLLQCCGALDNAIEREDEL5 43
Db :|||: ||: |::|:|||:|||||: |||: |||: |||:
47 DLKRMFLPLGVFSDEEQRQNLLQCNALDNAISSEELS 89
RESULT 11
TYEA VERPS
ID TYEA VERPS STANDARD; ID TYEA VERPS PRT; 92 AA.
AC P69969; P16161; Q663K2;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Protein tyea.
GN Name:tyeaA; OrderedLocusNames=pYV0064;
OS Yersinia pseudotuberculosis.
OC Plasmid pIB1, and plasmid pGV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=633;
RN [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91312137; PubMed=1857212;
RA Forsberg A., Viitanen A.-M., Skurnik M., Wolf-watz H.;
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Search completed: June 16, 2006, 19:22:53  
Job time : 38.9122 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 8.67398 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-1  
Perfect score: 234  
Sequence: 1 ELKRLIRLLPVLFSEERQ.....QGALDNIAREDELSGSS 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pcp:\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pcp:\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp:\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp:\*
  - 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/pCTUS COMB.pcp:\*
  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pcp:\*
  - 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	153	65.4	97	2	US-09-252-991A-30054
2	65	27.8	240	1	US-08-114-555A-6
3	65	27.8	240	2	US-08-559-397A-12
4	65	27.8	5032	2	US-09-538-092-979
5	59.5	25.4	1244	2	US-09-949-016-11702
6	58.5	25.0	155	2	US-09-902-540-11918
7	57	24.4	221	2	US-09-384-162-4
8	56.5	24.1	517	2	US-09-107-532A-6058
9	55.5	23.7	423	2	US-09-248-796A-16012
10	55.5	23.7	515	2	US-09-107-532A-5603
11	55	23.5	99	2	US-09-543-681A-8306
12	55	23.5	181	2	US-09-902-540-14043
13	55	23.5	240	1	US-08-114-555A-8
14	55	23.5	240	2	US-08-559-397A-14
15	55	23.5	616	2	US-09-690-185A-2
16	55	23.5	1231	2	US-09-595-684B-23
17	55	23.5	5037	2	US-09-424-783-4
18	54	23.1	506	2	US-09-117-250-1
19	54	23.1	665	2	US-09-949-016-10993
20	54	23.1	781	1	US-08-675-631-3
21	54	23.1	781	2	US-08-359-316A-3
22	54	23.1	781	2	US-09-248-776-3
23	52.5	22.4	376	2	US-10-094-749-2760
24	52.5	22.4	1040	2	US-09-564-805-238
25	52	22.2	136	2	US-10-104-047-3252
26	52	22.2	719	2	US-10-094-749-2001

ALIGNMENTS

RESULT 1  
US-09-252-991A-30054  
; Sequence 30054, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30054  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30054

Query Match 65.4%; Score 153; DB 2; Length 97;  
Best Local Similarity 70.5%; Pred. No. 1.6e-13;  
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
QY 1 ELKRLIRLLPVLFSEERQNLQCCQALDNIAREDELSG 44  
Db 52 ELKRLIRLLPVLFSEERQNLQCCQALDNIAREDELSG 95

RESULT 2  
US-08-114-555A-6  
; Sequence 6, Application US/08114555A  
; Patent No. 5854392  
; GENERAL INFORMATION:  
; APPLICANT: Manly, Susan P.  
; APPLICANT: Kozlowski, Michael R.  
; APPLICANT: Neve, Rachael L.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100  
; TITLE OF INVENTION: RECEPTOR (C100-R)  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

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; ORGANISM: Human
US-09-949-016-11702

Query Match      25.4%; Score 59.5; DB 2; Length 1244;
Best Local Similarity 28.6%; Pred. No. 24;
Matches 16; Conservative 10; Mismatches 19; Indels 11; Gaps 2;

QY 2 LKRLRLPVLFSBEEQRNLQCC-----CGALDNAIERREDELSGSS 47
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Db 919 LQEVTAIETKJQRKSRHLLQACKMQDIKPLSKGTMD-ISOEGSSQGEDS 973

RESULT 6
US-09-902-540-11918
; Sequence 11918, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11918
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11918

Query Match      25.0%; Score 58.5; DB 2; Length 155;
Best Local Similarity 32.6%; Pred. No. 2.8;
Matches 15; Conservative 10; Mismatches 10; Indels 11; Gaps 2;

QY 12 ELFSEBEEQRN-LQCCQGALDNA-----IEREDELSGES 46
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 66 KLFREPKEQNPLCDKCEGSLKNQPIGTILRLDKKDDWNSGGS 111

RESULT 7
US-09-384-162-4
; Sequence 4, Application US/09384162
; Patent No. 6376747
; GENERAL INFORMATION:
; APPLICANT: Xing, Ti
; APPLICANT: Malik, Kamal
; APPLICANT: Martin-Heller, Teresa
; APPLICANT: Miki L., Brian
; TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
; FILE REFERENCE: 08-884280US
; CURRENT APPLICATION NUMBER: US/09/384,162
; CURRENT FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-384-162-4

Query Match      24.4%; Score 57; DB 2; Length 221;
Best Local Similarity 36.8%; Pred. No. 7;
Matches 14; Conservative 7; Mismatches 7; Indels 10; Gaps 2;

QY 4 RUIRLPLVLFSEBEEQRNLL-----QCCQGALD 32
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Db 25 RIIALKKINIF-EKEKRQQLLTIRLCEAPCCQGLVE 61
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RESULT 8
US-09-107-532A-6058
; Sequence 6058, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6058:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...517
; SEQUENCE DESCRIPTION: SEQ ID NO: 6058:
US-09-107-532A-6058

Query Match      24.1%; Score 56.5; DB 2; Length 517;
Best Local Similarity 41.9%; Pred. No. 22;
Matches 18; Conservative 5; Mismatches 15; Indels 5; Gaps 2;

QY 3 KRLIRLPLVLFSEBEEQ-RQNLQCCQCAL-----DNAIERED 40
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Db 349 KGNIRLLTVDFQAEEQNREETVSVLGGLLVQDQLAIENEDE 391

RESULT 9
US-09-248-796A-16012
; Sequence 16012, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
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; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF BETA APP-C100-R)
; TITLE OF INVENTION: CLONING AND EXPRESSION OF BETA APP-C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-114-555A-8

Query Match      23.5%; Score 55; DB 1; Length 240;
Best Local Similarity 26.8%; Pred.No.14;
Matches 11; Conservative 14; Mismatches 10; Indels

QY      1 ELKRLRLPLVLEEEERQNLLCCGALDNAIEREDE 41
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Db      95 DVQILKMTEPVFTTDEE-----EEEEEEEEDE 129

RESULT 14
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF
; TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77286
; LENGTH: 4558
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3773)..(3773)
; OTHER INFORMATION: X=any amino acid
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; NAME/KEY: MISC FEATURE
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; OTHER INFORMATION: X=any amino acid
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; NAME/KEY: MISC FEATURE
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; OTHER INFORMATION: X=any amino acid
; US-10-282-122A-77286

Query Match 29.3%; Score 68.5; DB 4; Length 4558;
Best Local Similarity 35.4%; Pred. No. 52;
Matches 17; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

QY 2 LKSLIRLLPVLSEESFORQLQCCGALDNATEREDE---LSGES 46
DB 3123 LSPLTRENNELYGDKARRKIGITOTLLDHAVERGESQKITLQGEA 3170

RESULT 3
US-10-282-122A-50910
; Sequence 50910, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20

```

```

RESULT 7
US-10-756-149-5039
; Sequence 5039, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aaiz, Natasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF INVENTION
; TITLE OF INVENTION: METHODS OF SCREENING
; FILE REFERENCE: file

```

```

RESULT 9
US-10-450-763-35328
; Sequence 35328, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/080
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Cutoff
; SEQ ID NO 35328
; LENGTH: 5081
; TYPE: PRT
; ORGANISM: Homo sapiens

```

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; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (811)..(833)
; OTHER INFORMATION: Domain in Sp1a and the Ryanodine Receptor domain identified
; OTHER INFORMATION: by eMATRIX, accession number PF006228, p-value=5.821e-14, raw score
; OTHER INFORMATION: of 21.00
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (44)..(689)
; OTHER INFORMATION: Calcium channel extracellular region domain identified by
; OTHER INFORMATION: Pfam, accession name RYDR_ITPR, E-value=0, Pfam score of 1582.7
US-10-450-763-35328

Query Match      27.8%; Score 65; DB 5; Length 5081;
Best Local Similarity 29.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;

QY 1 ELKRLIRLLPVELFSEERQNLQCCQGAALDNAIEREDE 41
:::||||: |:|:||||: : : |:|:|
Db 1901 DVKQILKMIPEVFTSEEDDEE--EGEEDDEKEDE 1939

RESULT 10
US-11-177-894-11
; Sequence 11, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Homo sapiens
US-11-177-894-11

Query Match      26.1%; Score 61; DB 6; Length 840;
Best Local Similarity 44.4%; Pred. No. 72;
Matches 16; Conservative 6; Mismatches 8; Indels 6; Gaps 2;

QY 7 RLLPVELFSEERQNLQCCQGAALDNAIEREDE 41
::| ||||| ||| :|:|:| ||:|
Db 781 KVLWVLFMRBEQDKQLLETCMEK-----BRQKDE 811

RESULT 11
US-10-506-454-77
; Sequence 77, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Koz'yavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
```

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; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-77

Query Match      25.9%; Score 60.5; DB 5; Length 385;
Best Local Similarity 37.5%; Pred. No. 35;
Matches 18; Conservative 8; Mismatches 19; Indels 3; Gaps 1;

QY 1 ELKRLIRLLPVELFSEERQNLQCCQGA---LDNAIEREDELSG 45
||:|:|: : :|:|:|: :|:|:|: :|:|:|:
Db 301 ELRLLNVREPVVNEELQGLVGLCDGAGDGLLGIVIREIDFASGE 348

RESULT 12
US-11-188-298-11708
; Sequence 11708, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 11708
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus subsp. marinus str. CCMP1375
US-11-188-298-11708

Query Match      25.9%; Score 60.5; DB 6; Length 437;
Best Local Similarity 28.6%; Pred. No. 40;
Matches 16; Conservative 10; Mismatches 11; Indels 19; Gaps 3;

QY 5 LIRLLPVELFSEEE---BQRQNLQCCQG---ALDNAIEREDELSG 44
|:|:|:|: |:|:|:|: |:|:|:|: |:|:|:|:
Db 183 LKLVP---FAKEGRMAAVQLRKAVVNSQNLTLCCQAMENAMDTVIQQGRQSIGG 235

RESULT 13
US-10-437-963-183489
; Sequence 183489, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 183489
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80576C.1.pep
US-10-437-963-183489

Query Match      25.4%; Score 59.5; DB 4; Length 804;
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Best Local Similarity 34.2%; Pred. No. 1.1e+02;  
Matches 13; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

Qy	<div></div>	7 RLLPV---ELFSEEEQRNWLQQCGALDNAIEREDE 41   :     ::   ::   :   :   :   :
Db	<div></div>	172 KXPIFDSTFSKAPTOSLISVANGIMDESIEKKGE 209   :     ::   ::   :   :   :   :

**RESULT 14**

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US-10-408-765A-166
; Sequence 166, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166
; LENGTH: 1225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-166

```

Query Match	25.4%;	Score 59.5;	DB 4;	Length 1225;
Best Local Similarity	28.6%;	Pred. NO. 1.7e+02;		
Matches 16;	Conservative	10;	Mismatches 19;	Indels 11; Gaps 2;

Qy	2 LKRLIRLLPVELFSEEEQRQNLOCC-----QGALDNAIEREDELSSGESS 47   : : : :   :         : : : :   : : : :   : : : :
Db	900 LQKEVTAIETKLEQKRSDRNLHLQAACKMODIKLPLSGKTWDD-ISOEEGSGSGEDS 954

RESULT 15

```

US-10-473-127-1129
; Sequence 1129, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1129
; LENGTH: 1225
; TYPE: ERT
; ORGANISM: Homo sapiens
US-10-473-127-1129

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Query Match 25.4%; Score 59.5; DB 5; Length 1225;

Best Local Similarity 28.6%; Pred. No. 1.7e+02;  
Matches 16; Conservative 10; Mismatches 19; Indels 11; Gaps

Qy 2 LKRLIRLLPVLFSFEEQRNLLOCC-----QGALDNVIEREDELSSGS 47  
          ::: : : | | | | : : : : : : : : : :  
Db 900 LQKEVTATIKLEQRSDRHNLQAQMOKIPLKSGTKMDD-ISOEGSSOGEDS 954

Search completed: June 16, 2006, 20:24:53  
Job time : 28.2894 secs

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Result No.	Score	Query		DB	ID	Description
		Match	%			
1	63	26.9	370	6	US-10-449-902-46118	Sequence 46118, A
2	63	26.9	661	6	US-10-449-902-54195	Sequence 54195, A
3	56	23.9	453	6	US-10-449-902-35701	Sequence 35701, A
4	56	23.9	783	6	US-10-449-902-55443	Sequence 55443, A
5	54	23.1	198	6	US-10-449-902-39618	Sequence 39618, A
6	53	22.6	440	6	US-10-449-902-43167	Sequence 43167, A
7	53	22.6	797	6	US-10-449-902-50327	Sequence 50327, A
8	53	22.6	940	6	US-10-449-902-54166	Sequence 54166, A
9	52	22.2	379	6	US-10-953-349-19483	Sequence 19483, A
10	52	22.2	392	6	US-10-953-349-19482	Sequence 19482, A
11	52	22.2	401	6	US-10-953-349-19481	Sequence 19481, A
12	52	22.2	719	7	US-11-293-697-3841	Sequence 3841, A
13	52	22.2	914	6	US-10-527-411-60	Sequence 60, Appl
14	51.5	22.0	249	6	US-10-449-902-38739	Sequence 38739, A
15	51	21.8	952	7	US-11-221-332-86	Sequence 86, Appl
16	50.5	21.6	856	6	US-10-449-902-4567	Sequence 4567, A
17	50.5	21.6	926	6	US-10-449-902-43257	Sequence 43257, A
18	50.5	21.6	991	6	US-10-449-902-46978	Sequence 46978, A
19	50	21.4	286	7	US-11-134-228A-27	Sequence 27, Appl
20	50	21.4	551	7	US-11-293-697-3946	Sequence 3946, A
21	50	21.4	667	7	US-11-311-555-16	Sequence 16, Appl
22	50	21.4	667	7	US-11-311-561-16	Sequence 16, Appl
23	50	21.4	700	6	US-10-449-902-50309	Sequence 50309, A
24	50	21.4	895	7	US-11-293-697-3081	Sequence 3081, A
25	50	21.4	971	6	US-10-449-902-53924	Sequence 53924, A





Query Match 22.6%; Score 53; DB 6; Length 440;  
Best Local Similarity 37.8%; Pred. No. 34;  
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELKRLRLPVELFSEEQRLNLLQCCGALDINAIER 37  
DB 315 ELRRKIRLUEEIHKEKAQSSSELGVQCQNLKEQFTSR 351

RESULT 7  
US-10-449-902-50327  
; Sequence 50327, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50327  
; LENGTH: 797  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-50327

Query Match 22.6%; Score 53; DB 6; Length 797;  
Best Local Similarity 37.8%; Pred. No. 66;  
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELKRLRLPVELFSEEQRLNLLQCCGALDINAIER 37  
DB 672 ELRRKIRLUEEIHKEKAQSSSELGVQCQNLKEQFTSR 708

RESULT 8  
US-10-449-902-54166  
; Sequence 54166, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54166  
; LENGTH: 940  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-54166

Query Match 22.6%; Score 53; DB 6; Length 940;  
Best Local Similarity 33.3%; Pred. No. 80;  
Matches 11; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 12 ELFSEEQRLNLLQCCGALDINAIEREDELSG 44  
DB 693 QLFIEEQEKRLTEETFEADLDSAMDHKYQKDG 725

RESULT 9  
US-10-953-349-19483  
; Sequence 19483, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19483  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-19483

Query Match 22.2%; Score 52; DB 6; Length 379;  
Best Local Similarity 36.4%; Pred. No. 38;  
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 BEQRQNLQCCGALDINAIERE 38  
DB 154 KENREKLYNCCDGLNSSFKN E 175

RESULT 10  
US-10-953-349-19482  
; Sequence 19482, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19482  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-19482

Query Match 22.2%; Score 52; DB 6; Length 392;  
Best Local Similarity 36.4%; Pred. No. 40;  
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 BEQRQNLQCCGALDINAIERE 38  
DB 167 KENREKLYNCCDGLNSSFKN E 188

RESULT 11  
US-10-953-349-19481  
; Sequence 19481, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19481  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-19481

Query Match 22.2%; Score 52; DB 6; Length 401;  
Best Local Similarity 36.4%; Pred. No. 41;  
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 EQRONLLOCCGALDINAIERE 38  
DB 176 KENREKLYNCCDPLNSFPKNE 197

RESULT 12  
US-11-293-697-3841  
; Sequence 3841, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3841  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3841

Query Match 22.2%; Score 52; DB 7; Length 719;  
Best Local Similarity 30.8%; Pred. No. 78;  
Matches 12; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 9 LPVLFSEEEQRQNLQCCGALDINAIEREDELSSGESS 47  
DB 585 LPQSVSKQAVGHEENAQCCKATSDNVIOSETCSQDSS 623

RESULT 13  
US-10-527-411-60  
; Sequence 60, Application US/10527411  
; Publication No. US20060110410A1  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford  
; APPLICANT: Foster, Keith Alan  
; APPLICANT: Chaddock, John  
; APPLICANT: Marks, Philip  
; APPLICANT: Sutton, J. Mark  
; APPLICANT: Stancombe, Patrick  
; APPLICANT: Wayne, Jonathan  
; TITLE OF INVENTION: Recombinant Toxin Fragments  
; FILE REFERENCE: 1581.0130005  
; CURRENT APPLICATION NUMBER: US/10/527,411  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: PCT/GB2003/003824  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 10/241,596  
; PRIOR FILING DATE: 2002-09-12  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 60  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Clostridium botulinum  
US-10-527-411-60

Query Match 22.2%; Score 52; DB 6; Length 914;  
Best Local Similarity 35.9%; Pred. No. 1e+02;  
Matches 14; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 9 LPVLFSEEEQRQNLQCCGALDINAIEREDELSSGESS 47  
DB 852 IPFQL-SKYVDNQRLSLSTC-GGLTDTTLQAETDQLEDEKS 888

RESULT 14  
US-10-449-902-38739  
; Sequence 38739, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38739  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-38739

Query Match 22.0%; Score 51.5; DB 6; Length 249;  
Best Local Similarity 31.0%; Pred. No. 28;  
Matches 13; Conservative 11; Mismatches 13; Indels 5; Gaps 1;

QY 1 ELKELIRLLPVLFSEEEQRQNLQCCGALDINAIEREDEL 42  
DB 157 DVQQLVRSLAVENDSLREEMRTLQRACA-----ALSKENDKL 193

RESULT 15  
US-11-221-332-86  
; Sequence 86, Application US/11221332  
; Publication No. US20060121498A1  
; GENERAL INFORMATION:  
; APPLICANT: Eirx Therapeutics  
; TITLE OF INVENTION: Enzymes invovled in apoptosis  
; FILE REFERENCE: 8912/2042  
; CURRENT APPLICATION NUMBER: US/11/221,332  
; CURRENT FILING DATE: 2005-09-07  
; PRIOR APPLICATION NUMBER: PCT/GB2004/00957  
; PRIOR FILING DATE: 2004-03-05  
; PRIOR APPLICATION NUMBER: GB0305267.7  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86  
; LENGTH: 952  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-221-332-86

Query Match 21.8%; Score 51; DB 7; Length 952;  
Best Local Similarity 32.8%; Pred. No. 1.4e+02;  
Matches 19; Conservative 7; Mismatches 18; Indels 14; Gaps 3;

QY 2 LKRLIRLLPVLFSEEEQRQNLQCCO-----GALDNAI-----EREDELSSGESS 47  
DB 582 LLRWCRY--VKISTETEETEGSLHCKDQNGINGNPGNGIHEGSPSEMETDEPDDESS 637

Search completed: June 16, 2006, 20:25:52  
Job time : 4.0252 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 81.5 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-2  
Perfect score: 630  
Sequence: 1 MNWIEPLLVOFCQDLGITG.....POLHOAVTTLRLQREVLAAS 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	123	5	ABB80770 A. salmon
2	180	28.6	262	7	ABO81423 Pseudomon
3	118	18.7	106	7	ABO81215 Pseudomon
4	84	13.3	167	7	ABO79119 Pseudomon
5	82.5	13.1	235	2	AAY59756 Human nor
6	82	13.0	176	7	ADM26981 Hyperther
7	80	12.7	253	2	AAR13507 P.denitri
8	79.5	12.6	96	5	ABP01518 Human ORF
9	77	12.2	652	8	ADN25464 Bacterial
10	75	11.9	314	9	ADZ75794 Mouse pho
11	75	11.9	318	8	ADR27701 Mouse PAC
12	74.5	11.8	420	6	ABU50529 Protein e
13	74.5	11.8	742	5	ABP65368 Bifidobac
14	74	11.7	354	8	ADP30112 Human sec
15	74	11.7	1224	6	ABU39626 Protein e
16	73	11.6	421	2	AAR5055 IL-2-DETA
17	73	11.6	450	6	ABU39628 Protein e
18	73	11.6	565	7	ADB64142 Human pro
19	73	11.6	852	5	ABP69443 Human pol
20	72.5	11.5	496	2	AAR04934 Immunotox
21	72.5	11.5	3084	2	AAW50891 Mouse lam
22	72.5	11.5	3084	4	AAE11215 Mouse lam
23	72	11.4	117	9	ADx40246 HIV Rev p

24	71.5	11.3	243	4	AAE03548 Human mit
25	71.5	11.3	243	5	AAE21799 Human pep
26	71.5	11.3	243	6	ABO00588 Novel hum
27	71.5	11.3	289	4	ABG11298 Novel hum
28	71.5	11.3	289	6	ABO00850 Polypepti
29	71.5	11.3	455	3	AAG59392 Arabidops
30	71.5	11.3	486	3	AAG59391 Arabidops
31	71.5	11.3	530	3	AAG59390 Arabidops
32	71.5	11.3	939	7	ADC87071 Human GPC
33	71	11.3	332	7	ABO72413 Pseudomon
34	71	11.3	361	6	ABU01324 S. pneumo
35	71	11.3	361	8	ADK48614 Streptoco
36	71	11.3	365	8	ADR95921 Novel S.
37	71	11.3	365	9	AEA59791 Streptoco
38	71	11.3	408	3	AAG57790 Arabidops
39	71	11.3	413	3	AAG57789 Arabidops
40	71	11.3	482	8	ADN26175 Bacterial
41	71	11.3	560	4	ABB64311 Drosophil
42	71	11.3	1162	6	ABU41801 Protein e
43	70.5	11.2	434	7	ABO78655 Pseudomon
44	70	11.1	402	8	ADS44505 Bacterial
45	70	11.1	618	7	ABO76713 Pseudomon

ALIGNMENTS

RESULT 1  
ABB80770  
ID ABB80770 standard; protein; 123 AA.  
XX  
AC ABB80770;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE A. salmonicida type III secretion protein acr2 sequence.

XX  
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
XX  
KW acrV; acrH; antibiotic; vaccine; fish.  
XX

OS Aeromonas salmonicida.

XX WO200240514-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001WO-CA001589.

XX 15-NOV-2000; 2000US-0248864P.

XX (FREY/) FREY J.

XX (STUB/) STUBER K.

XX (THOR/) THORNTON J C.

XX (KUZ/) KUZIK M A.

XX (BURI/) BURIAN J.

XX Frey J, Stuber K, Thornton JC, Kuzik MA, Burian J;

XX WPI: 2002-537338/57.

XX N-PSDB; ABN86172.

XX Novel protein from Aeromonas salmonicida and nucleic acid encoding the

XX protein, useful for reducing susceptibility of fish to infection by a

XX virulent strain of Aeromonas salmonicida.

XX Claim 13; Page 26; 39pp; English.

XX The invention relates to A. salmonicida type III secretion genes and

XX encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrH, or AcrI.

XX A. salmonicida type III secretion apparatus is useful for producing

XX selected products, especially Aext. AcrV in vaccine, epitope or epitopic

XX region of AcrV or any other protein of A. salmonicida type III secretion

XX apparatus is useful for reducing the susceptibility of fish to infection

XX



XX SQ Sequence 106 AA;  
Query Match 18.7%; Score 118; DB 7; Length 106;  
Best Local Similarity 32.3%; Pred. No. 1.5e-05;  
Matches 31; Conservative 16; Mismatches 27; Indels 22; Gaps 4;  
QY 49 WLAR-AVP--WHOSGEAIRRAMVLT-----AAQGPALPVRSGWLGE 87  
DB 12 WISRTAPCSWNAMANSRSGWPTWPTGTRPIAAPGRCALCHARAAG-SLPLRCAWSGE 70  
QY 88 EQLILFVSLDERAVTLPOLHOAVTTLRLQREVLA 123  
DB 71 SRLLLCITLBARQVGIPTLHQALRSARSEVILAA 106  
RESULT 4  
ABO79119  
ID ABO79119 standard; protein; 167 AA.  
XX  
AC ABO79119;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #11294.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
XX 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
DR N-PSDB; ABD12690.  
XX  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
PS Disclosure; SEQ ID NO 27865; 455pp; English.  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biotech technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 167 AA;  
Query Match 13.3%; Score 84; DB 7; Length 167;  
Best Local Similarity 32.4%; Pred. No. 0.28;

Matches 24; Conservative 10; Mismatches 24; Indels 16; Gaps 3;  
QY 30 ELEQSGTLQERHQGOLTLWLARAVPW-----OSGEAIRRAMVLTAAQGPALP--- 79  
DB 14 EIDTGDLSHTTTPGLDALWLTENVRLREEQAGPLEDSEAVRQAL-----AQGSLPRRI 68  
QY 80 -VRSGWLGEQIL 92  
DB 69 LTRAHWLGRREGIL 82  
RESULT 5  
AAY59756  
ID AAY59756 standard; protein; 235 AA.  
XX  
AC AAY59756;  
XX  
DT 18-JAN-2000 (first entry)  
XX  
DE Human normal ovarian tissue derived protein 33.  
XX  
KW Human; ovary; screening; ovarian cancer; treatment.  
XX  
OS Homo sapiens.  
XX  
PN DE19816395-A1.  
XX  
PD 07-OCT-1999.  
XX  
PF 03-APR-1998; 98DE-01016395.  
XX  
PR 03-APR-1998; 98DE-01016395.  
XX  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX  
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
XX  
DR WPI; 1999-552352/47.  
DR N-PSDB; AA241237.  
XX  
PT Nucleic acid sequences potentially useful in diagnosis or therapy of  
PT ovarian cancer.  
XX  
PS Claim 23; Page 229; 274pp; German.  
XX  
XX This invention describes novel nucleic acid sequences that are highly  
CC expressed in normal ovary tissue. Artificial chromosomes and cosmid  
CC clones containing the sequences can be used as gene transfer vehicles.  
CC The sequences can be used to produce DNA fragments containing full-length  
CC genes. Host cells transfected with the sequences can be used to produce  
CC polypeptides or polypeptide fragments, which can be used to screen phage  
CC displays for polypeptides that bind to them, or as tools for identifying  
CC agents active against ovarian cancer, or to prepare medicaments for  
CC treating ovarian cancer. The cDNA sequences can be used to obtain genomic  
CC genes, their promoters, enhancers, silencers, exon structures, intron  
CC structures and their splice variants. AAY59724-Y59837 represent protein  
CC fragments encoded by the cDNA sequences represented in AA241222-241324  
CC which are derived from normal human ovarian tissue  
XX  
SQ Sequence 235 AA;  
Query Match 13.1%; Score 82.5; DB 2; Length 235;  
Best Local Similarity 24.6%; Pred. No. 0.67;  
Matches 32; Conservative 16; Mismatches 67; Indels 15; Gaps 5;  
QY 5 EPLIVQFQDLCITGDNPHSLIQLELQSGT---LQLERHQGOLTLWLARAVPW----- 56  
DB 49 EPLVLKVSQAQHGCTNISGEPEGIQHWQEKGVAGVTEFGDGDGVVMAVSPMGVIOD 108  
QY 57 HQSGEAI---RRAMVLTAAQGPALPVRSGWLGEQILFVSLDERAVTLP---QLHQAV 110  
DB 109 HNAGEVTVDHREVLDVAALQQLSAVLVSPLKNASAIQVFI-CHSRAIDLHACCKHHQLV 167

Qy 111 TTLRLQREV 120  
 Db 168 PLAHFQSEI 177

## RESULT 6

ADM26981  
 ID ADM26981 standard; protein; 176 AA.

AC ADM26981;

XX 20-MAY-2004 (first entry)

DE Hyperthermophile Methanopyrus kandleri protein #1587.

XX hyperthermophile; protein stability enhancement;

KW protein activity enhancement.

XX Methanopyrus kandleri.

OS WO2003076575-A2.

PN 18-SEP-2003.

XX 04-MAR-2003; 2003WO-US006664.

PF 04-MAR-2002; 2002US-0361742P.

PR 14-MAY-2002; 2002US-0380423P.

PR 16-SEP-2002; 2002US-0410974P.

XX (FIDE-) FIDELITY SYSTEMS INC.

PA (MALY/) MALYKH A.

XX Slesarev AI, Pavlov A, Pavlova N, Kozayavkin S;

XX WPI; 2003-748383/70.

DR N-PSDB; ADM27081.

XX New isolated nucleic acids encoding any of about 1700 Methanopyrus  
 PT kandleri proteins, and the encoded proteins, useful as a medicaments or  
 PT as diagnostic agents.

XX Claim 31; SEQ ID NO 1587; 1023pp; English.

XX The invention comprises the amino acid sequence of proteins from the  
 CC hyperthermophile Methanopyrus kandleri, the invention also comprises the  
 CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
 CC proteins of the invention are useful for enhancing the stability and/or  
 CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
 CC a variety of diagnostic and analytical methods. The present amino acid  
 CC sequence represents a Methanopyrus kandleri protein of the invention.

XX Sequence 176 AA;

Query Match 13.0%; Score 82; DB 7; Length 176;

Best Local Similarity 29.7%; Pred. No. 0.52;

Matches 30; Conservative 21; Mismatches 38; Indels 12; Gaps 5;

Qy 10 QFCODLGTIGDNPHSLIQ--LELEQSGTLQLERHQGTLTLWLRAR-----VPHHQSGEA 62

Db 53 EIABELGITVSGVRNHLHEQARKMKVNDNFQIARIIGKLEMSLGPALVIAIVPVDKSEDV 112

Qy 63 IRRAMTLTAAAGQ-PALPVRSGWLGEQQLILF-VSLDERAV 101

Db 113 INR---LIQEGEGVTMTGRGYTGEEQSVLFIITEDEKV 150

## RESULT 7

AAR13507  
 ID AAR13507 standard; protein; 253 AA.

XX AAR13507;

XX AAR13507;

DT 25-MAR-2003 (revised)  
 DT 25-OCT-1991 (first entry)  
 XX P.denitrificans COB M.  
 DE cob gene; corrinoid; descobaltocorrinoid; cor gene.  
 KW Pseudomonas denitrificans.  
 XX WO9111518-A.  
 XX 08-AUG-1991.  
 XX 31-JAN-1990; 90FR-00001137.  
 XX 31-JAN-1990; 90FR-00001137.  
 XX (RHON ) RHONE-POULENC BIOCH.  
 XX Blanche F, Meron B, Crouzet J, Debussche L, Levyschil S;  
 PI Thibaut D;  
 XX WPI; 1991-252650/34.  
 DR N-PSDB; AAQ13285.  
 XX New polypeptide(s) involved in cobalamin and cobamide biosynthesis - and  
 PT DNA encoding them, for amplification of cobalamin, esp. coenzyme B12  
 PT prodn.  
 XX Claim 17; Fig 16; 299pp; French.

XX This sequence corresponds to one of 24 polypeptides obtained from

CC P.denitrificans and implicated in the biosynthesis of cobalamines and/or  
 CC cobamides, specifically in catalysing the transfer of a methyl group to  
 CC positions C1, C5, C11, C15 or C17 in the conversion of precorrin-3 to  
 CC cobyrrinic acid a,c-diamide. It is encoded by part of the 8.7kb EcoRI-  
 CC EcoRI fragment of plasmid pXL367. The plasmid was isolated from a  
 CC P.denitrificans genomic DNA bank constructed in vector pXL59. See  
 CC AAQ13284-Q13288. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 253 AA;

Query Match 12.7%; Score 80; DB 2; Length 253;

Best Local Similarity 23.3%; Pred. No. 1.5;

Matches 35; Conservative 24; Mismatches 49; Indels 42; Gaps 7;

Qy 4 IEPILVQFCQDLGTIGDNPHSLIQLELE-----QSGTLQLER-HQGTLTLWLRARVPHQ 58

Db 37 VSPPELLRYCPGARIVDTAPMSLDEIEAEYVKAEGLDVARLHSGDLSVMSAVA----- 91

Qy 59 SGEAIRR-----AMTLTAAAGQPALPVRSGWLGE-----QLILFVSLDERAVTLPQ 105

Db 92 --EQIRRLKKGIAIYTTTPGV--PSFAAASALGRELTIAPAQSLVILTRVSGRASPMNP 147

Qy 106 -----LHOAVTTLRLQREV 120

Db 148 SETLSARGATGSLTAIHAIHALQOVVEEL 177

## RESULT 8

ABP01518

ID ABP01518 standard; protein; 96 AA.

XX AC ABP01518;

XX 24-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:3018.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;





Db 81 VYGMGFAEDPAFAELCEQLGVTFICPSPHAMRQLG-DKIGAKLLAEQVG-----VPVA 133

QY 55 PMHQ5-----GFAIRRAMT-----LTAAGGALPVR 81

Db 134 PWSRGPVTTLDFAIAARTIGYPLMLKAAAGGGGRGIR 171

RESULT 10

ADZ75794

ID ADZ75794 standard; protein; 314 AA.

XX

AC ADZ75794;

XX

DT 14-JUL-2005 (first entry)

XX

DE Mouse phosphatase of activated cells 1 (PAC1) protein - SEQ ID 2.

XX

KW transgenic animal; animal disease model; cancer; cytostatic;

KW inflammation; antiinflammatory; immune disorder; neurological disease;

KW neuroprotective; PAC1; phosphatase of activated cells 1.

XX

OS Mus sp.

XX

PN WO2005039281-A1.

XX

PD 06-MAY-2005.

XX

PF 22-OCT-2004; 2004WO-AU001457.

XX

PR 23-OCT-2003; 2003AU-00905822.

XX

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX

PI Gerondakis S, Grumont RJ;

XX

DR WPI; 2005-322895/33.

DR N-PSDB; ADZ75793.

XX

PT New genetically modified organism (i.e. mouse) comprising modifications to a gene encoding phosphatase of activated cells 1 (PAC1), useful as an animal model for diseases, for characterizing gene functions or in drug discovery.

PS

Claim 10; SEQ ID NO 2; 78pp; English.

XX

CC The invention comprises a genetically modified non-human organism (e.g. mouse) having cells which contain a modification to the phosphatase of activated cells 1 (PAC1) gene or to a regulatory region required for expression of the PAC1 gene, resulting in the cells producing altered levels of PAC1. The genetically modified organism of the invention is useful as an animal model for diseases or for identifying agents that modulate PAC1 - these may be used in the treatment of cancer, inflammatory diseases/disorders, immunological disorders, and neurological disorders. The present amino acid sequence represents the mouse PAC1 protein.

XX

Sequence 314 AA;

Query Match 11.9%; Score 75; DB 9; Length 314;

Best Local Similarity 32.2%; Pred. NO. 7.6;

Matches 37; Conservative 10; Mismatches 42; Indels 26; Gaps 5;

QY 28 QLEEQSTQLQERHOGQTLWL-----ARAVPMHQSGEAI--RRAMTLT 70

Db 8 ELECAAGALLREPREARETILLDCRPFLACRSHVRAARVPWN----ALLRRARGTP 63

QY 71 AAAGGALPVR5--GWLGEQQLILFVSLDERAVT---LPQLHQAVTTLRLQRE 120

Db 64 AAALACLIPDRALRGLRGELARAVLDESSASVAELPPDGPAPHLLLAALQHEM 118

RESULT 11

ADR27701

ID

XX ADR27701 standard; protein; 318 AA.

AC ADR27701;

XX

DT 18-NOV-2004 (first entry)

XX

DE Mouse PAC-1 protein SEQ ID NO:4.

XX

KW inflammation; immune response; phosphatase of activated cells-1; PAC-1;

KW inflammatory disorder; antiinflammatory; antiarthritic; antirheumatic;

KW antiasthmatic; analgesic; antiallergic; antiatherosclerotic;

KW immunosuppressive; vasotropic; neuroprotective; respiratory; antiulcer;

KW gastrointestinal; dermatological; antipsoriatic; cytostatic; anti-HIV;

KW PAC-1 modulator; immunosuppression; rheumatoid arthritis; asthma; pain;

KW joint swelling; allergy; atherogenesis; anaphylaxis; malignancy;

KW chronic inflammation; acute inflammation; allergic reaction; shock;

KW atherosclerosis; multiple sclerosis; allograft rejection;

KW fibrotic disease; inflammatory glomerulopathy;

KW respiratory allergic disease; allergic rhinitis;

KW hypersensitivity lung disease; interstitial lung disease;

KW hypersensitivity response; drug allergy; insect sting allergy;

KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW spondyloarthropathy; scleroderma; psoriasis; inflammatory dermatoses;

KW dermatitis; eczema; atopic dermatitis; allergic contact dermatitis;

KW urticaria; vasculitis; autoimmune disease; cancer; mouse; enzyme.

XX

OS Mus musculus.

XX

PN WO2004072298-A1.

XX

PD 26-AUG-2004.

XX

PF 12-FEB-2004; 2004WO-AU000168.

XX

PR 12-FEB-2003; 2003AU-00900639.

XX

PA (GTWO-) G2 THERAPIES LTD.

XX

PI Jeffrey K, Mackay C, Rolph M;

XX

DR WPI; 2004-625885/60.

DR N-PSDB; ADR27700.

XX

PT Screening for a compound that reduces inflammation/promotes immune response, useful for treating e.g. allergy, comprises determining phosphatase of activated cells-1 (PAC-1) activity/expression levels with/without a compound.

PT

Claim 28; SEQ ID NO 4; 96pp; English.

XX

CC The present invention describes a method of screening for a compound that suppresses or reduces inflammation or promotes an immune response. The method comprises determining the activity or expression levels of phosphatase of activated cells-1 (PAC-1) in the presence and absence of a candidate compound, where altered PAC-1 activity or expression in the presence of the compound indicates that the compound suppresses or reduces inflammation or promotes an immune response. Also described: (1) a method of detecting a PAC-1-associated transcript in a biological sample; (2) a method of diagnosing an inflammatory disorder in a human or animal subject being tested; and (3) a method of monitoring the efficacy of a therapeutic treatment of an inflammatory disorder. The compound has an antiinflammatory, antiarthritic, antirheumatic, antiasthmatic, analgesic, antiallergic, antiatherosclerotic, immunosuppressive, vasotropic, neuroprotective, respiratory, antiulcer, gastrointestinal, dermatological, antipsoriatic, cytostatic and anti-HIV activities, and can be used as a PAC-1 modulator. The method that administers a compound that modulates or alters PAC-1 activity, or alters the level of expression of functional PAC-1, in an amount to inhibit or reduce inflammation or to treat immunosuppression, is useful for treating or preventing an inflammatory disease or immunosuppression in the subject, where the method reduces or inhibits PAC-1 activity or functional PAC-1 expression in an amount to inhibit or reduce inflammation, or the compound increases or enhances PAC-1 activity or expression in an amount

CC to treat immunosuppression. The method is useful for screening compounds  
CC that treats and inhibits the signs and symptoms of inflammatory disorders  
CC such as rheumatoid arthritis and asthma, and particularly reduces the  
CC pain, inflammation, joint swelling, and lesions associated with the  
CC diseases. Other disease which can be treated are allergy, atherogenesis,  
CC anaphylaxis, malignancy, chronic and acute inflammation, histamine and  
CC immunoglobulin E-mediated allergic reactions, shock, atherosclerosis,  
CC multiple sclerosis, allograft rejection, fibrotic disease, inflammatory  
CC glomerulopathies, respiratory allergic diseases such as allergic  
CC rhinitis, hypersensitivity lung diseases, interstitial lung diseases,  
CC anaphylaxis or hypersensitivity responses, drug allergies, insect sting  
CC allergies, inflammatory bowel diseases such as Crohn's disease and  
CC ulcerative colitis, spondyloarthropathies, scleroderma, psoriasis and  
CC inflammatory dermatoses such as dermatitis, eczema, atopic dermatitis,  
CC allergic contact dermatitis, urticaria, vasculitis, other autoimmune  
CC diseases, cancers with leukocyte infiltration of the skin or organs and  
CC other diseases or conditions which can be treated with promoters of PAC-1  
CC function such as immunodeficiency syndromes such as AIDS. The present  
CC sequence represents mouse PAC-1, which is used in the exemplification of  
CC the present invention.

XX Sequence 318 AA;

Query Match 11.9%; Score 75; DB 8; Length 318;

Best Local Similarity 32.2%; Pred. No. 7.7;

Matches 37; Conservative 10; Mismatches 42; Indels 26; Gaps 5;

QY 28 QLEQSGTLQERHOGQLTML-----ARAVPWQSGEAI--RRAMTLT 70

DB 12 ELECAALGALLPREAETLLDCRPFLACFESHVRAARPVWN----ALLRRARGTF 67

QY 71 AAAQGALPVR--GWLGEQLILFVSLDERAVT---LPOLHQAVTTLRLQREV 120

DB 68 AAALACLLPDRLARLGRGELARAVVLDESSASVAELPPDGPAAHLLAALQHEM 122

RESULT 12

ABU50529

ID ABU50529 standard; protein; 420 AA.

AC ABU50529;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #36056.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Yersinia pestis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002NO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA54399.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 78453; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 420 AA;

Query Match 11.8%; Score 74.5; DB 6; Length 420;

Best Local Similarity 24.3%; Pred. No. 13;

Matches 33; Conservative 16; Mismatches 44; Indels 43; Gaps 4;

QY 24 HSLIQLELEQSGTL-----QLERHQQLILFWL-----RAVPWHQ 58

DB 33 NSLLQQLVQGGVWLSTCNRTLYLSVQQLNLHEQLTAWLNCYHKLSPDDVRQSLYWHH 92

QY 59 SCEARRAMTLTAAAGPALPVRSGWLGBEQLILFV-----SLDERAVTLPOLH 107

DB 93 GNDVTRHLMRVASG-----LDSQVLGEPQLIGQVKAFASQSGSLSELERLFOXS 145

QY 108 QAVTTLRLQREVLAS 123

DB 146 FSVAKRVRTETEIGAS 161

RESULT 13

ABP65368

ID ABP65368 standard; protein; 742 AA.

XX AC ABP65368;

XX DT 19-NOV-2002 (first entry)

XX DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:112.

XX KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;

XX KW antidiarrheic; antibacterial; inhibitor of Salmonella; detection;

XX KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;

XX KW rotavirus; food composition; pharmaceutical composition.

XX OS Bifidobacterium longum.

XX PN EP1227152-A1.

XX XX





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Nature 413, 523-527, 2001  
A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AB0246  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-420 <KUR>  
A;Cross-references: UNIPROT:Q8ZEX9; UNIPARC:UPI000012C442; GB:AL590842; PIDN:CAC90830.1  
C;Genetics:  
A;Gene: hema  
C;Superfamily: glutamyl-tRNA reductase  
C;Keywords: oxidoreductase

Query Match	11.8%;	Score	74.5;	DB	2;	Length	420;	
Best Local Similarity	24.3%;	Pred.	No. 6.6;					
Matches	33;	Conservative	16;	Mismatches	44;	Indels	43; Gaps	4;
Qy	24	HSLIQLEQGSGTL-----QLRHOGQLTMLA-----RAVPHWQ	58					
Dd	33	NLSLQQPVLGGVVLTNCNTELYLSVEQENLHEQTAWLCNYHKULSPDDVRSLYWHH	92					
Qy	59	SGEAIRAMTLITAAAGPALPVRSGLWGSEQLIFV-----SLDERAVTLPQLH	107					
Dd	93	GNDAVRHLMRVASG-----LDSVLGEPQILGVKKAFAESQRQSLSSELERLFQKS	145					
Qy	108	QAVTTLTRLOREVLAS	123					
Dd	146	FSVAKRVRVTETETIGAS	161					

RESULT 11

B57126

dual specificity phosphatase (EC 3.1.3.-) 2 - mouse

N/Alternate names: mitogen-induced nuclear protein-tyrosine-phosphatase PAC-1

C/Species: Mus musculus (house mouse)

C/Date: 03-Nov-1995 #sequence\_revision 03-Nov-1995 #text\_change 05-Oct-2004

C/Accession: B57126

R/Rohan, P.J.; Davis, P.; Moskaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Kell

Science 259, 1763-1766, 1993

A/Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.

A/Reference number: A57126; MUID:93206122; PMID:7681221

A/Accession: B57126

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-314 <ROH>

A/Crossa-references: UNIPARC:UPI0000150A61; GB:L11330

C/Supefamily: dual specificity protein phosphatase (MAP kinase phosphatase); VHL-type d

F/Keywds: nucleus; phosphoprotein; phosphoric monoester hydrolase

F/180-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

F/257/Active site: Cys (phosphocysteine intermediate) #status Predicted

F/263/Binding site: substrate phosphate (Arg) #status Predicted

```

Query Match      11.7%; Score 74; DB 2; Length 314;
Best Local Similarity 32.2%; Pred.No. 5.3;
Matches 37; Conservative 10; Mismatches 42; Indels 26; Gaps 5;

Qy   28 QLELGSGTQLERHQQLTLWL-----ARAVPHOSGEAI--RRAMTLT 70
       :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db    8 ELECAALGALLREPREAERTLLDCRPFLAFCSRHVRAARPVWN----ALLRRRAPGTP 63

Qy   71 AARGGPALPVRS--GWLGEESQLILFVSLDERAVT---LPQLHOAVNTLTBLQREV 120
       :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db   64 AAALACILLPRALARLGRGELARAVVLDDSSASVTBEPDGGPAHLLLAAALOHEM 118

```

RESULT 12  
AG2227  
DNA repair and genetic recombination protein [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AG2227  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchishima, I.

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, T.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AG2227  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-376 <KUR>  
 A:Cross-references: UNIPROT:Q8YR89; UNIPARC:UPI0000133552; GB:BA000019; PIDN:BA075073.1  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: recF  
 C:Superfamily: recF protein

Query Match	11.7%;	Score 73.5;	DB 2;	Length 376;			
Best Local Similarity	20.3%;	Pred. No. 7.4;					
Matches	29;	Conservative 21;	Mismatches 64;	Indels 29;	Gaps 3;		
QY	2	NMIEPLLVQF-----	-----	---CODLGITIGDNP	SHLSLIQLE	EQSGTL	37
Db	134	NMLDITLLIQLEPVYAHILQYQNVQLRQRYNAYLKKUQDSALT	TTQDSALATWDAOLVTTGK	193			
QY	38	QLERHOGQITLMLARAVPHHGGSEAIRRMATLTTAAAGG	PALPVRSGWLGEEQLILFVSLD	97			
Db	194	VIRRRDALARLAPLATANAHTSISGSTEVLQINYT---	ENVQLVKNPQPEVQQAFLSOLQ	250			
QY	98	ERAVTLPQLHQAVTTTLRLQREV	120				
Db	251	QRAV--PEIYRGTTLVGPHRDEV	271				

RESULT 13  
G87398  
ActB/AcrD/AcrF family protein [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: G87398  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Emdolava, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: G87398  
A:Status: preliminary  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1047 <STO>  
A:Cross-references: UNIPROT:Q9A821; UNIPARC:UPI00000C72B9; GB:AE005673; NID:g13422529; I  
C:Genetics:  
A:Gene: CC1204

Query Match	11.5%; Score 72.5; DB 2; Length 1047;
Best Local Similarity	20.7%; Pred.No.30;
Matches	25; Conservative 27; Mismatches 34; Indels 35; Gaps 4;
QY	2 NWIEPLLVFQCGLGIT-----IGDNPHSLIQLEQSGTQLERHQGOLTLWLARAVP 55    ::  : : :   :       ::     : 685 NMLKPIIAEQNPGLARRPLRYEPTAPLLVQIDLDKAATLGV----- 728
QY	56 WHQSGEAIRAMTLTAAAGCPALPVRSRGMVGEEQTILFVSJDERAVTLPQLHQAQVTLTR 115 :::   : : : :   :       :   :     : 729 ----SAGSVGRALETWFGSRPRATYIKSG--QEYDVILOTNLQOR-----RSIEDLNLR 775
QY	116 L 116
Db	 776 L 776

RESULT 14  
MMMSA  
laminin alpha-1 chain precursor - mouse  
N;Alternate names: laminin chain A1  
C:Species: Mus musculus (house mouse)

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004  
C;Accession: A3171; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670  
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.  
J. Biol. Chem. 263, 16536-16544, 1988  
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and he  
A;Reference number: A3171; PMID:89034134; PMID:3182802  
A;Accession: A3171  
A;Molecule type: mRNA  
A;Residues: 1-3084 <SAS>  
A;Cross-references: UNIPARC:UPI0000278CA; EMBL:J04064; NID:G309419; PID  
A;Accession: A30449  
A;Molecule type: protein  
A;Residues: 183-195;570-571 'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPR  
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SAS>  
A;Cross-references: UNIPARC:UPI0000173C92; UNIPARC:UPI0000173C93; UNIPARC:UPI0000173C94;  
C99; UNIPARC:UPI0000173C9A; UNIPARC:UPI0000173C9B; UNIPARC:UPI0000173C9C; UNIPARC:UPI000  
10000173CA2  
R;Hartl, L.; Oberbaumer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A;Title: The N terminus of laminin A chain is homologous to the B chains.  
A;Reference number: S00624; PMID:88225080; PMID:3267223  
A;Accession: S00624  
A;Molecule type: mRNA  
A;Residues: 1-208,'T',210-334 <HAR>  
A;Cross-references: UNIPARC:UPI000016CE8F; EMBL:X07737; NID:952857; PIDN:CAA30561.1; PID  
A;Accession: A30450  
A;Molecule type: protein  
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;  
3-1389;1449-1459 <HA2>  
A;Cross-references: UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CA5;  
CAA; UNIPARC:UPI0000173CAB; UNIPARC:UPI0000173CAC  
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile  
R;Mann, K.; Deutzmann, R.; Timpl, R.  
Eur. J. Biochem. 178, 71-80, 1988  
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th  
A;Reference number: S08895; PMID:89078415; PMID:2462498  
A;Accession: S08895  
A;Molecule type: protein  
A;Residues: 153-169 <MAN>  
A;Cross-references: UNIPARC:UPI0000173CAD  
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A;Reference number: S02678; PMID:88326259; PMID:2458101  
A;Accession: S02678  
A;Molecule type: protein  
A;Residues: 630-642,'D',644;2690-2704 <FUJ>  
A;Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE  
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.  
Eur. J. Biochem. 177, 33-45, 1988  
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te  
A;Reference number: S01790; PMID:89030693; PMID:3181157  
A;Accession: S01790  
A;Molecule type: mRNA  
A;Residues: 2338-3084 <DEU>  
A;Cross-references: UNIPARC:UPI000016CE8E; EMBL:X13459; NID:955499; PIDN:CAA31807.1; PID  
A;Accession: A30451  
A;Molecule type: protein  
A;Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120  
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;  
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>  
A;Cross-references: UNIPARC:UPI0000173CB6; UNIPARC:UPI0000173CB7; UNIPARC:UPI0000173CB8;  
CBD; UNIPARC:UPI0000173CBE; UNIPARC:UPI0000173CBF; UNIPARC:UPI0000173CC0; UNIPARC:UPI000  
10000173CC6; UNIPARC:UPI0000173CC7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CC9; UNIPAR  
A;Note: 2256-Val was also found  
R;Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
Lab. Invest. 60, 772-782, 1989  
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A;Reference number: A34961; PMID:89280632; PMID:2733383  
A;Accession: S14670  
A;Molecule type: protein  
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2  
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083

A;Cross-references: UNIPARC:UPI0000173C95; UNIPARC:UPI0000173CAE; UNIPARC:UPI0000173CB  
C7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CCA; UNIPARC:UPI0000173CCB; UNIPARC:UPI00  
1000173CD1; UNIPARC:UPI0000173CD2; UNIPARC:UPI0000173CD3; UNIPARC:UPI0000173CD4; UNIPAR  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:  
A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>  
F;25-277/Domain: VI <DOM6>  
F;277-331/Domain: laminin-type EGF-like homology <LE01>  
F;278-519/Domain: V <DOM5>  
F;334-401/Domain: laminin-type EGF-like homology <LE02>  
F;404-458/Domain: laminin-type EGF-like homology <LE03>  
F;461-507/Domain: laminin-type EGF-like homology <LE04>  
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;520-715/Domain: IVb <DO4B>  
F;716-1166/Domain: IIIB <DO3B>  
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F;749-795/Domain: laminin-type EGF-like homology <LE07>  
F;798-853/Domain: laminin-type EGF-like homology <LE08>  
F;830-834/Region: cell adhesion #status predicted  
F;856-906/Domain: laminin-type EGF-like homology <LE09>  
F;909-955/Domain: laminin-type EGF-like homology <LE10>  
F;958-1002/Domain: laminin-type EGF-like homology <LE11>  
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>  
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>  
F;1097-1116/Domain: laminin-type EGF-like homology <LE14>  
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>  
F;1147-1149/Region: cell attachment (R-G-D) motif  
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>  
F;1167-1368/Domain: IIVa <DO4A>  
F;1369-1561/Domain: IIVa <DO3A>  
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>  
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>  
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>  
F;1562-2133/Domain: II/I <DOM2>  
F;1562-2133/Region: heptad repeats  
F;2134-3084/Domain: G <DOM2>  
F;2150-2308/Domain: laminin G repeat homology <LG1>  
F;2317-2492/Domain: laminin G repeat homology <LG2>  
F;2518-2683/Domain: laminin G repeat homology <LG3>  
F;2748-2897/Domain: laminin G repeat homology <LG4>  
F;2925-3082/Domain: laminin G repeat homology <LG5>  
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F;45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,171  
e (Asn) (covalent) #status predicted  
F;304-312/Disulfide bonds: #status experimental  
F;770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status exper  
F;845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent  
  
Query Match 11.5%; Score 72.5; DB 1; Length 3084;  
Best Local Similarity 32.7%; Pred. No. 1e+02;  
Matches 32; Conservative 16; Mismatches 39; Indels 11; Gaps 6;  
  
QY 33 QSGTLQLEHOGQLTLWARAVPHWQSGEAI-----BRAMTLTAAAGCA--LPVRSGLG 86  
Db 1836 QDTLTQLEHRRDELLW-ARKTRSHVDLVQMQRARDLVHRAEQHASELOSAGALD 1894  
  
QY 87 EE-QILFVSLDERAVTLFQLHQAVTTLTLRLQREVLSA 123  
Db 1895 RDLNVRNVSIN--ATSAAHVHSNIQTLTTE-EAEMLAA 1929  
  
RESULT 15  
G83602  
hypoetical protein PA0345 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revison 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: G83602  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.: Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: G83602  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-461 <STO>  
A;Cross-references: UNIPROT:Q9I6E8; UNIPARC:UPI000000C5019; GB:AE004472; GB:AE004091; NID  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA0345  
C;Superfamily: Neisseria meningitidis hypothetical protein NMB1645

Query Match 11.4%; Score 72; DB 2; Length 461;  
Best Local Similarity 33.9%; Pred. No. 13;  
Matches 21; Conservative 8; Mismatches 17; Indels 16; Gaps 3;

QY 42 HQGQLTLWLARAVPWH-----OSGEAIRRAMTLTAAAGPALP-----VRSGLGEEQL 90  
Db 6 HPGLDALWLTEAVRLREEQAGPLEDSEAVRQAL-----AQQGLPRILTRAHWLGRREG 60

QY 91 IL 92  
Db 61 LL 62

Search completed: June 16, 2006, 19:25:13  
Job time : 13.5 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 96.6 Seconds  
(without alignments)  
1177.815 Million cell updates/sec

Title: US-10-813-908A-2  
Perfect score: 630  
Sequence: 1 MNWIEPLLVOFCQDLGITIG.....PQLHQAVTTTLRLQREVLAS 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	630	100.0	123	2	Q8GA94_AERSA	Q8GA94 aeromonas s
2	591	93.8	123	2	Q699R6_AERHY	Q699R6 aeromonas h
3	556	88.3	123	2	Q5XLI0_AERHY	Q5XLI0 aeromonas h
4	524	83.2	123	2	Q6TLM8_AERHY	Q6TLM8 aeromonas h
5	419	66.5	123	2	Q7N0W5_PHOLL	Q7N0W5 photorhabdu
6	418	66.3	123	2	Q84GZ1_PHOLL	Q84GZ1 photorhabdu
7	396	62.9	123	1	SYCN_YEREN	Q2095 yersinia en
8	392	62.2	123	1	SYCN_YERPE	P61380 yersinia pe
9	392	62.2	123	1	SYCN_YERPS	P61381 yersinia ps
10	279	44.3	123	2	Q9I329_PSEAE	Q9I329 pseudomonas
11	277	44.0	123	2	Q30533_PSEAE	Q30533 pseudomonas
12	241.5	38.3	124	2	Q6QVR6_VIBHA	Q6QVR6 vibrio harv
13	239.5	38.0	123	2	Q87P53_VIBPA	Q87P53 vibrio para
14	239.5	38.0	124	2	Q66PUI_PASPI	Q66PUI pasteurella
15	97	15.4	125	2	Q2SH41_9GAMM	Q2SH41 habella che
16	92.5	14.7	124	2	Q72WM4_DESVH	Q72WM4 desulfovibr
17	89.5	14.2	252	2	Q2JZV2_RHIET	Q2JZV2 rhizobium e
18	89	14.1	252	2	Q92LV3_RHIME	Q92LV3 rhizobium m
19	88.5	14.0	989	2	Q3W8C4_9ACTO	Q3W8C4 frankia sp.
20	87	13.8	150	2	Q4BLG3_BURVI	Q4BLG3 burkholderi
21	87	13.8	518	2	Q579G4_BRUAB	Q579G4 brucella ab
22	87	13.8	518	2	Q8FV99_BRUSU	Q8FV99 brucella su
23	87	13.8	518	2	Q2YLB4_BRUA2	Q2YLB4 brucella ab
24	87	13.8	622	2	Q2JU70_SCYAN	Q2JU70 cyanobacter
25	85.5	13.6	289	2	Q748U7_GEOSL	Q748U7 geobacter s
26	83	13.2	518	2	Q8YDZ7_BRUME	Q8YDZ7 brucella me
27	83	13.2	606	2	Q8RIU9_MOUSE	Q8RIU9 mus musculu
28	83	13.2	654	2	Q8RI33_MOUSE	Q8RI33 mus musculu
29	83	13.2	675	2	Q8C8I6_MOUSE	Q8C8I6 mus musculu
30	83	13.2	940	2	Q3U6C0_MOUSE	Q3U6C0 mus musculu
31	83	13.2	960	2	Q8BSZ1_MOUSE	Q8BSZ1 mus musculu

32	83	13.2	960	2	Q8CIE4_MOUSE	Q8CIE4 mus musculu
33	82	13.0	176	2	Q8TVI4_METKA	Q8TVI4 methanopyru
34	81.5	12.9	98	2	Q5TY81_ANOGA	Q5TY81 anopheles g
35	81	12.9	125	2	Q2SC38_9GAMM	Q2SC38 habella che
36	80	12.7	253	1	COBM_PSEDE	P21922 pseudomonas
37	80	12.7	960	2	Q3TIV7_MOUSE	Q3TIV7 mus musculu
38	79.5	12.6	450	2	Q7SGI1_NEUCR	Q7SGI1 neurospora
39	79.5	12.6	459	2	Q7V8L4_PROMM	Q7V8L4 prochloroco
40	79.5	12.6	984	2	Q6IEE7_HUMAN	Q6IEE7 homo sapien
41	79	12.5	289	2	Q82MI5_STRAW	Q82MI5 streptomyce
42	79	12.5	398	2	Q4BS00_BURVI	Q4BS00 burkholderi
43	79	12.5	1224	2	Q2XDN4_PSEPU	Q2XDN4 pseudomonas
44	78.5	12.5	268	2	Q52433_PSESP	Q52433 pseudomonas
45	78	12.4	321	2	Q339I3_ORYSA	Q339I3 oryza sativ

ALIGNMENTS

RESULT 1

Q8GA94\_AERSA  
ID Q8GA94\_AERSA PRELIMINARY; PRT; 123 AA.  
AC Q8GA94  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE Acr2 protein.  
GN Name=acr2;  
OS Aeromonas salmonicida subsp. salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RX MEDLINE=22826111; PubMed=12374830;  
RX DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida.";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type =III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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CC -----  
DR EMBL; AJ458292; CAD30215.1; -; Genomic\_DNA.  
DR EMBL; AF616218; CAB83102.1; -; Genomic\_DNA.  
DR SMR; Q8GA94; 2-122.  
DR InterPro; IPR012673; TTSS\_SynN.  
DR TIGRFAMs; TIGR02503; type III; 1.  
SQ SEQUENCE 123 AA; 13738 MW; D80B2EC9F9AAD806 CRC64;

Query Match 100.0%; Score 630; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 3.5e-57;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNWIEPLLVOFCQDLGITIGDNDPHSLIOLELESGTQLERHOGQLTLWLARAVPHQSG	60
Db	1	MNWIEPLLVOFCQDLGITIGDNDPHSLIOLELESGTQLERHOGQLTLWLARAVPHQSG	60
Qy	61	EAIRRAMTLTAAAGGALPVRSGLWGEQILFVSLDERAVTLPQLHQAVTTTLRLQREV	120
Db	61	EAIRRAMTLTAAAGGALPVRSGLWGEQILFVSLDERAVTLPQLHQAVTTTLRLQREV	120
Qy	121	LAS 123	

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Db 121 LAS 123

RESULT 2
ID Q699R6_AERHY PRELIMINARY; PRT; 123 AA.
AC Q699R6;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acr2.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919 (2004).
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CC -----
DR EMBL; AY528667; AAS91813.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 13741 MW; 01301E03BA6B7D8C CRC64;

Query Match 93.8%; Score 591; DB 2; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.9e-53;
Matches 113; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
Db 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
QY 121 LA 122
Db 121 VA 122

RESULT 3
ID Q5XL10_AERHY PRELIMINARY; PRT; 123 AA.
AC Q5XL10;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acr2.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Brova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457 (2005).
CC -----
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CC -----
DR EMBL; AY763611; AAV30227.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 13995 MW; 5DB076AD0BD3FF42 CRC64;

Query Match 88.3%; Score 556; DB 2; Length 123;
Best Local Similarity 87.8%; Pred. No. 1.7e-49;
Matches 108; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
Db 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
QY 121 LAS 123
Db 121 LVS 123

RESULT 4
Q6TLM8_AERHY PRELIMINARY; PRT; 123 AA.
AC Q6TLM8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acr2.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256 (2004).
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CC -----
DR EMBL; AY394563; AAR26333.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 14008 MW; 8751D98C0FE97500 CRC64;

Query Match 83.2%; Score 524; DB 2; Length 123;
Best Local Similarity 82.0%; Pred. No. 3.5e-46;
Matches 100; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGTTGDNPHSLIQLELESGTQLERHOGQLTLMLARVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
Db 61 DAIRHAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAVTTLTRIQREV 120
QY 121 LA 122
Db 121 LA 122
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RESULT 5
Q7N0W5 PHOLL PRELIMINARY; PRT; 123 AA.
AC Q7N0W5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Similar to YopN chaperone SynC.
GN OrderedLocusNames=plu3764;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Deroo R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanolis A., Powell K., Signier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
DR EMBL; BX571871; CAE161136.1; -; Genomic_DNA.
DR Photolista; plu3764; -.
DR BioCyc; PLUM243265:PLU3764-MONOMER; -.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III; 1.
KW Complete proteome.
SQ SEQUENCE 123 AA; 14111 MW; 689775086FFDFE92 CRC64;

Query Match 66.5%; Score 419; DB 2; Length 123;
Best Local Similarity 63.4%; Pred. No. 2.8e-35;
Matches 78; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCQDLGITIGDNPHSLIQLELEQSGTLQLERHQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGMEVDSSPLQIDFEYSGTLQIERYGGLTLWLAREIPWHQKG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLMBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGLWGEDRLLLFVTLDERDITLPLHQAFLRLRVQREV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 6
Q84GZ1 PHOLU PRELIMINARY; PRT; 123 AA.
AC Q84GZ1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE LessN.
GN Name=LessN;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=23488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0956-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., French-Constant R.H.;
RT "Genomic islands in Photorhabdus.";

Qy 1 MNWIEPLLVOFCQDLGITIGDNPHSLIQLELEQSGTLQLERHQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGMEVDSSPLQIDFEYSGTLQIERYGGLTLWLAREIPWHQKG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLMBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGLWGEDRLLLFVTLDERDITLPLHQAFLRLRVQREV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 7
SYCN YERN STANDARD; PRT; 123 AA.
ID SYCN_YERN STANDARD; PRT; 123 AA.
AC Q52095; P16162; Q93KT9;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Chaperone protein synC.
GN Name=synC;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OG Plasmid pYva127/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Serotype O:3; PLASMID=pYV;
RX MEDLINE=90264308; PubMed=2160939;
RA Vaitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrB gene is part of an operon in the lcr region of Yersinia
RT enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYve227;
RA Iriarte M., Lambert M., Kerbouch C., Cornells G.R.;
RT "Detailed genetic map of the pYve227 plasmid of Yersinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RY DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Shellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYva127/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foulter B., Cornells G.R.;
RT "DNA sequence and analysis of the pYva127/90 virulence plasmid of
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RL Trends Microbiol. 10:541-545(2002).
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CC -----
DR EMBL; AY144116; AA018047.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III; 1.
SQ SEQUENCE 123 AA; 14174 MW; 0247D3A1D26A088A CRC64;

Query Match 66.3%; Score 418; DB 2; Length 123;
Best Local Similarity 63.4%; Pred. No. 3.5e-35;
Matches 78; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCQDLGITIGDNPHSLIQLELEQSGTLQLERHQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCQDLGMEVDSSPLQIDFEYSGTLQIERYGGLTLWLAREIPWHQKG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLMBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGLWGEDRLLLFVTLDERDITLPLHQAFLRLRVQREV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 7
SYCN YERN STANDARD; PRT; 123 AA.
ID SYCN_YERN STANDARD; PRT; 123 AA.
AC Q52095; P16162; Q93KT9;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Chaperone protein synC.
GN Name=synC;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OG Plasmid pYva127/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Serotype O:3; PLASMID=pYV;
RX MEDLINE=90264308; PubMed=2160939;
RA Vaitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrB gene is part of an operon in the lcr region of Yersinia
RT enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYve227;
RA Iriarte M., Lambert M., Kerbouch C., Cornells G.R.;
RT "Detailed genetic map of the pYve227 plasmid of Yersinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RY DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Shellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYva127/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foulter B., Cornells G.R.;
RT "DNA sequence and analysis of the pYva127/90 virulence plasmid of
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RT Yersinia enterocolitica strain A127/90.;
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RP FUNCTION.
RC PLASMID=pfV;
RX MEDLINE=99102236; PubMed=9882687;
RA Iriarte M., Cornelis G.R.;
RT "Identification of SYN, YscX, and YscY, three new elements of the
RT Yersinia Yop virulon".
RL J. Bacteriol. 181:675-680(1999).
RN [6]
RP FUNCTION, AND SUBUNIT.
RC STRAIN=W22703 / Serotype O:9 / Biotype 2;
RX PubMed=11514512; DOI=10.1128/JB.183.18.5293-5301.2001;
RA Cheng L.W., Kay O., Schneewind O.;
RT "Regulated secretion of YopN by the type III machinery of Yersinia
RT enterocolitica.";
RL J. Bacteriol. 183:5293-5301(2001).
CC -!- FUNCTION: Functions as a specific chaperone for YopN. It could
CC facilitate the secretion and the subsequent translocation of YopN.
CC -!- SUBUNIT: Interacts with YscB to form a complex which specifically
CC binds to YopN.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane (By similarity).
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CC -----
DR EMBL; M32097; AAA98431.1; -; Genomic DNA.
DR EMBL; AF102990; AAD16821.1; -; Genomic DNA.
DR EMBL; AF336309; AAK69220.1; -; Genomic DNA.
DR EMBL; AY150843; AAN37520.1; -; Genomic DNA.
DR PIR; C35392; C35392.
DR SNR; Q52095; 2-122.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynC; 1.
KW Chaperone; Plasmid.
FT CHAIN 1 123 Chaperone protein SYN.
FT /FTID=PRO_0000072359.
FT VARIANT 58 58 Q -> R (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT VARIANT 77 77 A -> T (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT VARIANT 88 88 N -> S (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT SEQUENCE 123 AA; 13608 MW; 37732AA55A3FF9AD CRC64;
Query Match 62.9%; Score 396; DB 1; Length 123;
Best Local Similarity 62.3%; Pred. No. 6.8e-33;
Matches 76; Conservative 19; Mismatches 27; Indels 0; Gaps 0;
QY 1 MNWIEPLLQVFCODLGITTDGNPHSLIQLESGTQLQERHQGQTLWLARVPHQSG 60
Db 1 MSWIEPIIHFCDLGVPTSSPLIQLEMAQSGTLQEQHGATLTLWLARSLAHQCE 60
QY 61 EAIRRAMTITAAAGPALVRSGWLGEEQILFVSLDSRAVTLPOLHQAVTTTLRLQREV 120
Db 61 DANVKALTITAAQKSCALPLRAGWLGENQLVLFVSLDSRLTLPLLHQAFQLRLQREV 120
QY 121 LA 122
Db 121 LA 122
RESULT 8
SYCN_YERPE STANDARD; PRT; 123 AA.
AC P61380; P16162;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE Chaperone protein synC.
GN Name=synC; OrderedLocusNames=YPCD1.37c. y5041, y0044, pCD46;
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OS Yersinia pestis.
OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT Yersinia pestis KIM5.";
RL Infect. Immun. 66:4611-4623(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCreedy P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RT pestis.";
RL J. Bacteriol. 180:5192-5202(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Farhikhi J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Meule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Zhou Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Shou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
RN [5]
RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC STRAIN=KIM5 / Biovar Mediaevalis, and KIM8;
RX PubMed=10094626; and KIM8;
RA Day J.B., Plano G.V.;
RT "A complex composed of SynC and YscB functions as a specific chaperone
RT for YopN in Yersinia pestis.";
RL Mol. Microbiol. 30:777-788(1998).
RN [6]
RP FUNCTION.
RC STRAIN=KIM5 / Biovar Mediaevalis, and KIM8;
RX PubMed=12535078; DOI=10.1046/j.1365-2958.2003.03343.x;
RA Day J.B., Ferracci F., Plano G.V.;
RT "Translocation of YopE and YopN into eukaryotic cells by Yersinia
RT pestis YopN, yscA, synC, yscB and lcrG deletion mutants measured using
RT a phosphorylatable peptide tag and phosphospecific antibodies.";
RL Mol. Microbiol. 47:807-823(2003).
CC -!- FUNCTION: Functions as a specific chaperone for YopN. It could
CC facilitate the secretion and the subsequent translocation of YopN.
CC -!- SUBUNIT: Interacts with YscB to form a complex which specifically
CC binds to YopN.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane.
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CC EMBL; AF074612; AAC69794.1; -; Genomic DNA.
DR EMBL; AF053946; AAC62567.1; -; Genomic DNA.
DR EMBL; AL117189; CAB54914.1; -; Genomic DNA.
DR EMBL; AE017043; AAS58565.1; -; Genomic DNA.
DR PIR; T43588; T43588.
DR PDB; 1XKP; X-ray; B1-123.
DR GenomeReviews; AE017043.GR; pCD46.
DR GenomeReviews; AL117189.GR; YPCD1.37C.
DR BioCyc; YPES229193:PCD46-MONOMER; -.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynN; 1.
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FT TURN 15 16
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FT HELIX 103 121
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Qy 1 MNWIEPLLVPQCQDLGITIGNPHSLIQLELEQSGTLQERHOGQTLTLARAVPWHQSG 60
Db 1 MSWIEPIISHFCQDLGVPTSPSLPLIQLEMAQSGTLQERHOGATLTLARSLAWHRCE 60
Qy 61 EAIRAMTLTAAAGPALPVRSGLGEGQLILFVSLDERAVTLFQLHQAATTLRLQREV 120
Db 61 DAMVKALTTLTAQKSGALPLRAGWLGESQLVLFVSLDERSUTLPLHQAEPQLRLQREV 120
Qy 121 LA 122
Db 121 LA 122

RESULT 9
SYCN_YERPS STANDARD; PRT; 123 AA.
AC P61381; P16162; Q663K3;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 14.
DE Chaperone protein synN.
GN Name=synN; OrderedLocusNames=PYV0063;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91312137; PubMed=1857212;
RA Forsberg A., Vitanan A.-M., Skurnik M., Wolf-Watz H.;
RT "The surface-located YopN protein is involved in calcium signal

transduction in Yersinia pseudotuberculosis.";
RL Mol. Microbiol. 5:977-986(1991).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I; PLASMID=pYV.
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC FUNCTION: Functions as a specific chaperone for yopN. It could
CC facilitate the secretion and the subsequent translocation of yopN
CC (By similarity).
CC -! SUBUNIT: Interacts with yscB to form a complex which specifically
CC binds to YOPN (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane (By similarity).
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CC -----
DR EMBL; X51833; CAA36131.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25406.1; -; Genomic DNA.
DR PIR; S15322; S15322.
DR SMR; P61381; 2-122.
DR GenomeReviews; BX936399.GR; pYV0063.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynN; 1.
KW Chaperone; Complete proteome; Plasmid.
FT CHAIN 1 123
FT SEQUENCE 123 AA; 13609 MW; 3771F865B6E3D9AD CRC64;

Query Match 62.2%; Score 392; DB 1; Length 123;
Best Local Similarity 61.5%; Pred. No. 1.8e-32;
Matches 75; Conservative 20; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVPQCQDLGITIGNPHSLIQLELEQSGTLQERHOGQTLTLARAVPWHQSG 60
Db 1 MSWIEPIISHFCQDLGVPTSPSLPLIQLEMAQSGTLQERHOGATLTLARSLAWHRCE 60
Qy 61 EAIRAMTLTAAAGPALPVRSGLGEGQLILFVSLDERAVTLFQLHQAATTLRLQREV 120
Db 61 DAMVKALTTLTAQKSGALPLRAGWLGESQLVLFVSLDERSUTLPLHQAEPQLRLQREV 120
Qy 121 LA 122
Db 121 LA 122

RESULT 10
SYCN_PSEAE PRELIMINARY; PRT; 123 AA.
AC Q9I329;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocusNames=PA1700;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mitzoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
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RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RL opportunistic pathogen.";
RL Nature 406:959-964(2000).
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CC -----
DR EMBL; AE004597; A050589.1; -; Genomic_DNA.
DR F1R; A83432.
DR B1CVC; PAER287:PA1700-MONOMER; -.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 123 AA; 13674 MW; 500B35C61D4B757E CRC64;

Query Match 44.3%; Score 279; DB 2; Length 123;
Best Local Similarity 44.7%; Pred. No. 9.4e-21;
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DB 1 MDWVELPVAQFCODLQVSPAPLARVVQLDFEDSGTLQERHGEQSLWLACDLAWHQAY 60
QY 61 EAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLOREV 120
DB 61 RGTLRALRLCHARAAGSLPLRCAWSGESRLLCITLEARQVGIPTLHQALQALRSARSEV 120
QY 121 LAS 123
DB 121 LAA 123

RESULT 11
ID O30533 PSEAE PRELIMINARY; PRT; 123 AA.
AC O30533;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Pcr2.
GN Name=pCr2;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RA MEDLINE=38037517; PubMed=9371466;
RX Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chapterone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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DR EMBL; AF010150; AAC45941.1; -; Genomic_DNA.
DR ENBL; DQ000666; AAY17108.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.

SQ SEQUENCE 123 AA; 13682 MW; 000B24C6169073A5 CRC64;

Query Match 44.0%; Score 277; DB 2; Length 123;
Best Local Similarity 44.7%; Pred. No. 1.5e-20;
Matches 55; Conservative 24; Mismatches 44; Indels 0; Gaps 0;

QY 1 MNWIEPLLQVFCODLGTITGDNPHSLIQLESGTQLQERHOGQLTLWLARAVPMHQSG 60
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QY 61 EAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLOREV 120
DB 61 RGTLRALRLCHARAAGSLPLRCAWSGESRLLCITLEARQVGIPTLHQALQALRSARSEV 120
QY 121 LAS 123
DB 121 LAA 123

RESULT 12
ID O6QVR6 VIBHA PRELIMINARY; PRT; 124 AA.
AC O6QVR6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Vcr2.
GN Name=vcr2;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY524044; AAS13315.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.
SQ SEQUENCE 124 AA; 13832 MW; 687C707B69C08A5C CRC64;

Query Match 38.3%; Score 241.5; DB 2; Length 124;
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DB 1 MNWIDASVDVDFCRGMGLEAVDFSSAGRVQLSFQSGTLHIEKHQDCFLFLAKPLPHQS 60
QY 60 GEAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLOREV 119
DB 61 NELIKKALSFCAGQGWPELTKTGLLDEQTMVPSAQIEGDEVTLPTIEQAFALLVRLHKD 120
QY 120 VLAS 123
DB 121 VVGS 124

RESULT 13
ID Q87P53 VIBPA PRELIMINARY; PRT; 123 AA.
AC Q87P53;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative type III secretion protein.
GN OrderedLocNames=VP1665;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RA MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
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DR EMBL; BA000031; BAC59928.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III; 1.
KW Complete proteome.
SQ SEQUENCE 123 AA; 13841 MW; C061A5EEA2BAB0A3 CRC64;
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Best Local Similarity 42.1%; Pred. No. 1.2e-16;
Matches 51; Conservative 22; Mismatches 47; Indels 1; Gaps 1;
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Qy 60 GEATRRAMTLTAAAGPALPVRSGLWGEQILFVSLDERAVTLPOLHOAVTTLRLQRE 119
Db 61 GERIQHARLNCNAEQGWPFEMKGTGLDDTLVFSAKIEGDEVTLPTUEQAFALLVRLH 120
Qy 120 V 120
Db 121 V 121
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AC Q66PUL
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative TTSS chaperone.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
RT three secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY647223; AAU11475.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III; 1.
SQ SEQUENCE 124 AA; 13861 MW; 882888F4CDC6C9386 CRC64;
Query Match 38.0%; Score 239.5; DB 2; Length 124;
Best Local Similarity 39.5%; Pred. No. 1.2e-16;
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Qy 120 VLAS 123
Db 121 VAGS 124
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Q2SH41 9GAMM
ID Q2SH41 9GAMM PRELIMINARY; PRT; 125 AA.
AC Q2SH41;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE YopN chaperone, SyncN-like protein.
GN ORFNames=HCH_03276;
OS Haella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haellaceae; Haella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gki1016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
RT an algicidal agent.";
RL Nucleic Acids Res. 33:7066-7073(2005).
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DR EMBL; CP000155; ABC30033.1; -; Genomic_DNA.
SQ SEQUENCE 125 AA; 14010 MW; F1F95617AC9257E1 CRC64;
Query Match 15.4%; Score 97; DB 2; Length 125;
Best Local Similarity 27.7%; Pred. No. 0.075;
Matches 33; Conservative 25; Mismatches 49; Indels 12; Gaps 4;
Qy 8 LVQFCQDLG---ITIGDNPHSLIQLEQSGTLQLERHQGLTLWLARAVPMHQSGBAI 63
Db 11 ITEFLQQLGFADFIWRGEP---LTAFERSGTLMIPEHQGLLVRLQEISETDCADLI 66
Qy 64 RRAMTLTAAAGPALPVR--SGWLGEQILFVSLDERAVTLPOLHOAVTTLRLQREV 120
Db 67 PKA--LRVHYDQPLPLRAHTGMKGASQLAFIVALSRQQLSIAGLNEALGVLVHLQOL 123
Search completed: June 16, 2006, 19:23:07
Job time : 98.6 secs
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29961
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29961

Query Match
Best Local Similarity 18.7%; Score 118; DB 2; Length 106;
Matches 31; Conservative 16; Mismatches 27; Indels 22; Gaps 4;

Qy 49 WLAR-AVP--WQSGEARRMTLT-----AAAQGPALPVRSGWLGE 87
Db 12 WISRTAACSWMANAMSCSGWPVTWPTRTPIAFCGRCALCHARAAG-SLPLRCANSGE 70

Qy 88 EQLILFVSLDERAVTLPOLHQAHTTLRLQREVLAAS 123
Db 71 SRLLLCITLEARQVGIPTLHQAQLRSARSEVLAA 106

RESULT 3
US-09-252-991A-27865
; Sequence 27865, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27865
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27865

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Best Local Similarity 13.3%; Score 84; DB 2; Length 167;
Matches 24; Conservative 10; Mismatches 24; Indels 16; Gaps 3;

Qy 30 ELEOSGTLQLERHQQLTLWLARAVPWH-----QSGEARRMTLTAAQGPALP--- 79
Db 14 EIDTGGDLSTTHPGLDALMLLTAVALRLREQAGPLEDSEAVRQAL-----AQGGLPRRI 68

Qy 80 -VRSCWLGEEQLIL 92
Db 69 LTRAHWLGRREGLL 82

RESULT 4
US-08-426-630-28
; Sequence 28, Application US/08426630
; Patent No. 6656709
; GENERAL INFORMATION:
; APPLICANT: BLANCHE, FRANCIS; CAMERON, BEATRICE; CROUZET,
; APPLICANT: JOEL; DEBUSSCHE, LAURENT; LEVY SCHIL, SOPHIE;
; APPLICANT: THIBAUT, DENIS
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE
; TITLE OF INVENTION: BIOSYNTHESIS OF COBALAMINS AND/OR COBAMIDES, DNA SEQUENCES
; TITLE OF INVENTION: CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 555 13TH STREET, N.W.
; CITY: WASHINGTON
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426.630
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,151
; FILING DATE: 14-SEP-1992
; APPLICATION NUMBER: PCT/FR91/00054
; FILING DATE: 30-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: F. F. CALVETTI
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: 1290-7213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas denitrificans
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: COBM
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Translation product of SEQ ID NO:27
US-08-426-630-28

Query Match 12.7%; Score 80; DB 2; Length 253;
Best Local Similarity 23.3%; Pred. No. 0.1;
Matches 35; Conservative 24; Mismatches 49; Indels 42; Gaps 7;

Qy 4 IEPLLVQFCQDLGITIGNPHSLIQLELE-----QSGTLQLER-HQGQLTLWLARAVPMHQ 58
Db 37 VSPPELLRYCPCGARI VDTAPMSLDEIEAEYVKAEGLDVARLHSGDLSVMSAVA----- 91

Qy 59 SGEAIRR-----AMTLTAAQGPALPVRSGWLGE-----QLILFVSLDERAVTLPO 105
Db 92 --EQIRLEKHGIAYTMTPGV--PSFAAASALGRELTI PAVAAQSLVTLRVSGRASPMPN 147

Qy 106 -----LHQA VTTTLRLQREV 120
Db 148 SETLSAFGATGSTLAIHLAIHALQOQVVEEL 177

RESULT 5
US-08-990-379-7
; Sequence 7, Application US/089990379
; Patent No. 5998188
; GENERAL INFORMATION:
; APPLICANT: Stork, Philip J
; APPLICANT: Misra-Press, Anita
```



US-10-104-047-2296  
; Sequence 2296, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241el full length cdNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2296  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2296

Query Match 11.6%; Score 73; DB 2; Length 565;  
Best Local Similarity 27.4%; Pred. No. 2.6;  
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;  
QY 12 CQDLGITGDNDPHSLIQLEQSGTQLQER-----HOGQLTLMAR-----AVPWHQSG 60  
Db 189 CSDTGVV-----SSSLGPARRREASQPSLHRQLSDPNHGSPPOLYRANLGLGAYPWSQSS 244  
QY 61 EAIRRAMT--LTAAGGALPVRSWGLGEEQILFVSLDERAVTLPOLHQAVTTLTR 115  
Db 245 PALNINSTSPLTAVESPLP-----RSRPLLOPHRGAPALSR 282

RESULT 10  
US-09-252-991A-21159  
; Sequence 21159, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21159  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21159

Query Match 11.3%; Score 71; DB 2; Length 332;  
Best Local Similarity 28.5%; Pred. No. 2.1;  
Matches 37; Conservative 20; Mismatches 53; Indels 20; Gaps 7;  
QY 5 EPLLVOFCQDLGITGDNDPHSLIQLEQSGTQLQERHOGQLTLMAR---RAVPWHQSGEA 62  
Db 146 DAFLVEFCEEA-----PHRTTQLDVDPGGGL-VEDQQARLVDOQAGDHOAPLHAAGEH 197  
QY 63 IRRAMTLTAAQAQ--GPALPVRSWGLGERQLTLFVSLD--ERAVTLPOL-----HOAVTTLT 114  
Db 198 PRGFVALVPQALQGVALLGLDRLRDVAVAGLGHDDVDLELLEVEVLLRHAKATLE 257  
QY 115 --RLQREVLA 122  
Db 258 AGRVLVEVVA 267

RESULT 11  
US-09-583-110-5129

; Sequence 5129, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 5129  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-5129

Query Match 11.3%; Score 71; DB 2; Length 361;  
Best Local Similarity 33.9%; Pred. No. 2.4;  
Matches 20; Conservative 7; Mismatches 28; Indels 4; Gaps 2;  
QY 38 QLERHOGQLTLMARAVPWHQSGEAIRRAMT--LTAAGGPA--LPVRSWGLGEEQLIL 92  
Db 15 EYEPHGTLMWPTPGSWPFGAKAKRAFTQIETIAEGSERVYLLVEQAYLSEAQSYL 73

RESULT 12  
US-09-107-433-4556  
; Sequence 4556, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 4556:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 365 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear



```

RESULT 14
US-09-252-991A-25459
; Sequence 25459, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25459
; LENGTH: 618
; TYPE: PRT

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Query Match	11.1%	Score 70;	DB 2;	Length 1028;
Best Local Similarity	25.6%;	Pred. No. 15;		
Matches	32;	Conservative 17;	Mismatches 40;	Indels 36; Gaps 6;
QY	1	MNWI-----EPLLVOFCODLGITTDGPHSLIQLELESGTQLQHERHOGQLTLWLARA	53	
DB	114	MMWIYNEKQPSTPLTLQFKONNOVALS-----FKTELNFTG-----MRGIA	154	
QY	54	VPWH-OSGEAIRRAMTLTAAAOQPALPVRSNGEQLILFVSLDER----	AVTLPOLHQ	108
DB	155	VFRDMKGSATGKLDKLIVITA-----PDQAGTLFFDQIIMSVELDRNWPIDYQIPVNN	209	
QY	109	AVTTL	113	
DB	210	AVNTM	214	

Search completed: June 16, 2006, 19:29:01  
Job time : 23.7 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 68.8 Seconds  
(without alignments)  
828.131 Million cell updates/sec

Title: US-10-813-908A-2  
Perfect score: 630  
Sequence: 1 MNWIEPLLQVFCQDLGITIG.....POLHQA VTTLT LRLQREVLA S 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : Published Applications AA Main: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	123	5	US-10-813-908-2
2	89	14.1	252	5	US-10-732-923-2161
3	82	13.0	176	5	US-10-506-454-1585
4	80	12.7	253	5	US-10-732-923-2165
5	80	12.7	253	5	US-10-724-598-28
6	79	12.5	289	4	US-10-156-761-9384
7	78	12.4	558	4	US-10-437-963-153335
8	77	12.2	652	4	US-10-369-493-8117
9	74.5	11.8	420	4	US-10-282-122A-78453
10	74	11.7	1224	4	US-10-282-122A-78453
11	73	11.6	450	4	US-10-282-122A-67552
12	73	11.6	565	4	US-10-104-047-2296
13	73	11.6	565	6	US-11-072-512-2296
14	72.5	11.5	3084	3	US-09-938-275-4
15	72.5	11.5	3084	4	US-10-262-670-2
16	71.5	11.3	243	3	US-09-866-099-2
17	71.5	11.3	243	4	US-10-149-256-6
18	71.5	11.3	243	4	US-10-243-552-594
19	71.5	11.3	289	5	US-10-450-763-41657
20	71.5	11.3	760	5	US-10-732-923-12022
21	71.5	11.3	939	4	US-10-087-099-9073
22	71.5	11.3	939	4	US-10-292-798-1524
23	71.5	11.3	1068	5	US-10-017-161-1868
24	71	11.3	361	5	US-10-472-928-1798
25	71	11.3	365	5	US-10-617-320-4556
26	71	11.3	482	4	US-10-369-493-8828
27	71	11.3	560	6	US-11-097-143-19725

28	71	11.3	1162	4	US-10-282-122A-69725	Sequence 69725, A
29	71	11.3	1814	4	US-10-367-094-162	Sequence 162, App
30	70	11.1	402	4	US-10-369-493-22935	Sequence 22935, A
31	70	11.1	641	6	US-11-097-143-12591	Sequence 12591, A
32	69.5	11.0	305	4	US-10-437-963-186976	Sequence 186976, A
33	69	11.0	551	4	US-10-238-075-847	Sequence 847, App
34	69	11.0	747	4	US-10-408-765A-1495	Sequence 1495, App
35	69	11.0	2241	4	US-10-369-493-5240	Sequence 5240, App
36	69	11.0	2261	4	US-10-369-493-5241	Sequence 5241, App
37	69	11.0	6145	4	US-10-156-761-7962	Sequence 7962, App
38	68.5	10.9	412	4	US-10-282-122A-63228	Sequence 63228, A
39	68.5	10.9	502	4	US-10-282-122A-65008	Sequence 65008, A
40	68.5	10.9	788	5	US-10-485-395A-6	Sequence 6, Appli
41	68.5	10.9	788	6	US-11-097-143-19737	Sequence 19737, A
42	68.5	10.9	827	4	US-10-347-470A-26	Sequence 26, Appl
43	68	10.8	364	6	US-11-096-568A-15334	Sequence 15334, A
44	68	10.8	390	6	US-11-096-568A-15333	Sequence 15333, A
45	68	10.8	1403	5	US-10-732-923-8710	Sequence 8710, App

ALIGNMENTS

RESULT 1

US-10-813-908-2  
; Sequence 2, Application US/10813908  
; Publication No. US20050058662A1  
; GENERAL INFORMATION:  
; APPLICANT: Frey, Joachim Stuber  
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and U  
; FILE REFERENCE: MICO1/2315/WO  
; CURRENT APPLICATION NUMBER: US/10/813,908  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US/10/416,902  
; PRIOR FILING DATE: 2003-05-15  
; PRIOR APPLICATION NUMBER: PCT/CA01/01589  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Aeromonas salmonicida  
US-10-813-908-2

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QY	1	MNWIEPLLQVFCQDLGITIGDNPHSLIQLELEQSGTQLQERHQGQLTLWLARAVPWHQSG	60	
Db	1	MNWIEPLLQVFCQDLGITIGDNPHSLIQLELEQSGTQLQERHQGQLTLWLARAVPWHQSG	60	
QY	61	EAIRAMTILTAQAQCPALPVRSGWLGESQLILFVSLDERAVTLPOLHQA VTTLT LRLQREV	120	
Db	61	EAIRAMTILTAQAQCPALPVRSGWLGESQLILFVSLDERAVTLPOLHQA VTTLT LRLQREV	120	
QY	121	LAS 123		
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RESULT 2				
US-10-732-923-2161				
; Sequence 2161, Application US/10732923				
; Publication No. US20050108791A1				
; GENERAL INFORMATION:				
; APPLICANT: Egerton, Michael D				
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES				
; FILE REFERENCE: 38-15(52796)C				
; CURRENT APPLICATION NUMBER: US/10/732,923				
; CURRENT FILING DATE: 2003-12-10				
; PRIOR APPLICATION NUMBER: 10/310,154				



SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: Amino Acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: No  
ORIGINAL SOURCE:  
ORGANISM: Pseudomonas denitrificans  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
FEATURE:  
NAME/KEY: COBM  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION: Translation product of SEQ ID NO:28  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-10-724-598-28  
Query Match 12.7%; Score 80; DB 5; Length 253;  
Best Local Similarity 23.3%; Pred. No. 2.2;  
Matches 35; Conservative 24; Mismatches 49; Indels 42; Gaps 7;  
QY 4 IEPLVQFCODLGITIGDNPHSLIQLELE-----QSGTQLQLER-HQGQLTLWLAARVPWHQ 58  
DB 37 VPELLRYCPGARIVDTTPMSLDEIEAEYVKAEGLDVAUHSGLDSVWSAVA----- 91  
QY 59 SGEAIRR-----AMTLTAAAGPALPVRSGMLGEE-----QLILFVSLDERAVTLTPQ 105  
DB 92 --EQIRRLKKGIAVTMTFGV--PSFAAASALGRELTIPTAVALQSLVLTFRVSGRASPMPN 147  
QY 106 -----LHQAVTTLTRLQREV 120  
DB 148 SETLSAFGATGSTLAHLAHLAHLAQVVEEL 177  
RESULT 6  
US-10-156-761-9384  
; Sequence 9384, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 9384  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-9384  
Query Match 12.5%; Score 79; DB 4; Length 289;  
Best Local Similarity 31.9%; Pred. No. 3.4;  
Matches 23; Conservative 10; Mismatches 25; Indels 14; Gaps 1;

QY 21 DNPHSLIQLELEQSGTQLQLERHOGQLTLWLAARVPWHQSGEAIIRRAMTTLTAAAGPALPV 80  
DB 115 DPEVDLELTVELSGTTLHEQLAAGKLDLVLAKRPPQDPRGELVRHD----- 160  
QY 81 RSGMLGEEOLIL 92  
DB 161 RUVWIGAERLRL 172  
RESULT 7  
US-10-437-963-153335  
; Sequence 153335, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 153335  
; LENGTH: 558  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_532C.1.pap  
US-10-437-963-153335  
Query Match 12.4%; Score 78; DB 4; Length 558;  
Best Local Similarity 32.6%; Pred. No. 10;  
Matches 30; Conservative 6; Mismatches 36; Indels 20; Gaps 5;  
QY 39 LERHOGQLTLWLAARVP--WHQSGEAIIRRAMTTLTAAAGPALPVRSGW-----LGEEQLI 91  
DB 89 LQTHNGSLT---GRVPPDAWHGVGHAANSVF-----VLPFRKRWALRRIGAHL 136  
QY 92 LRVSLDERAVTIPQLHQAVTTLTRLQREVLA 123  
DB 137 SARQLDGRRL-LPLLRDAVLDRRVSEMSAA 167  
RESULT 8  
US-10-369-493-8117  
; Sequence 8117, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 8117  
; LENGTH: 652  
; TYPE: PRT  
; ORGANISM: Thermobifida fusca  
; FEATURE:  
; NAME/KEY: unsure



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QY 114 TRLQREVLA 122
Db 317 QHLQOQLQA 325

RESULT 11
US-10-282-122A-67552
; Sequence 67552, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; FILE OF INVENTION: Identification of Essential Genes in Microorganisms
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67552
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-67552

Query Match 11.6%; Score 73; DB 4; Length 450;
Best Local Similarity 36.9%; Pred. No. 28;
Matches 24; Conservative 7; Mismatches 16; Indels 18; Gaps 4;

QY 7 LLVQFCQ-----DLGITGDNPHSLIQLEEQSGTLQLER-----HQQQLTLWLARA 53
Db 387 LLEQCCQRAVAQRHLRAVLIGDEP---QVSAELSGE-ELDRLLDPAHYLGQARVWVARA 441

QY 54 VFWHQ 58
Db 442 VSEHQ 446

RESULT 12
US-10-104-047-2296
; Sequence 2296, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; FILE OF INVENTION: No. US20030236392A1e1 full length cDNA
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2296
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2296

Query Match 11.6%; Score 73; DB 6; Length 565;
Best Local Similarity 27.4%; Pred. No. 37;
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;

QY 12 CODLGITIGDNPHSLIQLEEQSGTLQLER-----HQQQLTLWLAR-----AVPMHQSG 60
Db 189 CSDTGWV----SSSLGPARREASQPSLHRQLSDPNHGSPPGLYRANLGLGAYPWSQSS 244
QY 61 EAIRRAMT--LTAARQGPALPVRSGWLGEELILFVSLDERAVTLPOLHOAVTTLTR 115
Db 245 PALNHNSTSPLTAVESPLP-----RSRPLLOFHRGAPALSR 282

RESULT 13
US-11-072-512-2296
; Sequence 2296, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAOJU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; FILE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2296
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2296

Query Match 11.6%; Score 73; DB 6; Length 565;
Best Local Similarity 27.4%; Pred. No. 37;
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;

QY 12 CODLGITIGDNPHSLIQLEEQSGTLQLER-----HQQQLTLWLAR-----AVPMHQSG 60
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Db189CSDTGW-----SSSIGPARREASGQPSLHRQLSDPNHGSPPCLYRANLGLGAYPWSOSS244

Qy61EAIRRAMT--LTAAAGPALPVRSGWLGEQILILFVSLDERAVTLPOLHQAVTTLTTRLQREVLTAS123

Db245PALNHSTSPITLAVESPLP-----RSRPLLQPHRGAPALSR282

RESULT 14

US-09-938-275-4

Sequence 4, Application US/09938275

Patent No. US20020111309A1

GENERAL INFORMATION:

APPLICANT: Gerardo Castillo

APPLICANT: Alan Snow

TITLE OF INVENTION: Therapeutic and Diagnostic Applications

TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments

FILE REFERENCE: PROTEO.P03

CURRENT APPLICATION NUMBER: US/09/938,275

PRIOR FILING DATE: 2001-08-16

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 3084

TYPE: PRT

ORGANISM: Mus musculus

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Swissprot P19137

DATABASE ENTRY DATE: 1990-11-01

US-09-938-275-4

Query Match11.5%; Score 72.5; DB 3; Length 3084;

Best Local Similarity32.7%; Pred. No. 3.6e+02;

Matches32; Conservative16; Mismatches39; Indels11; Gaps6;

Qy33QSGTLQLERHOGQLTLWLARAVPHVHQSGEAI-----RRAMTLTAAAGQGA--LPVRSGLWG86

Db1836QDTLTQLEHHRDELLW-ARKIRSHVDDLVNMQSKRRARDLVHRAEQHASELQSRAGALD1894

Qy87EE-QLILFVSLDERAVTLPOLHQAVTTLTTRLQREVLTAS123

Db1895RDLENVRNVSLN--ATSAAHVHSNIQILTTE-EAEMTLAA1929

RESULT 15

US-10-262-670-2

Sequence 2, Application US/10262670

Publication No. US20030108540A1

GENERAL INFORMATION:

APPLICANT: Kalluri, Raghuram

TITLE OF INVENTION: Anti-Angiogenic and Anti-Tumor

TITLE OF INVENTION: Properties of Matin and Other Laminin Domains

FILE REFERENCE: 1440-2004-008

CURRENT APPLICATION NUMBER: US/10/262,670

CURRENT FILING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: PCT/US01/09921

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 60/192,875

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 3084

TYPE: PRT

ORGANISM: Mus musculus

US-10-262-670-2

Query Match11.5%; Score 72.5; DB 4; Length 3084;

Best Local Similarity32.7%; Pred. No. 3.6e+02;

Matches32; Conservative16; Mismatches39; Indels11; Gaps6;

Qy33QSGTLQLERHOGQLTLWLARAVPHVHQSGEAI-----RRAMTLTAAAGQGA--LPVRSGLWG86

Db1836QDTLTQLEHHRDELLW-ARKIRSHVDDLVNMQSKRRARDLVHRAEQHASELQSRAGALD1894



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 5.3 Seconds  
(without alignments)  
523.484 Million cell updates/sec

Title: US-10-813-908A-2  
Perfect score: 630  
Sequence: 1 MNWIEPLLVQFQDLGITIG.....POLHQAVTTLTLQREVLAAS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	10.8	441	US-10-449-902-32870	Sequence 32870, A
2	67	10.6	557	US-10-449-902-47436	Sequence 47436, A
3	65.5	10.4	305	US-11-122-986-5	Sequence 5, Appli
4	65.5	10.4	305	US-11-122-986-7	Sequence 7, Appli
5	65.5	10.4	308	US-10-449-902-28824	Sequence 28824, A
6	65	10.3	557	US-10-449-902-50128	Sequence 50128, A
7	64.5	10.2	249	US-10-953-349-32013	Sequence 32013, A
8	64.5	10.2	307	US-10-953-349-32012	Sequence 32012, A
9	64.5	10.2	354	US-10-953-349-32011	Sequence 32011, A
10	64.5	10.2	1333	US-10-449-902-41289	Sequence 41289, A
11	63.5	10.1	673	US-11-121-154-11	Sequence 11, Appli
12	63	10.0	152	US-10-449-902-38951	Sequence 38951, A
13	62	9.8	231	US-10-449-902-30176	Sequence 30176, A
14	61.5	9.8	153	US-10-953-349-12335	Sequence 12335, A
15	61.5	9.8	153	US-10-953-349-25973	Sequence 25973, A
16	61.5	9.8	156	US-10-449-902-51435	Sequence 51435, A
17	61.5	9.8	508	US-10-449-902-38213	Sequence 38213, A
18	61	9.7	433	US-10-953-349-17176	Sequence 17176, A
19	61	9.7	436	US-10-953-349-17175	Sequence 17175, A
20	61	9.7	454	US-10-953-349-17174	Sequence 17174, A
21	61	9.7	619	US-10-449-902-44299	Sequence 44299, A
22	60.5	9.6	163	US-11-293-697-2811	Sequence 2811, Ap
23	60	9.5	183	US-10-449-902-38622	Sequence 38622, A
24	60	9.5	485	US-11-293-697-2858	Sequence 2858, Ap
25	60	9.5	497	US-10-953-349-35183	Sequence 35183, A

ALIGNMENTS

RESULT 1

US-10-449-902-32870  
; Sequence 32870, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 32870  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-32870

Query Match 10.8%; Score 68; DB 6; Length 441;  
Best Local Similarity 29.3%; Pred. No. 3.4;  
Matches 27; Conservative 11; Mismatches 34; Indels 20; Gaps 5;  
QY 16 GITIGDNPHSLIQLEBOSGTLQERHOGQLTLWLRARVPHQSGETIRRAMTLTAAG 75  
Db 179 GFLVWQKPELMSLVSGCKISAGSDGKA-W--RQTPWHQS-----HASRG 224

QY 76 PALPVRSGLGHEQLI---LF---VSLDERAV 101  
Db 225 PPRPULRSLOGLDPLMTATSLFADAVCIGERSV 256

RESULT 2

US-10-449-902-47436  
; Sequence 47436, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

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; FILE REFERENCE: MOA-A0205V1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47436
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47436

Query Match      10.4%; Score 67; DB 6; Length 557;
Best Local Similarity 25.4%; Pred. No. 5.9;
Matches 29; Conservative 17; Mismatches 46; Indels 22; Gaps 4;

Qy      26 LIQLEQSGTQLER-----HQQQLTLMLAR-----AVPWHQSGEAIRAM 67
Db      403 LLSYEDESGKLQATKVLGTHVYVHPNGSSMEIVRVGSPSTETFPWQTDDES--RAV 460

Qy      68 TLTAQAQGPALPVRSG--WLGEQILFVSLDERAVTLPQLHQAVTTTLRLQRE 119
Db      461 EINRSFAGEIATGYGFRYPGSKGSLFVLLDGLRAFLVRENKAVTLTLQLDLLE 514

RESULT 3
US-11-122-986-5
; Sequence 5, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-5

Query Match      10.4%; Score 65.5; DB 7; Length 305;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 24; Conservative 14; Mismatches 23; Indels 23; Gaps 4;

Qy      57 HOSGE-AIRRAMTLTAAAGPALPV-----RSGWLGEQIL-----FVS----- 95
Db      73 HKSGEKALNRYMNRNTASAALKDQVDVIFVDRTRWTEEDQWLVQVQVSCPVLIAVNKT 132

Qy      96 --LDERAVTLPQLHQAVTTTLRLQ 117
Db      133 DRIEKAADLLPHLEWLTQQLPKAE 156

RESULT 4
US-11-122-986-7
; Sequence 7, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-7

Query Match      10.4%; Score 65.5; DB 7; Length 305;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 24; Conservative 14; Mismatches 23; Indels 23; Gaps 4;

Qy      57 HOSGE-AIRRAMTLTAAAGPALPV-----RSGWLGEQIL-----FVS----- 95
Db      73 HKSGEKALNRYMNRNTASAALKDQVDVIFVDRTRWTEEDQWLVQVQVSCPVLIAVNKT 132

Qy      96 --LDERAVTLPQLHQAVTTTLRLQ 117
Db      133 DRIEKAADLLPHLEWLTQQLPKAE 156

RESULT 5
US-10-449-902-28824
; Sequence 28824, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
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; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30176
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30176

Query Match          9.8%; Score 62; DB 6; Length 231;
Best Local Similarity 23.8%; Pred. No. 7.5;
Matches 19; Conservative 15; Mismatches 36; Indels 10; Gaps 3;

QY 44 GQLTLMARAVPHQSGEARRAMTLTAAAGGALPVRSGWLGEQILFVSLDERAVTL 103
Db 161 GYLDVSLGAMIGMRAGEALHGRRTDATRS----PLLNAMWR-----FAALDAAKAAM 211

QY 104 PQLHQAVTTLRLQREVLA 123
Db 212 PDNNKLIV-EFVRVRAAAN 230

RESULT 14
US-10-953-349-12335
; Sequence 12335, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12335
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12335

Query Match          9.8%; Score 61.5; DB 6; Length 153;
Best Local Similarity 34.4%; Pred. No. 5.2;
Matches 21; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 30 ELEQSGTLQLERHQGLTLMARAVPHQSGEARRAMTLTAAAGGALPVRSGWLGEQ 89
Db 32 EREMAKSLRSKREKRLTLRREITAEFPYDKKEAKQA-AQAAALEAPKLPVRVHPAYEES 90

QY 90 L 90
Db 91 L 91

RESULT 15
US-10-953-349-25973
; Sequence 25973, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25973
; LENGTH: 153
; TYPE: PRT
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; ORGANISM: Triticum aestivum
US-10-953-349-25973

Query Match          9.8%; Score 61.5; DB 6; Length 153;
Best Local Similarity 34.4%; Pred. No. 5.2;
Matches 21; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 30 ELEQSGTLQLERHQGLTLMARAVPHQSGEARRAMTLTAAAGGALPVRSGWLGEQ 89
Db 32 EREMAKSLRSKREKRLTLRREITAEFPYDKKEAKQA-AQAAALEAPKLPVRVHPAYEES 90

QY 90 L 90
Db 91 L 91

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-3  
Perfect score: 609  
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Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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2: geneseqp1990s:\*  
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7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	266	43.7	262	7	ABO81423 Pseudomon
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4	83.5	13.7	353	2	AAR20178 P. glumae
5	83	13.6	10917	6	AAR36132 Streptomy
6	81.5	13.4	366	4	AAU53181 Propionib
7	81.5	13.4	366	6	ABM49700 Propionib
8	81.5	13.4	452	6	ABU25842 Protein e
9	80	13.1	1132	8	ADY06856 Plant ful
10	78.5	12.9	165	3	ABU41479 Human ORF
11	78.5	12.9	165	5	ABP10391 Human ORF
12	78.5	12.9	4924	4	AAB70968 S. spinos
13	78.5	12.9	4928	2	AAV39300 Spnd a po
14	78	12.8	294	8	ADJ67793 B. subtil
15	78	12.8	294	8	ADJ68005 B. subtil
16	78	12.8	294	8	ADK01083 DNA polym
17	78	12.8	294	8	ADJ79302 B. subtil
18	78	12.8	294	8	ADJ84742 B. subtil
19	78	12.8	294	8	ADM77530 DNA polym
20	78	12.8	294	8	ADM66197 B. subtil
21	78	12.8	294	8	ADO04250 B. subtil
22	78	12.8	294	8	ADP82327 DNA polym
23	78	12.8	294	8	ADS15534 DNA polym

24	78	12.8	294	9	ADY55025 B. subtil
25	78	12.8	294	9	ADZ76601 Bacillus
26	78	12.8	294	9	AEA24609 B. subtil
27	78	12.8	294	9	AEA34032 B. subtil
28	78	12.8	294	9	AEB51436 DNA polym
29	77.5	12.7	1486	4	ABB63035 Drosophil
30	77	12.6	673	8	ADS28904 Bacteri
31	76.5	12.6	322	8	ABM85037 Human dia
32	76.5	12.6	662	4	AAE00477 sgal prot
33	76	12.5	810	7	ABO63231 Klebsiell
34	74.5	12.2	602	7	ABO81712 Pseudomon
35	73.5	12.1	340	4	ABB71440 Drosophil
36	73.5	12.1	429	7	ABO81630 Pseudomon
37	72.5	11.9	524	8	ADT60176 Plant pol
38	72.5	11.9	602	8	ADG22680 Cyanophag
39	72	11.8	294	8	ADX71223 Plant ful
40	72	11.8	610	8	ADX89677 Plant ful
41	72	11.8	2216	9	ABM93022 M. xanthu
42	71.5	11.7	393	8	ADY22840 Plant ful
43	71.5	11.7	482	8	ADY04623 Plant ful
44	71	11.7	261	8	ADN27057 Bacteri
45	71	11.7	293	7	ABO71150 Pseudomon

ALIGNMENTS

RESULT 1  
ABB80771 ID ABB80771 standard; protein; 121 AA.  
XX AC ABB80771;  
XX DT 23-SEP-2002 (first entry)  
XX DE A. salmonicida type III secretion protein acr3 sequence.

XX KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
XX KW acrV; acrH; antibiotic; vaccine; fish.  
XX OS Aeromonas salmonicida.

XX PN WO200240514-A2.  
XX PD 23-MAY-2002.  
XX PF 15-NOV-2001; 2001WO-CA001589.

XX PR 15-NOV-2000; 2000US-0248864P.

XX PA (FREY/) FREY J.  
XX PA (STUB/) STUBER K.  
XX PA (THOR/) THORNTON J C.  
XX PA (KUZY/) KUZYSK M A.  
XX PA (BURI/) BURIAN J.  
XX PI Frey J, Stuber K, Thornton JC, Kuzysk MA, Burian J;  
XX DR WPI: 2002-537338/57.  
XX DR N-PSDB: ABN86172.

XX PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the  
XX FT protein, useful for reducing susceptibility of fish to infection by a  
XX PS virulent strain of Aeromonas salmonicida.

XX CC Claim 13; Page 27; 39pp; English.

XX CC The invention relates to A. salmonicida type III secretion genes and  
XX CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.  
XX CC A. salmonicida type III secretion apparatus is useful for producing  
XX CC selected products, especially Aext. AcrV in vaccine, epitope or epitopic  
XX CC region of AcrV or any other protein of A. salmonicida type III secretion  
XX CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the A.salmonicida type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from A.salmonicida or its genes. The present  
CC sequence represents the A. salmonicida type III secretion protein acr3  
XX  
XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 609; DB 5; Length 121;  
Best Local Similarity 100.0%; Pred. No. 3.3e-60;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPEPHISRILYPERLADRVLLDFA 60  
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPEPHISRILYPERLADRVLLDFA 60  
QY 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGQSPELRAAAALLEGQWHADEQLMQMTLLHLHK 120  
DB 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGQSPELRAAAALLEGQWHADEQLMQMTLLHLHK 120  
QY 121 V 121  
DB 121 V 121

RESULT 2  
ABO81423  
ID ABO81423 standard; protein; 262 AA.  
AC ABO81423;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #13598.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
XX Pseudomonas aeruginosa.

XX US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
XX 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
XX WPI; 2003-615309/58.  
DR N-PSDB; ABD14994.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 30169; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biocchip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
XX SQ Sequence 262 AA;

Query Match 43.7%; Score 266; DB 7; Length 262;  
Best Local Similarity 46.3%; Pred. No. 3.4e-21;  
Matches 56; Conservative 20; Mismatches 45; Indels 0; Gaps 0;  
QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPEPHISRILYPERLADRVLLDFA 60  
DB 142 MSRVGAWHIGIERLDLAHAEPFAPPLPERHLLAPDGRPVETHVASLYPQAQOQLFDYA 201  
QY 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGQSPELRAAAALLEGQWHADEQLMQMTLLHLHK 120  
DB 202 RPQLEFPHGLRPGDFRQALRLRLATLPRQALQAACLLGGERDEQRLLOMAPNLLHK 261  
QY 121 V 121  
DB 262 V 262

RESULT 3  
AEC75797  
ID AEC75797 standard; protein; 259 AA.  
XX  
AC AEC75797;  
XX  
DT 01-DEC-2005 (first entry)  
XX  
DE P. cellulosum ambruticin ORF5 protein.

XX ambruticin; fungal infection; fungicide; polyketide.

XX Polyangium cellulosum.

XX WO2005086907-A2.

XX 22-SEP-2005.

XX 08-MAR-2005; 2005WO-US007924.

XX 08-MAR-2004; 2004US-0551103P.

XX 04-MAY-2004; 2004US-0568290P.

XX 07-MAR-2005; 2005US-00075185.

XX (KOSA-) KOSAN BIOSCIENCES INC.

XX Reeves CD, Julien B, Reid RC;

XX WPI; 2005-639088/65.

XX N-PSDB; AEC75775.

XX New nucleic acids encoding polyketide synthases and polyketide  
PT modification enzymes involved in or required for the biosynthesis of  
PT ambruticin, useful for producing polyketides, e.g. ambruticins, for  
PT treating fungal infections.

XX Disclosure; SEQ ID NO 24; 285pp; English.

XX The invention relates to a purified or recombinant nucleic acid (I)  
CC comprising a nucleotide sequence encoding a polypeptide involved in or  
CC required for the biosynthesis of ambruticin. The complement of the  
CC nucleotide sequence hybridizes to a nucleic acid encoding a domain  
CC selected from beta-ketocacylsynthase, acyltransferase, beta-ketoreductase,  
CC dehydratase, enoylreductase, or acyl carrier protein domains of the  
CC Sorangium cellulosum (synonym: Polyangium cellulosum) ambruticin gene  
CC cluster, or where the complement of the nucleotide sequence hybridizes to  
CC a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO.  
CC 11-19 (AEC75784-AEC75792). The nucleic acid is useful for producing







XX Sequence 366 AA;  
SQ Query Match 13.4%; Score 81.5; DB 6; Length 366;  
Best Local Similarity 27.0%; Pred. No. 2.9;  
Matches 24; Conservative 18; Mismatches 32; Indels 15; Gaps 3;  
  
QY 8 HIGIEQLSALDDQERSLPGRYALLPDGQSIPEPHISRLYPERLADRVLLDFATPDGRGFH 67  
Db 237 HRWIEELGGMNF-----MAISKDGLVTPELAGTILRGVTRRSILEVA-PDLGLE 285  
  
QY 68 DLLRPVDFNQAMQGLRSVLARGQSPELRA 96  
Db 286 PVERKIDVELLDGVR-----GEPEVEFA 310  
  
RESULT 8  
ABU25842  
ID ABU25842 standard; protein; 452 AA.  
XX  
AC ABU25842;  
DT 19-JUN-2003 (first entry)  
DE Protein encoded by Prokaryotic essential gene #11369.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Corynebacterium diphtheriae.  
XX  
PN W0200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPT; 2003-029926/02.  
DR N-PSDB; ACA29712.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 53766; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 452 AA;  
  
Query Match 13.4%; Score 81.5; DB 6; Length 452;  
Best Local Similarity 23.5%; Pred. No. 3.8;  
Matches 36; Conservative 20; Mismatches 56; Indels 41; Gaps 4;  
  
QY 2 SRITAAHIGIEQLSALDDQERSLPGRYAL---LPDGQSIPEPHISRLYPERLADRVLLD 58  
Db 202 NRITISDEALEQLVLLSGGDARSLTYLEAASESLADGEELTPPIIR-----HNVDKAIVR 257  
  
QY 59 FATPDGRGFHDL-----LRPVDNFNQAMQGLRSVLARGQSPELRA----- 96  
Db 258 YDRDGDGHQYDVSAFIKSMRGSVDVDAALHYLARIMIDAGEDPRFTARRLVIHASEDVGWAD 317  
  
QY 97 -----AAALLEGVHADEQLMQMTLHL 117  
Db 318 PQALSVAAVAASQAVALTGMPEARINLAQATIH 350  
  
RESULT 9  
ADY06856  
ID ADY06856 standard; protein; 1132 AA.  
XX  
AC ADY06856;  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polypeptide seqid 62671.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
XX protein content.  
XX Unidentified.  
XX  
XX US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX

DR WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 62671; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at

CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring

CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous

CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or

CC content. This is the amino acid sequence of a plant full length insert

CC polypeptide that can be used in the recombinant DNA construct of the

CC invention.

XX Sequence 1132 AA;

XX

Query Match 13.1%; Score 80; DB 8; Length 1132;

Best Local Similarity 27.2%; Pred. No. 19;

Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;

QY 38 SIEPHSRUYPERLADRLVLLDFATPDGPHDLRLPVDNFQAMQGLRS-----VLAEGQ 90

Db 831 STEPH-----DVIAPDR-LTDLPLPPNDPNHTVMHIOAQSTAQSHALDGGK 874

QY 91 SPELRAAALAEQMHAD-EQLMQMTLHLHKV 121

Db 875 DPAHATSSLVKTHSNMEPVQKSISQLHDI 906

RESULT 10

AAB41479

ID AAB41479 standard; protein; 165 AA.

XX

XX AAB41479;

XX

08-FEB-2001 (first entry)

XX

Human ORFX ORF1243 polypeptide sequence SEQ ID NO:2486.

XX

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

XX vulnery; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;

XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

XX immunosuppressant; thrombolytic; coagulant; vasotropic; antidiabetic;

XX hypotensive; dermatological; immunosuppressive; antiinflammatory;

XX antiviral; antibacterial; antifungal; antirheumatic; antihypertensive;

XX antinaemic; gene therapy; cancer; proliferative disorder; hypertension;

XX neurodegenerative disorder; osteoarthritis; graft vs host disease;

XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

XX cholesterol ester storage; systemic lupus erythematosus; infection;

XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

XX bone damage; cartilage damage; antinflammatory disease; coagulation;

XX thrombosis; contraceptive.

XX

Homo sapiens.

OS

XX

WO200058473-A2.

PN

XX

05-OCT-2000.

PD

XX

31-MAR-2000; 2000WO-US008621.

XX

31-MAR-1999; 99US-0127607P.

PR

02-APR-1999; 99US-0127636P.

PR

05-APR-1999; 99US-0127728P.

PR

30-MAR-2000; 2000US-00540763.

XX

(CURA-) CURAGEN CORP.

PA

XX

Shinkets RA, Leach M;

PI

XX

WPI; 2000-602362/57.

DR

DR N-PSDB; AAC75688.

XX

Novel nucleic acids and peptides derived from open reading frame X,

PT useful for treating e.g. cancers, proliferative disorders,

PT neurodegenerative disorders and cardiovascular disease.

XX

Claim 11; Page 1789-1790; 5507pp; English.

XX

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX

CC sequences have activities such as: cytostatic; hepatotropic; vulnery;

CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; vulnery;

CC anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant;

CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;

CC dermatological; immunosuppressive; antiinflammatory; antibacterial;

CC antiviral; antifungal; antirheumatic; antihypertensive; antinaemic. The

CC sequences can be used for determining the presence of or predisposition

CC to, or preventing or treating pathological conditions associated with an

CC ORFX-associated disorder. The nucleic acids can be used to express ORFX

CC proteins in gene therapy vectors. The proteins and nucleic acids may be

CC used to treat cancers, proliferative disorders, neurodegenerative

CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,

CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester

CC storage, systemic lupus erythematosus, severe combined immunodeficiency

CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune

CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and

CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to

CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX

Sequence 165 AA;

XX

Query Match 12.9%; Score 78.5; DB 3; Length 165;

Best Local Similarity 25.8%; Pred. No. 2-2;

Matches 23; Conservative 19; Mismatches 32; Indels 15; Gaps 3;

QY 8 HIGIEQLSAISLDQERSLPGRYALLPDQGSIEPHISRLYPERLADRLVLLDFATPDGPH 67

Db 36 HRWIBELGGMNF-----MAISKQGLVTPELAGTILRGVTRKSILEVA-PDLGLE 84

QY 68 DLLRPVDFNQAMQGLRSVLAEQSPELRA 96

Db 85 PVERKIDVDELDDGVR-----GEFPEVFA 109

RESULT 11

ABP10391

ID ABP10391 standard; protein; 165 AA.

XX

ABP10391;

XX

24-JUN-2002 (first entry)

DT

XX

Human ORFX protein sequence SEQ ID NO:20764.

DE

XX

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

XX degenerative disorder; osteoarthritis; neurodegenerative disorder;

XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

XX hypertension; hypothyroidism; cholesterol ester storage disease;

XX immune deficiency; immune disorder; infectious disease;

XX

KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KW myasthenia gravis.

OS Homo sapiens.

PN WO200192523-A2.

XX 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN26143.

XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and autoimmune disorders.

XX Disclosure; SEQ ID NO 20764; 1037pp; English.

XX The present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
CC storage disease, various immune deficiencies and disorders, infectious  
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, or periodontal disease, and for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues and conditions resulting from  
CC systemic cytokine damage. N.B. The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 165 AA;

Query Match 12.9%; Score 78.5; DB 5; Length 165;  
Best Local Similarity 25.8%; Pred. No. 2.2;  
Matches 23; Conservative 19; Mismatches 32; Indels 15; Gaps 3;

QY 8 HIGIEQLSALSDDOERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFATPDRGFH 67

DB 36 HRWIEEGGNF-----MAISKDGLQVTPELAGTILRGVTRKSIILEVA-PDUGLE 84

QY 68 DLLRPVDFNQMGRLSVLAEGSQPELRA 96

DB 85 PVERKIDVDELLDGVR-----GEFPEVFA 109

RESULT 12

ID AAB70968

XX AAB70968 standard; protein; 4924 AA.

AC AAB70968;

XX

DT

XX 28-AUG-2001 (first entry)

DE S. spinosa protein fragment encoded by ORF21, SEQ ID 48.

XX

KW Forosamine; trimethylrhannose; polyketide synthase; biosynthesis;  
KW spinosyn; polyketide aglycone; transgenic plant; insect resistance;  
KW macrolide; insecticidal; polyketide synthase.

XX

OS Saccharopolyspora spinosa.

XX

PN DE19957268-A1.

XX

PD 08-MAR-2001.

XX

PF 29-NOV-1999; 99DE-01057268.

XX

PR 27-AUG-1999; 99DE-01040596.

XX

PA (FARB ) BAYER AG.

XX

PI Eberz G, Moehrlie V, Froede R, Velten R, Salas JA;

XX

DR WPI; 2001-267102/28.

DR

N-PSDB; AAF88338.

XX

New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for

recombinant production of insecticidal spinosyns and their derivatives.

PS

Claim 57; Page 264-284; 354pp; German.

XX

This invention describes a novel method nucleic acid (I) and its encoded  
CC polypeptide (II) containing at least one region that encodes an enzymatic  
CC activity involved in biosynthesis of spinosyns. (I) are used (i) to  
CC identify, inactivate or modulate genes involved in the biosynthesis of  
CC (ii); (ii) to generate a library of polyketide synthases; (iii) for  
CC adding forosamine or trimethylrhannose to a spinosyn or polyketide  
CC aglycone; and (iv) for recombinant production of the corresponding  
CC enzymes, which are used for production of (II), their precursors or  
CC derivatives, including production of transgenic plants that express (II)  
CC and thus have increased resistance to insects. (I) are also useful as  
CC markers for sequencing of the Saccharopolyspora spinosa genome. (II) are  
CC macrolides with insecticidal, but not antibacterial, activity, and can  
CC also be used to raise specific antibodies, useful for identifying  
CC expression clones in a gene bank. Cells transformed with (I) may produce  
CC (II) at significantly increased levels or produce new derivatives of  
CC (II). This sequence represents an S. spinosa polyketide synthase

XX Sequence 4924 AA;

Query Match 12.9%; Score 78.5; DB 4; Length 4924;  
Best Local Similarity 27.5%; Pred. No. 1.9e+02;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

QY 5 TAAHIGIEQLSALSDDOERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFATPDR 64

DB 4795 TFAELGFDLSLTAVELNRNLNAVTV--LRUPPTLVFDHPTLALSEQVLPALV---AFPDN 4849

QY 65 GFHDLRPVDFNQMGRLSVLAEGSQPELRAAAALLEGQMA 106

DB 4850 GIESLLAELD-----RLDTTLAQGFSPLEDOAKVAERLHA 4885

RESULT 13

AAV39300

ID AAV39300 standard; protein; 4928 AA.

XX

AC AAV39300;

XX

DT 01-DEC-1999 (first entry)

XX

DE Spnd a polyketide synthase.

XX

KW Spinosyn biosynthetic enzyme; open reading frame; ORF;

KW insecticidal microlides; arachnid; nematode; insect; polyketide;  
KW polyketide synthase; PKS; extender module; initiator module;  
KW acyl transferase domain; AT; acyl carrier protein; ACP;  
KW beta-ketosynthase domain; KS; KR; dehydratase domain; DH;  
KW enoyl reductase domain; ER; beta-ketoreductase; insecticide.  
XX Saccharopolyspora spinosa.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..424  
FT /label= KS5  
FT /note= "Beta-ketosynthase domain: part of extender module 5"  
FT Domain 539..866  
FT /label= AT5  
FT /note= "Acyl transferase domain: part of extender module 5"  
FT Domain 893..1078  
FT /label= DH5  
FT /note= "Dehydratase domain: part of extender module 5"  
FT Domain 1394..1565  
FT /label= KR5  
FT /note= "Beta-ketoreductase domain: part of extender module 5"  
FT Domain 1645..1726  
FT /label= ACP5  
FT /note= "Acyl carrier protein domain: part of extender module 5"  
FT Domain 1748..2172  
FT /label= KS6  
FT /note= "Beta-ketosynthase domain: part of extender module 6"  
FT Domain 2283..2613  
FT /label= AT6  
FT /note= "Acyl transferase domain: part of extender module 6"  
FT Domain 2916..3095  
FT /label= KR6  
FT /note= "Beta-ketoreductase domain: part of extender module 6"  
FT Domain 3188..3269  
FT /label= ACP6  
FT /note= "Acyl carrier protein domain: part of extender module 6"  
FT Domain 3291..3713  
FT /label= KS7  
FT /note= "Beta-ketosynthase domain: part of extender module 7"  
FT Domain 3825..4153  
FT /label= AT7  
FT /note= "Acyl transferase domain: part of extender module 7"  
FT Domain 4344..4638  
FT /label= KR7  
FT /note= "Beta-ketoreductase domain: part of extender module 7"  
FT Domain 4725..4806  
FT /label= ACP7  
FT /note= "Acyl carrier protein domain: part of extender module 7"  
XX  
PN WO9946387-A1.  
XX  
PD 16-SEP-1999.  
XX  
PF 16-FEB-1999; 99WO-US0003212.  
XX  
PR 09-MAR-1998; 98US-00036987.  
XX  
PA (DOWC ) DOW AGROSCIENCES LLC.  
XX Baltz RH, Broughton MC, Crawford KP, Madduri K, Merlo DJ;  
PI treadway PJ, Turner JR, Waldron C;

XX WPI: 1999-551414/46.  
DR N-PSDB; AA221501.  
XX New spinosyn biosynthetic genes from Saccharopolyspora spinosa, useful for production of insecticidal spinosyn compounds.  
FT  
XX  
PS Claim 1; Page 113-129; 190pp; English.  
XX  
XX This is the amino acid sequence of the product of the spnD gene. The protein is involved in spinosyn biosynthesis. The spnD gene is one of 23 genes and open reading frames contained in an 80kb DNA sequence AAZ21501. Spinosyns are insecticidal microlides which are useful for the control of arachnids, nematodes and insects. Biosynthesis of spinosyns occurs via stepwise condensation and modification of carboxylic acid precursors generating a linear polyketide which is modified further. The DNA sequence contains a central region of approximately 55kb which has homology to the DNA encoding the polyketide synthases (PKS) of known macrolide producers. The spinosyn PKS DNA region consists of 5 ORFs with stop codons at the end of acyl carrier protein (ACP) domains. Together the PKS polypeptides (AAV39297-Y39301) of which this sequence is one, form a complex consisting of an initiator module, spnA, and several extender modules spnB-spnE. Each extender module adds a specific acetyl Co-A precursor to a growing polyketide chain, and modifies the beta-keto group in a specific manner. A module in a PKS polypeptide consists of several domains with specific functions. The initiator module has an acyl transferase (AT) domain, and an acyl carrier protein (ACP) domain. The extender modules have the same domains plus a beta-ketosynthase (KS) domain, and optionally a beta-ketoreductase domain, a dehydratase (DH) domain, and an enoyl reductase (ER) domain. The last extender module terminates with a thiolester domain. The products of the genes present in the upstream region the PKS genes have been assigned names spnF-spnS CC AAV39302-Y39315 and are responsible for different modifications in CC spinosyn biosynthesis. There are also two ORFs ORF15 and ORF16 present CC immediately upstream of spnS, producing polypeptides AAY39316-Y39317, and CC two ORFs ORF1 and ORF2 present downstream of the PKS region producing CC polypeptides AAY39318-Y39319. The genes are useful to improve yields of CC spinosyns, and for creating new spinosyns e.g. by mutagenesis, or CC interruption of steps in spinosyn biosynthesis. The modified spinosyns CC may be a new insect control agent or serve as substrates for further CC chemical modification and the creation of new semi-synthetic spinosyns. CC The genes are also useful to isolate similar sequences from S. spinosa or CC other species by hybridization  
XX  
SQ Sequence 4928 AA;  
Query Match 12.9%; Score 78.5; DB 2; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 1.9e+02;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
QY 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDDQSTEPHISRLYPERLADRVLLDFATPDR 64  
Db 4799 TFAELGFDLSLTAVELNRLNAVVG--LRLPPTLVDFHPTPLALSEQLVPLV---AEPDN 4853  
QY 65 GFHDLRLPVDNFQAMQGLRSVLAEQGSPELRAAAALLEQMHA 106  
Db 4854 GIESLLAEUD-----RLDTTLAQGPSIPLEDOAKVAERLHA 4889  
RESULT 14  
ADJ67793  
ID ADJ67793 standard; protein; 294 AA.  
XX  
AC ADJ67793;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE B. subtilis gamma/tau ATP binding domain.  
XX  
KW DNA polymerase; DNA sequencing; DNA amplification.  
XX Bacillus subtilis.  
XX



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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 19:07:20 ; Search time 12.2967 Seconds  
(without alignments)  
946.773 Million cell updates/sec  
Title: US-10-813-908A-3  
Perfect score: 609  
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMQMTLHLHKV 121  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 80:\*  
1: Piri:\*  
2: Piri2:\*  
3: Piri3:\*  
4: Piri4:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304.5	50.0	122	2	T43589
2	302	49.6	122	2	D35392
3	276	45.3	121	2	B83432
4	83.5	13.7	353	2	S36249
5	76	12.5	761	2	S20458
6	74.5	12.2	275	2	E83412
7	74	12.2	355	2	T36273
8	73	12.0	369	2	B81039
9	73	12.0	403	2	B36151
10	72.5	11.9	429	2	JC4986
11	72.5	11.9	2218	2	B84683
12	72	11.8	491	2	E87270
13	71.5	11.7	186	2	B75590
14	71.5	11.7	986	2	AB2209
15	70	11.5	149	2	T03477
16	70	11.5	310	2	C95950
17	70	11.5	314	2	AC2878
18	70	11.5	325	2	E97654
19	70	11.5	489	2	F65125
20	70	11.5	9376	2	T14593
21	69	11.3	246	2	S39726
22	69	11.3	436	2	A75311
23	69	11.3	451	2	E90011
24	69	11.3	506	2	A99252
25	69	11.3	506	2	AC3034
26	69	11.3	563	2	S13786
27	69	11.3	820	2	T51186
28	68.5	11.2	302	2	B82036
29	68.5	11.2	420	2	AG0867

hypothetical protein Y0045 - Yersinia pestis plasmid pCD1  
C;Species: Yersinia pestis  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43589; T42884  
R;Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubake J. Bacteriol. 180, 5192-5202, 1998  
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.  
A;Reference number: 222578; MUID:98422474; PMID:9748454  
A;Accession: T43589  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-122 <HUP>  
A;Cross-references: UNIPROT:P61416; UNIPARC:UPI0000005173; EMBL:AF053946; NID:g29962222,  
A;Experimental source: strain KIM  
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998  
A;Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia  
A;Reference number: 222273; MUID:98427122; PMID:9746557  
A;Accession: T42884  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-122 <PER>  
A;Cross-references: UNIPARC:UPI0000005173; EMBL:AF074612; NID:g3822037; PIDN:AAC69795.1  
A;Experimental source: strain KIMS  
C;Genetics:  
A;Genome: plasmid pCD1  
A;Note: Y0045  
C;Superfamily: Yersinia pestis hypothetical protein Y0045

ALIGNMENTS

RESULT 1					
T43589					
hypothetical protein Y0045 - Yersinia pestis plasmid pCD1					
C;Species: Yersinia pestis					
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004					
C;Accession: T43589; T42884					
R;Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubake J. Bacteriol. 180, 5192-5202, 1998					
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.					
A;Reference number: 222578; MUID:98422474; PMID:9748454					
A;Accession: T43589					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: DNA					
A;Residues: 1-122 <HUP>					
A;Cross-references: UNIPROT:P61416; UNIPARC:UPI0000005173; EMBL:AF053946; NID:g29962222,					
A;Experimental source: strain KIM					
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998					
A;Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia					
A;Reference number: 222273; MUID:98427122; PMID:9746557					
A;Accession: T42884					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: DNA					
A;Residues: 1-122 <PER>					
A;Cross-references: UNIPARC:UPI0000005173; EMBL:AF074612; NID:g3822037; PIDN:AAC69795.1					
A;Experimental source: strain KIMS					
C;Genetics:					
A;Genome: plasmid pCD1					
A;Note: Y0045					
C;Superfamily: Yersinia pestis hypothetical protein Y0045					
Query Match	50.0%;	Score	304.5;	DB 2;	Length 122;
Best Local Similarity	54.1%;	Pred. No.	2e-23;		
Matches	66;	Conservative	19;	Mismatches	36;
Indels	1;	Gaps	1;		
Qy	1	MSR-ITAAHIGIEQLSAISLDQERSIPGRYALLPDQOSIEPHISRLYPERLADRVLLDF	59		
Db	1	MSRIITAPHIGIEKLSAISLEELSCGLPERYALPPDGHVPVEHLERLYPTAQSKESLWDF	60		
Qy	60	ATPDGRFHLLRPVDFNQAMQGLRSVLAEQSQSELRAAALLRQMHADEQLMQMTLHLH	119		
Db	61	ASPGYTFHGLHRAQDYRRELTQLSLTTSSQSELQAAAALLKCCQDDRLQLIILNLH	120		
Qy	120	KV	121		
Db	121	KV	122		
RESULT 2					
D35392					
hypothetical protein 3 - Yersinia enterocolitica					
C;Species: Yersinia enterocolitica					

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Jul-2000  
C/Accession: D35392  
R/Viitanen, A.M.; Toivanen, P.; Skurnik, M.  
J. Bacteriol. 172, 3152-3162, 1990  
A>Title: The lcrE gene is part of an operon in the lcr region of *Yersinia enterocolitica*  
A/Reference number: A35392; MUID:90264308; PMID:2160939  
A/Accession: D35392  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-122 <VII>  
A/Cross-references: UNIPARC:UPI00001798AF; GB:M32097  
C/Superfamily: *Yersinia pestis* hypothetical protein Y0045

Query Match 49.6%; Score 302; DB 2; Length 122;  
Best Local Similarity 53.4%; Pred. No. 3.5e-23;  
Matches 63; Conservative 19; Mismatches 36; Indels 0; Gaps 0;

QY 4 ITAAHTGIEOLSAISLDDQERSLPGRYALLPDGQSTIEPHISRLYPERLADRVLLDPATPD 63  
DB 5 ITAPHGIEKLSAISLEELSCGLPDRYALPDGHPVEPHLERLYPTAQSKRSLWDFASFG 64

QY 64 RGFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQMHAEQMLQMTLHLHKV 121  
DB 65 YTFGLHRAQDYRRELTQSLTTTSQSELOAAALLCQQDDDRLLQIILNLHKV 122

RESULT 3  
B83432  
Conserved hypothetical protein in type III secretion PA1701 [imported] - *Pseudomonas aeruginosa*  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: B83432  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: B83432  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-121 <STO>  
A/Cross-references: UNIPROT:O30534; UNIPARC:UPI00000D425B; GB:AE004597; GB:AE004091; NID:AE004091  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: PA1701  
C/Superfamily: *Yersinia pestis* hypothetical protein Y0045

Query Match 45.3%; Score 276; DB 2; Length 121;  
Best Local Similarity 47.9%; Pred. No. 1.4e-20;  
Matches 58; Conservative 19; Mismatches 44; Indels 0; Gaps 0;

QY 1 MSRTAAHTGIEOLSAISLDDQERSLPGRYALLPDGQSTIEPHISRLYPERLADRVLLDFA 60  
DB 1 MSRVGAHWGIERLDLAHAEPPAPPYPERHLLAPDGRPVETHVASLYPAQQAQQLFDYA 60

QY 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQMHAEQMLQMTLHLHK 120  
DB 61 RPQLEPHGLLRPGCDFQALRDLELATLPRQPALQAACLLGCDERDRLQALNLHLK 120

QY 121 V 121  
DB 121 V 121

RESULT 4  
S36249  
lipB protein - *Pseudomonas glumae*  
C/Species: *Pseudomonas glumae*  
C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: S36249  
R/Frenken, L.G.O.; Bos, J.W.; Visser, C.; Mueller, W.; Tommassen, J.; Verrige, C.T.  
Mol. Microbiol. 9, 579-589, 1993

A>Title: An accessory gene, lipB, required for the production of active *Pseudomonas glumae*  
A/Reference number: S36248; MUID:94018652; PMID:8412704  
A/Accession: S36249  
A/Molecule type: DNA  
A/Residues: 1-353 <PRE>  
A/Cross-references: UNIPROT:Q05490; UNIPARC:UPI000002CA54; EMBL:X70354; NID:949205; PID:949205  
C/Genetics:  
A/Gene: lipB  
C/Keywords: transmembrane protein  
F:19-40/Domain: transmembrane #status predicted <TMM>

Query Match 13.7%; Score 83.5; DB 2; Length 353;  
Best Local Similarity 33.6%; Pred. No. 1;  
Matches 36; Conservative 12; Mismatches 36; Indels 23; Gaps 5;

QY 21 DQERSLPGRYALLPDGQSTIEPHISRLYPER---LADRVLLDPATP-----DRGFHDLLR 71  
DB 157 DALAQLPDGGAVL--GDKLDPAAQMQLADRLTGEWAEPFGDEQRQRHDLR 214

QY 72 PVDFNQAMQGLRSVLAEGSQSPELRAA--AALAEQMHAEQMLQMTLH 116  
DB 215 -----IRIANDTTLSPEQKARLAALDAQLTPDERAQAALH 251

RESULT 5  
S20458  
pqgF protein - *Klebsiella pneumoniae*  
C/Species: *Klebsiella pneumoniae*  
C/Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
C/Accession: S20458  
R/Neulenberger, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.  
Mol. Gen. Genet. 232, 284-294, 1992  
A>Title: Nucleotide sequence and structure of the *Klebsiella pneumoniae* pqg operon.  
A/Reference number: S20452; MUID:92212293; PMID:1313537  
A/Accession: S20458  
A/Molecule type: DNA  
A/Residues: 1-761 <MEU>  
A/Cross-references: UNIPROT:P27508; UNIPARC:UPI0000132135; EMBL:X58778; NID:943903; PID:943903  
C/Genetics:  
A/Gene: pqgF  
C/Superfamily: pyrroloquinoline quinone synthesis F protein

Query Match 12.5%; Score 76; DB 2; Length 761;  
Best Local Similarity 29.4%; Pred. No. 15;  
Matches 32; Conservative 13; Mismatches 26; Indels 38; Gaps 6;

QY 33 LPDQSQI-----EP-HISRLYPE-----RLADR--VLLDFATPPRGPH 67  
DB 612 LPDGASLAALRLAQHCEPLFQRLRVEQQIGYVVSRYQRYVADRDLGLMALQSPDRRAG 671

QY 68 DLLR-----PVD---FNQAMQGLRSVLAEGSQSPELRAAAALAEQ 103  
DB 672 ELLRCGKDFLRQLAPMDENTFPLQORLAQAQRASRPPEARALSALRQE 720

RESULT 6  
E83412  
streptomycin 3''-phosphotransferase PA1858 [imported] - *Pseudomonas aeruginosa* (strain: 15-Sep-2000)  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: E83412  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: E83412  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-275 <STO>  
A/Cross-references: UNIPROT:O912N7; UNIPARC:UPI00000C54D6; GB:AE004612; GB:AE004091; NID:AE004091  
A/Experimental source: strain PA01

C;Genetics:  
A;Gene: str; PA1858  
C;Superfamily: streptomycin 6-kinase





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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 95.0293 seconds  
(without alignments)  
1177.815 Million cell updates/sec

Title: US-10-813-908A-3  
Perfect score: 609  
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMQMTLHLHKV 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	609	100.0	121	2	Q8GA93	aeromonas s
2	588	96.6	121	2	Q699R5	aeromonas h
3	585	96.1	121	2	Q5CCA2	aeromonas s
4	502	82.4	121	2	Q5XL09	aeromonas h
5	500	82.1	124	2	Q6TLW7	aeromonas h
6	381	62.6	121	2	Q7N0W6	photorhabdu
7	370	60.8	121	2	Q84GZ0	photorhabdu
8	305.5	50.2	122	1	YSCX_YEREN	P21208 yersinia en
9	304.5	50.0	122	1	YSCX_YERPE	P61416 yersinia pe
10	304.5	50.0	122	2	Q663K4	yersinia ps
11	276	45.3	121	2	Q30534	pseudomonas
12	193	31.7	125	2	Q6QVR7	vibrio harv
13	187	30.7	125	2	Q66PU0	pasteurella
14	180	29.6	126	2	Q87P34	vibrio para
15	112.5	18.5	125	2	Q2SC40	9GAMM
16	92.5	15.2	202	2	Q2J353	RHOA
17	90.5	14.9	722	2	Q4Q0R9	DESAC
18	84	13.8	464	2	Q6N0H8	RHOA
19	83.5	13.7	205	2	Q3IXK4	RHOA4
20	83.5	13.7	353	1	LIFO_BURGL	
21	83.5	13.7	3574	2	Q5Y9G5	9ACTO
22	83	13.6	1462	2	Q3XUH1	9PROT
23	83	13.6	10917	2	Q31N66	9ACTO
24	82.5	13.5	338	2	Q2IYP4	RHOA
25	82	13.5	456	2	Q7WP97	BORBR
26	82	13.5	589	2	Q3UJY8	MOUSE
27	82	13.5	618	2	Q3UK73	MOUSE
28	82	13.5	673	2	Q80T90	MOUSE
29	82	13.5	1316	2	Q6PGE3	MOUSE
30	81.5	13.4	325	2	Q6N3W9	RHOA
31	81.5	13.4	363	2	Q6A7Z4	PROAC

32	81.5	13.4	369	2	Q37N29	RHOA
33	81.5	13.4	456	2	Q6NGZ6	CORDI
34	81	13.3	252	2	Q407D6	9RHO
35	80.5	13.2	133	2	Q2SH42	9GAMM
36	80	13.1	233	2	Q91IE2	9REOV
37	80	13.1	332	2	Q3AUD6	CHLCH
38	80	13.1	688	2	Q3RJE9	RALME
39	79.5	13.1	202	2	Q37BB5	RHOA
40	79	13.0	331	2	Q2JN45	9CYAN
41	78.5	12.9	246	2	Q7MK07	VIBVY
42	78.5	12.9	450	2	Q5FU22	GLUOX
43	78.5	12.9	501	2	Q47T70	THERFY
44	78.5	12.9	514	2	Q2NHY0	XANOR
45	78.5	12.9	533	2	Q7U464	SYNXP

ALIGNMENTS

RESULT 1  
Q8GA93\_AERSA  
ID Q8GA93\_AERSA PRELIMINARY; PRT; 121 AA.  
AC Q8GA93;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE AsC protein.  
GN Name=ascX;  
OS Aeromonas salmonicida subsp. salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RX MEDLINE=22262111; PubMed=12374830;  
RA DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RA "Evidence for a type III secretion system in Aeromonas salmonicida  
subsp. salmonicida.";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;  
RA "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida  
type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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CC -----  
CC EMBL; AJ458292; CAD30216.1; -; Genomic DNA.  
DR EMBL; AJ616218; CAB83103.1; -; Genomic DNA.  
DR InterPro; IPR012672; TRSS\_YscX.  
DR TIGRFAMs; TIGR02502; type\_III\_YscX; 1.  
SQ SEQUENCE 121 AA; 13576 MW; 3016F377DA9080E CRC64;

Query Match 100.0%; Score 609; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2.8e-50;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSRTAAHIGIEQLSAISLDQDRLSPGRYALLPDGQSI	PHISRLRYPERLADRVLLDFA	60
Db	1	MSRTAAHIGIEQLSAISLDQDRLSPGRYALLPDGQSI	PHISRLRYPERLADRVLLDFA	60
Qy	61	TPDRGFHDLRLPVDVFNQAMQGLSVLAEGQSP	ELRAAAALLENQHADEQLMQMTLHLHK	120
Db	61	TPDRGFHDLRLPVDVFNQAMQGLSVLAEGQSP	ELRAAAALLENQHADEQLMQMTLHLHK	120
Qy	121	V	121	
Db	121	V	121	

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CC -----
DR EMBL; AJ749609; CAG44553.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13651 MW; 9EAF6B74CA9B7C91 CRC64;

Query Match 96.1%; Score 585; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 5.6e-48;
Matches 116; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
QY 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGOSPELRAAAALAEQMHAEQMLQMTLLHLHK 120
DB 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGOSPELRAAAALAEQMHAEQMLQMTLLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 4
Q5XL09_AERHY PRELIMINARY; PRT; 121 AA.
AC Q5XL09;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
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CC -----
DR EMBL; AY763611; AAV30228.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13674 MW; 5083CE413DD9F7D8 CRC64;

Query Match 82.4%; Score 502; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 4.9e-40;
Matches 98; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
QY 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGOSPELRAAAALAEQMHAEQMLQMTLLHLHK 120
DB 61 EPDRGFYDLRRPRDFSLAMQGLRAVLMEGQTAEKAGALLERHMEDEQLMQMTLLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 5
Q6TLW7_AERHY PRELIMINARY; PRT; 121 AA.
AC Q6TLW7;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91814.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13635 MW; A136E074CA84665B CRC64;

Query Match 96.6%; Score 588; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 2.9e-48;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
QY 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGOSPELRAAAALAEQMHAEQMLQMTLLHLHK 120
DB 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGOSPELRAAAALAEQMHAEQMLQMTLLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 3
Q5CCA2_AERSO PRELIMINARY; PRT; 121 AA.
AC Q5CCA2;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AscX protein.
GN Name=ascX;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burt S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150(2005).
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ID Q6TLM7_AERHY PRELIMINARY; PRT; 124 AA.
AC Q6TLM7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Mexino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
pathogenesis."
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL: AY394563; AAR26334.1; -; Genomic_DNA.
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 124 AA; 13979 MW; ECC3860471D7FBCE CRC64;

Query Match 82.1%; Score 500; DB 2; Length 124;
Best Local Similarity 81.0%; Pred. No. 7.9e-40;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFA 60
Db 4 MSRTAAHIGIEQLSALTDEQSLPGRYALLPDGQSIIEPHINRLYPERLAERALLDFA 63

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPQLRAAAALAEQMHADQLMOMTLHLHK 120
Db 64 APAHGFDLLRPDFTLMAQGLRLKEGGTDELMAASVLEQMHEDQLMOMTLHLHK 123

Qy 121 V 121
Db 124 V 124

RESULT 6
Q7N0W6_PHOLL PRELIMINARY; PRT; 121 AA.
AC Q7N0W6;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Type III secretion protein ScTx.
GN Name=ScTx; OrderedLocusNames=plu3763;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbr886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Bouraux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Detose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Signier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
DR EMBL: BX571871; CAE16135.1; -; Genomic_DNA.
DR Photolista; plu3763; -;
DR BioCyc: PLUM243265:PLU3763-MONOMER; -;
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
KW Complete proteome.
SQ SEQUENCE 121 AA; 13453 MW; E13DEE33DE590A48 CRC64;

Query Match 62.6%; Score 381; DB 2; Length 121;
Best Local Similarity 62.8%; Pred. No. 1.9e-28;
Matches 76; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFA 60
Db 1 MSRTAAHIGIEQLTAISREIEVSLPDRYALLPDGQSVETHAARLYPANKADQALLAFA 60

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPQLRAAAALAEQMHADQLMOMTLHLHK 120
Db 61 CPQDGFHALLRPDHFQAVSGLRTILQOGNDIRVQHAVSLLENMNDQEQLLQMALHLHK 120

Qy 121 V 121
Db 121 V 121

RESULT 7
Q84GZ0_PHOLU PRELIMINARY; PRT; 121 AA.
ID Q84GZ0;
AC Q84GZ0;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE LesB.
GN Name=LesB;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus."
RL Trends Microbiol. 10:541-545(2002).
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CC -----
DR EMBL: AY144116; AAO18048.1; -; Genomic_DNA.
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13472 MW; CEE63BE1ED0E3802 CRC64;

Query Match 60.8%; Score 370; DB 2; Length 121;
Best Local Similarity 61.2%; Pred. No. 2.1e-27;
Matches 74; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFA 60
Db 1 MSRTAAHIGIEQLTAISREIEVSLPDRYALLPDGQSVETHAARLYPANKADQALLAFA 60

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPQLRAAAALAEQMHADQLMOMTLHLHK 120
Db 61 CPQDGFHALLRPDHFQAVSGLRTILQOGNDIRVQHAVSLLENMNDQEQLLQMALHLHK 120

Qy 121 V 121
Db 121 V 121

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RESULT 8
YSCX_YEREN          STANDARD;          PRT;    122 AA.
AC P21208; O68696;
DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1991, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Yop proteins translocation protein X.
GN Names: yscX;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OG Plasmid pYval27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.
RC STRAIN=Serotype O:3; PLASMID=pYV;
RA MEDLINE=90264308; PubMed=2160939;
RX Viitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Yersinia
enterocolitica O:3";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:8 / Biotype 2; PLASMID=pYve227;
RA Iriarte M., Lambert M., Kerbourch C., Cornelis G.R.;
RT "Detailed genetic map of the pYve227 plasmid of Yersinia
enterocolitica serotype O:3";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RX DOI=10.1128/IAI.69.7.4627-4638.2001;
RX Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
calcium-response plasmid reveals a new virulence plasmid-associated
replicon";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYval27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foultier B., Cornelis G.R.;
RT "DNA sequence and analysis of the pYval27/90 virulence plasmid of
Yersinia enterocolitica strain A127/90";
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RP FUNCTION.
RC PLASMID=pYV;
RX MEDLINE=99102336; PubMed=9882687;
RA Iriarte M., Cornelis G.R.;
RT "Identification of SYN, yscX, and yscY, three new elements of the
Yersinia Yop virulon";
RL J. Bacteriol. 181:675-680(1999).
CC -!- INDUCTION: Temperature seems to play the major role in regulation
of transcription of the lcrE-containing operon of pYV, whereas
Ca(2+) concentration has only a moderate effect at 37 degrees
Celsius, and no effect at room temperature.
CC -!- DOMAIN: The region between residues 50 and 110, which contains the
predicted coiled coil domain, is essential for interaction with
yscY (By similarity).
CC -!- MISCELLANEOUS: May possess both an mRNA signal and a ysc-dependent
signal capable of directing its export through the type III
secretion system (By similarity).
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CC -----
DR EMBL; M32097; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL; AF102990; AD15820.1; -; Genomic_DNA.
DR EMBL; AF336309; AAK69218.1; -; Genomic_DNA.
DR EMBL; AY150843; AAN37521.1; -; Genomic_DNA.
DR InterPro; IPR012672; TSS YscX.
DR TIGRPFAMs; TIGR02502; type_III_YscX; 1.
KW Coiled coil; Plasmid.
FT CHAIN 1 122 Yop proteins translocation protein X.
FT FTID=PRO_0000086499.
FT COILED 71 87 Potential.
FT VARIANT 29 29 D -> E (in plasmid pYve8081 and plasmid
FT pYval27/90).
SQ SEQUENCE 122 AA; 13742 MW; 050F5E2D6909BB00 CRC64;
Query Match 50.2%; Score 305.5; DB 1; Length 122;
Best Local Similarity 54.1%; Pred. No. 3.2e-21;
Matches 66; Conservative 19; Mismatches 36; Indels 1; Gaps 1;
QY 1 MSR-ITAAHIGTEOLSAISLDDQERSLPGRYALLPDQSIPIHISLYPERLADRVLLDF 59
Db 1 MSRIITAPHIGIEKLSAISLELSCLPDRYALPPDCHPVEPHERLYPTAQSKRSLWDF 60
QY 60 ATPDGRGFHDLRPVDFNQAGLSRVLAEGQSPELRAAAALAEQMHADQLQMTHLLH 119
Db 61 ASPGYTFHGLHRAQDYRRELTQLSLTTTSQSSELQAAALAKCQDDRLQLILNLLH 120
QY 120 KV 121
Db 121 KV 122
RESULT 9
YSCX_YERPE
ID YSCX_YERPE STANDARD; PRT; 122 AA.
AC P61416; O68696;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAY-2006, entry version 17.
DE Yop proteins translocation protein X.
GN Name=yscX; Ordered locus names=YPCD1.36c, Y5042, Y0045, pCD47;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
Yersinia pestis KIMS";
RL Infect. Immun. 66:4611-4623(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCreedy P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
pestis";
RL J. Bacteriol. 180:5192-5202(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagele K., Karlyshev A.V.,
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RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Ewin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.B., Coulter S.N., Folger K.K., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forberg A., Francis M.S.;
RT "Mapping of a YacY Binding Domain within the LcrH Chapterone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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CC -----
DR EMBL; AF010150; AAC45942.1; -; Genomic_DNA.
DR EMBL; AE004597; AAG05090.1; -; Genomic_DNA.
DR EMBL; DQ000666; AAY17109.1; -; Genomic_DNA.
DR PIR; B83432; B83432.
DR BioCyc; PAER287; PA1701-MONOMER; -.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
KW Complete proteome.
SQ SEQUENCE 121 AA; 13722 MW; 91EBF2450DEC87B6 CRC64;
Query Match 45.3%; Score 276; DB 2; Length 121;
Best Local Similarity 47.9%; Pred. No. 2.1e-18;
Matches 58; Conservative 19; Mismatches 44; Indels 0; Gaps 0;
QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
DB 1 MSRVGAHWIGIERLDLAHAEFPAPPLPERHLLAPDGRPVETHVASLYPAQAQQLPFDYA 60
QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMADEQLMOMTLH 120
DB 61 RPQLEFGLRLPGDFRQALRDLRLALTLPQPALQAACLLGRDEDERLLQNALNLLHK 120
QY 121 V 121
DB 121 V 121
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Q6QVR7 VIBHA PRELIMINARY; PRT; 125 AA.
AC Q6QVR7;
DT 03-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE VscX.
GN Names=vscX;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Basler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY524044; AAS13314.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.

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SQ SEQUENCE 125 AA; 14484 MW; F48F6AD8560AA8F2 CRC64;
Query Match 31.7%; Score 193; DB 2; Length 125;
Best Local Similarity 36.0%; Pred. No. 2e-10;
Matches 45; Conservative 23; Mismatches 53; Indels 4; Gaps 1;
QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
DB 1 MSRTSLNVGIEGFTHSVLEQVENGFPPQRFQLPDQAATATHEKLYELRPSQYLMSLA 60
QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMADEQLMOMTLH 116
DB 61 KPKLTRSELLRPDKYRQQFDTTQORLREVAQKNGSHALNQALETLQSTQDQRYLTMALN 120
QY 117 LLHKV 121
DB 121 LLIQV 125
RESULT 13
Q66PU0 PASPI PRELIMINARY; PRT; 125 AA.
AC Q66PU0;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative TTSS protein X.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
RT three secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY647223; AAU11476.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 125 AA; 14447 MW; 0671D3457BD3860E CRC64;
Query Match 30.7%; Score 187; DB 2; Length 125;
Best Local Similarity 35.2%; Pred. No. 7.3e-10;
Matches 44; Conservative 24; Mismatches 53; Indels 4; Gaps 1;
QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
DB 1 MSRTSLNVGIEGFTHSVLEQVENGFPPQRFQLPDQAATATHEKLYELRPSQYLMSLA 60
QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMADEQLMOMTLH 116
DB 61 RPKLTHLELLRPDKYRQQFDTTQORLQELAQKNGSHALNQALETLQSTQDQRYLTMALN 120
QY 117 LLHKV 121
DB 121 LLIQV 125
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Q87P54 VIBPA PRELIMINARY; PRT; 126 AA.
AC Q87P54;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative type III secretion protein.
GN OrderedLocusNames=vPI664;
OS Vibrio parahaemolyticus.

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 22.3309 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-3  
Perfect score: 609  
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMQMTLLHLHKV 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA.\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	266	43.7	262	2	US-09-252-991A-30169
2	83.5	13.7	353	1	US-08-034-650-11
3	83.5	13.7	353	1	US-08-449-015-11
4	78.5	12.9	4928	2	US-09-036-987A-5
5	78.5	12.9	4928	2	US-09-370-700-5
6	78.5	12.9	4928	2	US-09-603-207-5
7	78.5	12.9	4928	3	US-10-329-148A-5
8	78	12.8	294	2	US-09-716-964B-23
9	76	12.5	810	2	US-09-489-039A-9748
10	74.5	12.2	602	2	US-09-252-991A-30458
11	73.5	12.1	429	2	US-09-252-991A-30376
12	73.5	12.1	513	2	US-09-833-745-50
13	72	11.8	2216	2	US-09-902-540-12221
14	71	11.7	293	2	US-09-252-991A-19896
15	71	11.7	386	2	US-09-270-767-42532
16	71	11.7	457	2	US-09-605-703B-2586
17	70.5	11.6	156	2	US-09-252-991A-31384
18	70.5	11.6	1651	2	US-09-543-681A-6604
19	69.5	11.4	235	2	US-09-489-039A-13178
20	69.5	11.4	502	2	US-09-489-039A-10638
21	69.5	11.4	574	2	US-09-605-703B-2288
22	69.5	11.4	927	2	US-09-252-991A-20340
23	69	11.3	233	2	US-09-489-039A-10313
24	69	11.3	273	2	US-10-104-047-2397
25	69	11.3	370	2	US-09-489-039A-8211
26	69	11.3	452	2	US-09-925-637-16

27	69	11.3	485	2	US-09-252-991A-24868	Sequence 24868, A
28	69	11.3	748	1	US-08-997-080-154	Sequence 154, App
29	69	11.3	748	1	US-08-997-362-154	Sequence 154, App
30	69	11.3	748	2	US-09-095-855-154	Sequence 154, App
31	69	11.3	748	2	US-09-324-542-154	Sequence 154, App
32	69	11.3	748	2	US-09-205-426-154	Sequence 154, App
33	68.5	11.2	700	2	US-09-252-991A-29072	Sequence 29072, A
34	68.5	11.2	2560	2	US-09-949-016-11554	Sequence 11554, A
35	68	11.2	1147	2	US-09-902-540-13965	Sequence 13965, A
36	67.5	11.1	255	2	US-09-252-991A-17010	Sequence 17010, A
37	67.5	11.1	275	2	US-09-036-987A-7	Sequence 7, Appli
38	67.5	11.1	275	2	US-09-370-700-7	Sequence 7, Appli
39	67.5	11.1	275	2	US-09-603-207-7	Sequence 7, Appli
40	67.5	11.1	275	3	US-10-329-148A-7	Sequence 7, Appli
41	67.5	11.1	291	2	US-09-489-039A-13316	Sequence 13316, A
42	67.5	11.1	544	2	US-09-252-991A-19064	Sequence 19064, A
43	67.5	11.1	612	2	US-09-902-540-13545	Sequence 13545, A
44	67.5	11.1	684	2	US-09-605-703B-654	Sequence 654, App
45	67.5	11.1	684	2	US-09-605-703B-656	Sequence 656, App

ALIGNMENTS

RESULT 1  
US-09-252-991A-30169  
; Sequence 30169, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30169  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30169

Query Match	43.7%	Score 266;	DB 2;	Length 262;
Best Local Similarity	46.3%	Pred. No. 1.3e-21;		
Matches	56;	Conservative	20;	Mismatches 45; Indels 0; Gaps 0;
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Db	142	MSRVGAWHIGIERLDLAHAEPFPAPPLPERHLLAPDGRPVETHVASLYPAQQAQORLFDYA	201	
Qy	61	TPDRGFHLLRPVDFNQMOGLRSVLAEQSGPELRAAALQEQMHADEQLMQMTLLHLHK	120	
Db	202	RPOLFGLLRPGDFRQALRDLRLATLPQPALQAACLLGERDEQRLIQMAPNLHK	261	
Qy	121	V 121		
Db	262	V 262		
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US-08-034-650-11				
; Sequence 11, Application US/08034650				
; Patent No. 5641671				
; GENERAL INFORMATION:				
; APPLICANT: BOS, Jannetje W.				
; APPLICANT: FRENKEN, Leon G.				
; APPLICANT: VEREIPS, Cornelis T.				
; APPLICANT: VISSER, Christiaan				
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE				

;; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS  
;; NUMBER OF SEQUENCES: 13  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
;; STREET: 1615 L. Street, N.W.  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20036-5601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/034,650  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/727,235  
;; FILING DATE: 03-JUL-1991  
;; NAME: Kokulis, Paul N.  
;; REGISTRATION NUMBER: 16,773  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 861-3000  
;; TELEFAX: (202) 822-0944  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 353 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-034-650-11

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/449,015  
;; FILING DATE: 24-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/727,235  
;; FILING DATE: 03-JUL-1991  
;; NAME: Kokulis, Paul N.  
;; REGISTRATION NUMBER: 16,773  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 861-3000  
;; TELEFAX: (202) 822-0944  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 353 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-449-015-11

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Best Local Similarity 33.6%; Pred. No. 0.46;  
Matches 36; Conservative 12; Mismatches 36; Indels 23; Gaps 5;  
  
QY 21 DQERSLPGRVALLPDGQSIPEHISRLYPER---LADRVLLDFATP-----DRGFHDLRL 71  
Db 157 DALAQLPGDGA VL--GDKLDPAAQALDQRAALADRTLGAEAPFFGDEQRQRHDLR 214  
  
QY 72 PVDFNQAMQGLRSVLAEGOSPELRAA--AALLEQMHADQLMQMTLH 116  
Db 215 -----IRIANDTTLSPEQKAARLAALDAQLTPDERAQQAAALH 251

Query Match 13.7%; Score 83.5; DB 1; Length 353;  
Best Local Similarity 33.6%; Pred. No. 0.46;  
Matches 36; Conservative 12; Mismatches 36; Indels 23; Gaps 5;  
  
QY 21 DQERSLPGRVALLPDGQSIPEHISRLYPER---LADRVLLDFATP-----DRGFHDLRL 71  
Db 157 DALAQLPGDGA VL--GDKLDPAAQALDQRAALADRTLGAEAPFFGDEQRQRHDLR 214  
  
QY 72 PVDFNQAMQGLRSVLAEGOSPELRAA--AALLEQMHADQLMQMTLH 116  
Db 215 -----IRIANDTTLSPEQKAARLAALDAQLTPDERAQQAAALH 251

RESULT 3  
US-08-449-015-11  
; Sequence 11, Application US/08449015  
; Patent No. 5804409  
; GENERAL INFORMATION:  
; APPLICANT: BOS, Jannette W.  
; APPLICANT: FRENKEN, Leon G.  
; APPLICANT: VERIPS, Cornelis T.  
; APPLICANT: VISSER, Christiaan  
; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1615 L. Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 4  
US-09-036-987A-5  
; Sequence 5, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.  
; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow AgroSciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R.  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608



; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4928 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-036-987A-5

Query Match 12.9%; Score 78.5; DB 2; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 61;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
  
Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64  
Db 4799 TFAELGFDLSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853  
  
Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMH 106  
Db 4854 GIESLLAEID-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

## RESULT 5

US-09-370-700-5  
; Sequence 5, Application US/09370700  
; Patent No. 6274350  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J  
; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 Div1  
; CURRENT APPLICATION NUMBER: US/09/370,700  
; PRIOR FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/36987  
; PRIOR FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 4928  
; TYPE: PRT  
; ORGANISM: Saccharopolyspora spinosa  
US-09-370-700-5

Query Match 12.9%; Score 78.5; DB 2; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 61;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
  
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Db 4799 TFAELGFDLSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853  
  
Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMH 106  
Db 4854 GIESLLAEID-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

## RESULT 6

US-09-603-207-5  
; Sequence 5, Application US/09603207B  
; Patent No. 6521406  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J

; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 Div1  
; CURRENT APPLICATION NUMBER: US/09/603,207B  
; CURRENT FILING DATE: 2000-06-23  
; EARLIER APPLICATION NUMBER: 09/370,700  
; PRIOR FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 4928  
; TYPE: PRT  
; ORGANISM: Saccharopolyspora spinosa  
US-09-603-207-5

Query Match 12.9%; Score 78.5; DB 2; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 61;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
  
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Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMH 106  
Db 4854 GIESLLAEID-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

## RESULT 7

US-10-329-148A-5  
; Sequence 5, Application US/10329148A  
; Patent No. 7015001  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J  
; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 Div1  
; CURRENT APPLICATION NUMBER: US/10/329,148A  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/603,207B  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/370,700  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 4928  
; TYPE: PRT  
; ORGANISM: Saccharopolyspora spinosa  
US-10-329-148A-5

Query Match 12.9%; Score 78.5; DB 3; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 61;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
  
Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64  
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Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMH 106  
Db 4854 GIESLLAEID-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

## RESULT 8

US-09-716-964B-23  
; Sequence 23, Application US/09716964B



## RESULT 12

US-09-833-745-50  
; Sequence 50, Application US/09833745  
; Patent No. 6939541

; GENERAL INFORMATION:  
; APPLICANT: ROBERTS, JOSEPH

; APPLICANT: SETHURAMAN, NATARAJAN  
; APPLICANT: MACALLISTER, THOMAS

; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF

; TITLE OF INVENTION: BIOACTIVE HISTIDINE AMMONIA LYASE

; FILE REFERENCE: 078728/0106

; CURRENT APPLICATION NUMBER: US/09/833,745

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/197,770

; PRIOR FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 50

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Vibrio cholerae

US-09-833-745-50

Query Match 12.1%; Score 73.5; DB 2; Length 513;

Best Local Similarity 26.0%; Pred. No. 10;

Matches 33; Conservative 17; Mismatches 44; Indels 33; Gaps 5;

QY 11 IEQLSAISLDDOERSL--PCRYALLPDGQSIPIHSLYPERLADRVLLDFATPDGRGPHD 68

DB 389 IAGVTAALASENKTLAHPASVDSLTSANQEDHVS--ATFAARLRDMGENTRG--- 442

QY 69 LRPVDFNQMOGL-----RSVLAEGQ-----SPELRAAALAEQM 104

DB 443 -ILAVEYLAAGQLDFRAPLKSPRIEAEARQLREKVPFYDKRYFAPDIEKANALLAQL 501

QY 105 HADEQLM 111

DB 502 AVNRLM 508

## RESULT 13

US-09-902-540-12221

; Sequence 12221, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 12221

; LENGTH: 2216

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-12221

Query Match 11.8%; Score 72; DB 2; Length 2216;

Best Local Similarity 24.7%; Pred. No. 1.le+02;

Matches 43; Conservative 21; Mismatches 48; Indels 62; Gaps 9;

QY 5 TAAHIGIE--QLSAISLDDOERSLPGRYALLPDG-----QSIPIHSLYPERLAD- 53

DB 520 SAPSAGIEPKSVDAEVDSEGIASVSLGICILPGAKDPETYQWIRKIGSIGIVDQGLLP 579

QY 54 RVLLDFA----TPDRGF-----HDLLRPVDF-----NQMOG 81

DB 580 ELVTDFAAGPAGTPDRTYTLTGYVRDEDLVPPGFDPTRFQQYVREQKLALIALSQAMQG 639

QY 82 LRSV-----LAEGOSPELRAAALAEQMADEQLMOWMTLHLLHKV 121

DB 640 LKPVASKTPGRTQCILGSLGTAEG-SABYDAALS-----VEAGEALLSARGERVHDI 688

## RESULT 14

US-09-252-991A-19896

; Sequence 19896, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 19896

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19896

Query Match 11.7%; Score 71; DB 2; Length 293;

Best Local Similarity 28.7%; Pred. No. 8.8;

Matches 33; Conservative 13; Mismatches 31; Indels 38; Gaps 7;

QY 11 IEQLSAISLDDOERSLPGRYALLPDGQSIPIHSLYLP-----ERLAD-----RVL 56

DB 14 VVQGSFASDTRQERQMP-RFA-----ANLSMLYPRHDFLERFAAAADGFEVYL 63

QY 57 LDFATP-----DRGFHDL-----RPVDFNQAMQGLRSVLAEGOSPELRAAAA 99

DB 64 PFYAVPAELKARLDDHGLRQMLFNAAAPGDWDKGERGLASL--PGREAEFRRAIA 116

## RESULT 15

US-09-270-767-42532

; Sequence 42532, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 42532

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-42532

Query Match 11.7%; Score 71; DB 2; Length 386;

Best Local Similarity 31.0%; Pred. No. 13;

Matches 26; Conservative 9; Mismatches 29; Indels 20; Gaps 4;

QY 46 LYPELADRVLLDFAT-PDRGFHDLRLRPVDFNQ-----AMQGLRSVLAEGOSPELRA 96

DB 110 LFPSPNF---VTADLSVDPER-----LDINQOHSKAAAGORELDSVAALQOKTEAAA 158

QY 97 AAALAEQMADEQLMOWMTLHLLHK 120

DB 159 AAAAAQPVEIDSKIDRLHLLHLE 182

Search completed: June 16, 2006, 19:29:00  
Job time : 23.3309 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 20:12:36 ; Search time 67.6813 Seconds  
(without alignments)  
828.131 Million cell updates/sec  
Title: US-10-813-908A-3  
Perfect score: 609  
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMNTLHLHKV 121  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2097797 seqs, 463214858 residues  
Total number of hits satisfying chosen parameters: 2097797  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications AA Main: \*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	609	100.0	121	5	US-10-813-908-3	Sequence 3, Appli
2	88.5	14.5	259	6	US-11-075-185-24	Sequence 24, Appl
3	83	13.6	10917	5	US-10-732-923-20606	Sequence 20606, A
4	81.5	13.4	452	4	US-10-282-122A-53766	Sequence 53766, A
5	80	13.1	1108	4	US-10-425-115-223719	Sequence 223719, A
6	80	13.1	1132	4	US-10-425-114-62671	Sequence 62671, A
7	78.5	12.9	4928	4	US-10-329-148A-5	Sequence 5, Appli
8	78	12.8	294	4	US-10-671-403-23	Sequence 23, Appl
9	78	12.8	294	4	US-10-671-419-23	Sequence 23, Appl
10	78	12.8	294	4	US-10-670-844-23	Sequence 23, Appl
11	78	12.8	294	4	US-10-671-134-23	Sequence 23, Appl
12	78	12.8	294	4	US-10-673-098-23	Sequence 23, Appl
13	78	12.8	294	4	US-10-672-638-23	Sequence 23, Appl
14	78	12.8	294	4	US-10-673-127-23	Sequence 23, Appl
15	78	12.8	294	4	US-10-670-817-23	Sequence 23, Appl
16	78	12.8	294	4	US-10-671-119-23	Sequence 23, Appl
17	78	12.8	294	4	US-10-671-207-23	Sequence 23, Appl
18	78	12.8	294	5	US-10-673-120-23	Sequence 23, Appl
19	78	12.8	294	5	US-10-671-412-23	Sequence 23, Appl
20	78	12.8	294	5	US-10-671-859-23	Sequence 23, Appl
21	78	12.8	294	5	US-10-671-106-23	Sequence 23, Appl
22	77.5	12.7	1486	6	US-11-097-143-15897	Sequence 15897, A
23	77	12.6	673	4	US-10-369-493-17937	Sequence 17937, A
24	76	12.5	709	6	US-11-188-298-11622	Sequence 11622, A
25	75	12.3	318	4	US-10-156-761-12913	Sequence 12913, A
26	75	12.3	326	4	US-10-425-115-223741	Sequence 223741, A
27	73.5	12.1	340	6	US-11-097-143-41112	Sequence 41112, A

28	73.5	12.1	513	3	US-09-833-745-50	Sequence 50, Appl
29	73.5	12.1	513	6	US-11-135-667-50	Sequence 50, Appl
30	72.5	11.9	524	5	US-10-739-930-10253	Sequence 10253, A
31	72.5	11.9	3571	5	US-10-732-923-8324	Sequence 8324, Ap
32	72.5	11.9	3574	5	US-10-732-923-8326	Sequence 8326, Ap
33	72.5	11.9	3574	5	US-10-732-923-8329	Sequence 8329, Ap
34	72	11.8	294	4	US-10-425-114-40589	Sequence 40589, A
35	72	11.8	313	4	US-10-425-115-306063	Sequence 306063, A
36	72	11.8	348	4	US-10-156-761-12267	Sequence 12267, A
37	72	11.8	413	4	US-10-425-115-306066	Sequence 306066, A
38	72	11.8	610	4	US-10-425-114-52341	Sequence 52341, A
39	72	11.8	689	4	US-10-437-963-125613	Sequence 125613, A
40	71.5	11.7	393	4	US-10-425-114-70624	Sequence 70624, A
41	71.5	11.7	393	4	US-10-425-115-292398	Sequence 292398, A
42	71.5	11.7	482	4	US-10-425-114-60438	Sequence 60438, A
43	71	11.7	261	4	US-10-369-493-9710	Sequence 9710, Ap
44	71	11.7	432	3	US-09-738-626-4678	Sequence 4678, Ap
45	71	11.7	477	5	US-10-494-672-246	Sequence 246, App

ALIGNMENTS

RESULT 1  
US-10-813-908-3  
; Sequence 3, Application US/10813908  
; Publication No. US20050058662A1  
; GENERAL INFORMATION:  
; APPLICANT: Frey, Joachim Stuber  
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and  
; FILE REFERENCE: MIC01/2315/MO  
; CURRENT APPLICATION NUMBER: US/10/813.908  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US/10/416.902  
; PRIOR FILING DATE: 2003-05-15  
; PRIOR APPLICATION NUMBER: PCT/CA01/01589  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Aeromonas salmonicida  
US-10-813-908-3

Query Match	100.0%	Score 609;	DB 5;	Length 121;
Best Local Similarity	100.0%	Pred. No. 8.3e-60;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA	60	
Db	1	MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA	60	
Qy	61	TPDGRFHLLRPVDFNQMGRLSVLAEGOSPELRARAAALLOMHADEQLMNTLHLHK	120	
Db	61	TPDGRFHLLRPVDFNQMGRLSVLAEGOSPELRARAAALLOMHADEQLMNTLHLHK	120	
Qy	121	V 121		
Db	121	V 121		

RESULT 2  
US-11-075-185-24  
; Sequence 24, Application US/11075185  
; Publication No. US20050266434A1  
; GENERAL INFORMATION:  
; APPLICANT: REEVES, CHRISTOPHER D  
; APPLICANT: JULIEN, BRYAN  
; APPLICANT: REID, RALPH  
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS  
; FILE REFERENCE: 010099.03  
; CURRENT APPLICATION NUMBER: US/11/075.185

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; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 24
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
; US-11-075-185-24

Query Match      14.5%; Score 88.5; DB 6; Length 259;
Best Local Similarity 28.1%; Pred. No. 0.28;
Matches 27; Conservative 19; Mismatches 29; Indels 21; Gaps 4;

QY 20 DDQERSLPGRYALLPDGQSIEPHISRLYPERLADRVLLDFATPDGRGHDLRLRPVDFNQAM 79
Db 73 NEREQQNIRWVWL-DGQADEPHRPLAPELLVPI-----RGFTTLMKPLADKQGV 123
QY 80 QGLRSVLAEQSPELRAAAALLEGQHADEQLMQMTL 115
Db 124 ----TIVEGGTDP-----RLVHADADQLQOAL 147

RESULT 3
US-10-732-923-20606
; Sequence 20606, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 20606
; LENGTH: 10917
; TYPE: PRT
; ORGANISM: Streptomyces nodosus
; US-10-732-923-20606

Query Match      13.6%; Score 83; DB 5; Length 10917;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 36; Conservative 14; Mismatches 37; Indels 30; Gaps 6;

QY 5 TAAHIGIEQ----LSAISLDQERSLPGRYALLPDGQSIEPHISRLYPERLADRV--LLDF 59
Db 3916 TNAHVILEQPVVAPAPATADVGDGAEPAVVPLILSGKS-----PEARLDQARLLDT 3966
QY 60 ATPDRGHDLRLRPVDFNQAMQGLRS-----VLAEGQSPELRAAAALLEGQHADEQ 109
Db 3967 VRE----HTALRPLDLGHSLSRSPAFDHRVAVLVATGREDALRALTAL-----ADDE 4014

RESULT 4
US-10-282-122A-53766
; Sequence 53766, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/369,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 53766
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Corynebacterium diptheriae
; US-10-282-122A-53766

Query Match      13.4%; Score 81.5; DB 4; Length 452;
Best Local Similarity 23.5%; Pred. No. 3.4;
Matches 36; Conservative 20; Mismatches 56; Indels 41; Gaps 4;

QY 2 SRITAAHIGIEQLSALSDQERSLPGRYAL----LPDQSQSIEPHISRLYPERLADRVLLD 58
Db 202 NRITISDEALEQLVLLSGGDARRSLTYLEAAASESLADGBELTPEIIR----HNVDKAIVR 257
QY 59 FATPDGRGHDL-----LRPVDFOAMQGLRSVLAEQSPELRA----- 96
Db 258 YDRDGDQHDVVSAPFTKSMRGSDVDAAHLHYLRMIDAGEDPRFIARRLVHASEDVGMD 317
QY 97 -----AAALLEQMHAEQLMQMTLHL 117
Db 318 PQALSVAVAASQAVALIGMPEARINLAQATLHL 350

RESULT 5
US-10-425-115-223719
; Sequence 223719, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 223719
; LENGTH: 1108
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_13561C.1.pep
```

US-10-425-115-223719

Query Match 13.1%; Score 80; DB 4; Length 1108;  
Best Local Similarity 27.2%; Pred. No. 16;  
Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;  
QY 38 STEPHISRLYPERLADRVLLDFATPDGFGHDLRPVDFNQMOGLRS-----VLAEGQ 90  
DB 807 STEPH-----DVIAPDR-LTDLPPNDPNHTVHIQASTAQSHALDGGK 850  
QY 91 SPELRAAALAEQMHAD-EQLMQMTLHLHLKV 121  
DB 851 DPDAHATSSLVKNTHSNMEPVVQKSISQLHDI 882

RESULT 6

US-10-425-114-62671  
; Sequence 62671, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 62671  
; LENGTH: 1132  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3689-238-A9\_FLI.pep  
US-10-425-114-62671

Query Match 13.1%; Score 80; DB 4; Length 1132;  
Best Local Similarity 27.2%; Pred. No. 17;  
Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;  
QY 38 SIEPHISRLYPERLADRVLLDFATPDGFGHDLRPVDFNQMOGLRS-----VLAEGQ 90  
DB 831 STEPH-----DVIAPDR-LTDLPPNDPNHTVHIQASTAQSHALDGGK 874  
QY 91 SPELRAAALAEQMHAD-EQLMQMTLHLHLKV 121  
DB 875 DPDAHATSSLVKNTHSNMEPVVQKSISQLHDI 906

RESULT 7

US-10-329-148A-5  
; Sequence 5, Application US/10329148A  
; Publication No. US20040023343A1  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J  
; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 DIV1  
; CURRENT APPLICATION NUMBER: US/10/329,148A  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/603,207B  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/370,700  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-09

; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 4928  
; TYPE: PRT  
; ORGANISM: Saccharopolyspora spinosa  
US-10-329-148A-5

Query Match 12.9%; Score 78.5; DB 4; Length 4928;  
Best Local Similarity 27.5%; Pred. No. 1.6e+02;  
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;  
QY 5 TAAHIGIEQLSAISLDDOERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64  
DB 4799 TFAELGFDLSLTAVELRNRLNAVTG--LRLPPTLVFDHPTPLALSEQLPALV---AEPDN 4853  
QY 65 GFHDLRLRPVDFNQMOGLRSVLAEGQSPELRAAALAEQMH 106  
DB 4854 GIESLLAELD-----RLDITTLAOGPSIPLEDQAKVAERLHA 4889

RESULT 8

US-10-671-403-23  
; Sequence 23, Application US/10671403  
; Publication No. US20040038289A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Donnell, Michael E.  
; APPLICANT: Yuzhakov, Alexander  
; APPLICANT: Yurieva, Olga  
; APPLICANT: Jeruzalmi, David  
; APPLICANT: Bruck, Irina  
; APPLICANT: Kuriyan, John  
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
; FILE REFERENCE: 22221/1030  
; CURRENT APPLICATION NUMBER: US/10/671,403  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US/09/716,964A  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/143,202  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 08/823,407  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 09/057,416  
; PRIOR FILING DATE: 1998-04-08  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 294  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-10-671-403-23

Query Match 12.8%; Score 78; DB 4; Length 294;  
Best Local Similarity 29.0%; Pred. No. 4.8;  
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;  
QY 5 TAAHIGIEQLSAISLDDOERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64  
DB 208 SAAHGGMR--DAUSLLDQAIISFGSDILKVEDALLITGVANSOLYIGKLA-----K 254  
QY 65 GFHDLRLRPVDFNQMOGLRSVLAEGQSPELRAAALAEQMH 104  
DB 255 SLHD----KNVSDALETLNELLOQKDP-----AKLIEDM 285

RESULT 9

US-10-671-419-23  
; Sequence 23, Application US/10671419  
; Publication No. US20040038290A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Donnell, Michael E.





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; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/673,098
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-673-098-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDQSTEPHISRLYPERLADRVLLDFATPDR 64
Db      208 SAAGGMR--DALSLLDQAISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQM 104
Db      255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 13
US-10-672-638-23
; Sequence 23, Application US/10672638
; Publication No. US20040077012A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/672,638
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-672-638-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDQSTEPHISRLYPERLADRVLLDFATPDR 64
Db      208 SAAGGMR--DALSLLDQAISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQM 104
Db      255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 13
US-10-672-638-23
; Sequence 23, Application US/10672638
; Publication No. US20040077012A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/672,638
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-672-638-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDQSTEPHISRLYPERLADRVLLDFATPDR 64
Db      208 SAAGGMR--DALSLLDQAISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQM 104
Db      255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285
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Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQM 104
Db      255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 14
US-10-673-127-23
; Sequence 23, Application US/10673127
; Publication No. US20040081995A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/673,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-673-127-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDQSTEPHISRLYPERLADRVLLDFATPDR 64
Db      208 SAAGGMR--DALSLLDQAISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEGSQSPELRAAAALAEQM 104
Db      255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 15
US-10-670-817-23
; Sequence 23, Application US/10670817
; Publication No. US20040106137A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/670,817
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US/09/716,964
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
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; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-670-817-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

QY      5  TAAHIGIEQLSAISLDDQERSLFGRYALLPDGQSIEPHISRLYPERLADRVLLDFATPDR 64
Db      208  SAAHGGMR--DALSLLDQAIISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

QY      65  GFHDLRLRPVDFNQAMQGLRSVLAEQSPELRAAAALAEQM 104
Db      255  SLHD-----KNVSDALETINELLOQKDP-----AKLIEDM 285
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Search completed: June 16, 2006, 20:25:00  
Job time : 69.6813 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 5.21382 Seconds  
(without alignments)  
523.484 Million cell updates/sec

Title: US-10-813-908A-3  
Perfect score: 609  
Sequence: 1 MSRTAHIGIEQLSAISLD.....EQMADEQLMONTLHLHKV 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pap:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pap:\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap:\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	11.5	562	6	US-10-449-902-47856
2	70	11.5	562	6	US-10-449-902-47856
3	69	11.3	451	6	US-10-471-571A-2280
4	68	11.2	467	6	US-10-449-902-49788
5	68	11.2	504	6	US-10-449-902-35636
6	68	11.2	547	6	US-10-449-902-55462
7	67	11.0	504	6	US-10-449-902-43064
8	67	11.0	504	6	US-10-449-902-53630
9	67	11.0	567	6	US-10-449-902-46221
10	66.5	10.9	458	6	US-10-449-902-37980
11	66	10.8	381	7	US-11-321-421-8
12	65.5	10.8	447	6	US-10-449-902-46260
13	65.5	10.8	3429	6	US-10-953-349-9275
14	65.5	10.8	3438	6	US-10-953-349-9274
15	65.5	10.8	3478	6	US-10-953-349-9273
16	65	10.7	800	6	US-10-449-902-53325
17	64	10.5	520	6	US-10-449-902-54451
18	64	10.5	521	6	US-10-449-902-43877
19	63.5	10.4	272	7	US-11-293-697-3682
20	63.5	10.4	343	6	US-10-449-902-43568
21	63.5	10.4	349	6	US-10-449-902-48899
22	63.5	10.4	489	6	US-10-449-902-41981
23	63.5	10.4	546	6	US-10-449-902-29819
24	63.5	10.4	859	6	US-10-449-902-51763
25	63.5	10.4	1568	7	US-11-330-363-5

26 63 10.3 846 6 US-10-449-902-43448 Sequence 43448, A  
27 62.5 10.3 493 6 US-10-449-902-53861 Sequence 53861, A  
28 62.5 10.3 839 7 US-11-293-697-3261 Sequence 3261, Ap  
29 62 10.2 291 7 US-11-252-276-10 Sequence 10, Appl  
30 62 10.2 513 6 US-10-953-349-8011 Sequence 8011, Ap  
31 62 10.2 553 6 US-10-953-349-8010 Sequence 8010, Ap  
32 62 10.2 571 6 US-10-449-902-42832 Sequence 42832, A  
33 62 10.2 580 6 US-10-953-349-8009 Sequence 8009, Ap  
34 62 10.2 910 6 US-10-953-349-9741 Sequence 9741, Ap  
35 62 10.2 991 6 US-10-449-902-55212 Sequence 55212, A  
36 62 10.2 1127 6 US-10-953-349-9740 Sequence 9740, Ap  
37 62 10.2 1139 6 US-10-953-349-9739 Sequence 9739, Ap  
38 61.5 10.1 810 6 US-10-953-349-33953 Sequence 33953, A  
39 61 10.0 226 6 US-10-953-349-16545 Sequence 16545, A  
40 61 10.0 479 6 US-10-449-902-55434 Sequence 55434, A  
41 61 10.0 1190 6 US-10-449-902-41233 Sequence 41233, A  
42 60.5 9.9 178 6 US-10-953-349-34473 Sequence 34473, A  
43 60.5 9.9 261 6 US-10-953-349-34472 Sequence 34472, A  
44 60.5 9.9 855 6 US-10-449-902-41097 Sequence 41097, A  
45 60.5 9.9 961 6 US-10-449-902-41296 Sequence 41296, A

#### ALIGNMENTS

##### RESULT 1

US-10-449-902-47856  
; Sequence 47856, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 47856

; LENGTH: 562

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-47856

Query Match 11.5%; Score 70; DB 6; Length 562;

Best Local Similarity 29.8%; Pred. No. 9.1;

Matches 25; Conservative 14; Mismatches 35; Indels 10; Gaps 3;

Qy 23 ERSLPGRYALLP-DGQSIPIHISRLYPERLADRVLLDFATPDRCGHLLRPVDNQAMQG 81

Db 225 EWSLPTVTFPHPHGLCIPIHKSRLSLKLGCCII----PPLOGFHALTK-----MTLQD 275

Qy 82 LRSVLAEGSQSPELRAAAALAEQWH 105

Db 276 LRNSVAKASYEDVFKPCPQLQVLH 299

##### RESULT 2

US-10-449-902-50502

; Sequence 50502, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF



```
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5462
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55462

Query Match      11.2%; Score 68; DB 6; Length 547;
Best Local Similarity 24.6%; Pred. No. 14;
Matches 28; Conservative 20; Mismatches 46; Indels 20; Gaps 4;

Qy 1 MSRTAAHIGIEQLSALSDDQERSLPCRYALLPDGOSIEPHISRL--YPERLADRVLLD 58
Db 261 LHKITDIINIDPNSSIS-----FPKGISFSFGMSEIIRFVEEHCDFCVID 306

Qy 59 FATPDGRGHDLLRPVDFNOAMOGRLSVLAEGSPELRAAAALLOMHADEQLMQ 112
Db 307 ---PFKNYPLDLRIQIEILIRLEGLSABGR-FALRAPCFKIESFCGSELQK 356

RESULT 7
US-10-449-902-43064
; Sequence 43064, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43064
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43064

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRPVDFNOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAIAVIMDK 400

Qy 91 SPELRAAAALLOMHADEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHESCGOCT 424

RESULT 8
US-10-449-902-53630
; Sequence 53630, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53630
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53630

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRPVDFNOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAIAVIMDK 400

Qy 91 SPELRAAAALLOMHADEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHESCGOCT 424

RESULT 9
US-10-449-902-46221
; Sequence 46221, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46221
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46221

Query Match      11.0%; Score 67; DB 6; Length 567;
Best Local Similarity 24.8%; Pred. No. 19;
Matches 33; Conservative 19; Mismatches 19; Indels 44; Gaps 8;

Qy 27 PGRYALLPDGOSTE---PHISRLYPER-----LADRVLLDFATPD-----RGFH 67
Db 336 PAR-AILPYSQALEKFAPHIQQLSMESNGKVSIDGVQLSFETGEIDFGSPGTNGQHSFY 394
Qy 68 DLLR-----PVDENQAMQGLRSVLAEGQ-----SPELRAAAALLOMHADE 108
Db 395 QLTHQGRVIPCDFIGVVKSQOPVYLKGEIVSNHDELMNSFFAQPDALAYKGTPEQLHSE- 453
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; Sequence 53630, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53630
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53630

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRPVDFNOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAIAVIMDK 400

Qy 91 SPELRAAAALLOMHADEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHESCGOCT 424

RESULT 9
US-10-449-902-46221
; Sequence 46221, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46221
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46221

Query Match      11.0%; Score 67; DB 6; Length 567;
Best Local Similarity 24.8%; Pred. No. 19;
Matches 33; Conservative 19; Mismatches 19; Indels 44; Gaps 8;

Qy 27 PGRYALLPDGOSTE---PHISRLYPER-----LADRVLLDFATPD-----RGFH 67
Db 336 PAR-AILPYSQALEKFAPHIQQLSMESNGKVSIDGVQLSFETGEIDFGSPGTNGQHSFY 394
Qy 68 DLLR-----PVDENQAMQGLRSVLAEGQ-----SPELRAAAALLOMHADE 108
Db 395 QLTHQGRVIPCDFIGVVKSQOPVYLKGEIVSNHDELMNSFFAQPDALAYKGTPEQLHSE- 453
```





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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 76.8618 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-4  
Perfect score: 602  
Sequence: 1 MTWVLTQQQDALLTTCWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	5	ABB80772 A. salmon
2	272	45.2	231	7	ABO81216 Pseudomon
3	111.5	18.5	470	9	ABM93219 M. xanthu
4	99	16.4	619	6	ABU22979 Protein e
5	96.5	16.0	143	2	AAI35024 Chlamydia
6	88.5	14.7	870	7	ABO79661 Pseudomon
7	86.5	14.4	719	8	ADX89002 Plant ful
8	84.5	14.0	122	3	AAI14133 Bordetell
9	84.5	14.0	737	8	ADX94619 Plant ful
10	83	13.8	1219	7	ABO80094 Pseudomon
11	83	13.8	1586	6	ABU21467 Protein e
12	81	13.5	953	9	ABM95482 M. xanthu
13	80	13.3	143	10	AE60312 Cat chlam
14	80	13.3	368	7	ABO81971 Pseudomon
15	79.5	13.2	517	9	AEBA49907 P. aerugi
16	79.5	13.2	956	7	ABM91196 M. xanthu
17	79.5	13.1	2519	7	ABM88218 Rice abio
18	78.5	13.0	169	2	AAW15044 G-CSF rec
19	78.5	13.0	1234	4	ABM68510 Drosophil
20	78	13.0	390	9	ABM97422 M. xanthu
21	78	13.0	577	9	AEBA1002 L. pneumo
22	78	13.0	587	9	AEBA37691 L. pneumo
23	77.5	12.9	171	2	AAW15045 G-CSF rec

24	77.5	12.9	171	2	AAW15046	Aaw15046 G-CSF rec
25	77.5	12.9	171	2	AAW15048	Aaw15048 G-CSF rec
26	77.5	12.9	171	2	AAW15050	Aaw15050 G-CSF rec
27	77.5	12.9	171	2	AAW15043	Aaw15043 G-CSF rec
28	77.5	12.9	171	2	AAW15049	Aaw15049 G-CSF rec
29	77.5	12.9	171	2	AAW15051	Aaw15051 G-CSF rec
30	77.5	12.9	238	2	AAW15089	Aay52089 Human ret
31	77.5	12.9	299	2	AAW17131	Aaw17131 Amino aci
32	77.5	12.9	302	2	AAW17108	Aaw17108 Amino aci
33	77.5	12.9	302	2	AAW17112	Aaw17112 Amino aci
34	77.5	12.9	302	2	AAW17106	Aaw17106 Amino aci
35	77.5	12.9	302	2	AAW17110	Aaw17110 Amino aci
36	77.5	12.9	302	2	AAW17845	Aaw17845 Multi-fun
37	77.5	12.9	302	2	AAW17839	Aaw17839 Multi-fun
38	77.5	12.9	302	2	AAW17841	Aaw17841 Multi-fun
39	77.5	12.9	302	2	AAW17843	Aaw17843 Multi-fun
40	77.5	12.9	317	2	AAW17113	Aaw17113 Amino aci
41	77.5	12.9	317	2	AAW17109	Aaw17109 Amino aci
42	77.5	12.9	317	2	AAW17111	Aaw17111 Amino aci
43	77.5	12.9	317	2	AAW17107	Aaw17107 Amino aci
44	77.5	12.9	317	2	AAW17842	Aaw17842 Multi-fun
45	77.5	12.9	317	2	AAW17840	Aaw17840 Multi-fun

ALIGNMENTS

RESULT 1  
ABB80772  
ID ABB80772 standard; protein; 116 AA.  
XX  
AC ABB80772;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE A. salmonicida type III secretion protein acr4 sequence.  
XX  
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
XX  
KW acrV; acrH; antibiotic; vaccine; fish.  
XX  
OS Aeromonas salmonicida.  
XX  
PN WO200240514-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 15-NOV-2001; 2001WO-CA001589.  
XX  
PR 15-NOV-2000; 2000US-0248864P.  
XX  
(FREY/) FREY J.  
PA (STUB/) STUBER K.  
PA (THOR/) THORNTON J C.  
PA (KOZI/) KOZYK M A.  
PA (BURI/) BURIAN J.  
XX  
PI Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;  
XX  
DR WPI; 2002-537338/57.  
XX  
DR N-PSDB; ABN86172.  
XX  
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the  
PT protein, useful for reducing susceptibility of fish to infection by a  
PT virulent strain of Aeromonas salmonicida.  
XX  
PS Claim 13; Page 27; 39pp; English.  
XX  
CC The invention relates to A. salmonicida type III secretion genes and  
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrV or AcrH.  
CC A. salmonicida type III secretion apparatus is useful for producing  
CC selected products, especially AexT. AcrV in vaccine, epitope or epitopic  
CC region of AcrV or any other protein of A. salmonicida type III secretion  
CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present  
CC sequence represents the *A. salmonicida* type III secretion protein acr4  
XX  
SQ Sequence 116 AA;

Query Match 100.0%; Score 602; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.1e-65;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60  
|||||  
DB 1 MTWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60  
|||||

QY 61 EAALAHVDQLMQQGEADGPIWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP 116  
|||||  
DB 61 EAALAHVDQLMQQGEADGPIWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP 116  
|||||

RESULT 2  
ABO81216  
ID ABO81216 standard; protein; 231 AA.

AC ABO81216;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #13391.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

OS Pseudomonas aeruginosa.

PN US6551795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD14787.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 29962; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
XX polynucleotides encoding them. The sequences are useful in diagnosis and  
XX therapy of pathological conditions, as molecular targets for diagnostics,  
XX prophylaxis and treatment of pathological conditions resulting from a  
XX bacterial infection, for evaluating a compound, such as a polypeptide,  
XX for the ability to bind a P. aeruginosa nucleic acid, as components of  
XX effective antibacterial targets, as targets for antibacterial drugs,  
XX including anti-P. aeruginosa drugs, as templates for recombinant  
XX production of P. aeruginosa-derived peptides or polypeptides, as target  
XX components for diagnosis and/or treatment of P. aeruginosa-caused  
XX infection, and in detection of P. aeruginosa sequences or other sequences  
XX of Pseudomonas species using biochip technology. Sequences ABO67826-  
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 231 AA;

Query Match 45.2%; Score 272; DB 7; Length 231;  
Best Local Similarity 55.1%; Pred. No. 1.2e-24;  
Matches 59; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 TWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEGE 61  
|||||  
DB 122 SMTLKQTQORLLTLMGLWHLQCGQPRRAQVLLLEALLSVAPERRDGRALLLQOGLGE 181  
|||||

QY 62 AALAHVDQLMQQGEADGPIWLCRSRACQAGRLDEARFAYQQYLELE 108  
|||||  
DB 182 PAVRLCRQLQEDGESEPEGLWLCLSRAEQLAGRLDAARAHAHALELE 228  
|||||

RESULT 3  
ABM93219  
ID ABM93219 standard; protein; 470 AA.

XX AC ABM93219;

XX DT 02-JUN-2005 (first entry)

XX DE M. xanthus protein sequence, seq id 12418.

XX KW Transgenic plant; DNA replication; gene regulation; gene expression.

XX OS Myxococcus xanthus.

XX PN US6833447-B1.

XX PD 21-DEC-2004.

XX PF 10-JUL-2001; 2001US-00902540.

XX PR 10-JUL-2000; 2000US-0217883P.

XX PA (MONS ) MONSANTO TECHNOLOGY LLC.

XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX DR WPI; 2005-028716/03.

XX PT New substantially purified Myxococcus xanthus nucleic acid molecule  
XX encoding a nitrite reductase, useful for determining gene expression,  
XX identifying mutations in a gene of interest, and for constructing  
XX mutations in a gene of interest.

XX Example 2; SEQ ID NO 12418; 25pp; English.

XX The invention relates to a substantially purified nucleic acid molecule  
XX encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
XX recombinant DNA construct for expression of a nitrite reductase gene in a  
XX plant cell, and a plant cell comprising the recombinant DNA construct.  
XX The nucleic acid is useful for determining gene expression, identifying  
XX mutations in a gene of interest, and for constructing mutations in a gene  
XX of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
XX a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from USPTO

XX SQ Sequence 470 AA;

Query Match 18.5%; Score 111.5; DB 9; Length 470;  
Best Local Similarity 36.6%; Pred. No. 0.00018;  
Matches 34; Conservative 8; Mismatches 44; Indels 7; Gaps 2;

QY 13 LLLTGMVLQLOY---GHPDK----ASVLLAALLQIHPDHQGGRTLLVALLKQEGEAALA 65  
|||||  
DB 56 LLLAGFLLDGYEPDGRPGQGPYAQLLRLLRSHPDHAGVHHAWVQAMLSNGRPEARD 115  
|||||

QY 66 HVDQLMOQGEADGPIWLCSRACQLAGRLDEAR 98  
DB 116 SAHRLVALAPRAGPALLSAGRLQRLVGLVAEAR 148

RESULT 4

ABU22979  
ID ABU22979 standard; protein; 619 AA.

XX AC ABU22979;  
XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by prokaryotic essential gene #8506.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Bordetella pertussis.

XX PN WO200277183-A2.  
XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342933P.

XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.  
XX DR N-PSDB; ACA26849.

XX PT New antisense nucleic acids, useful for identifying proteins or screening  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX PT isolate candidate molecules for rational drug discovery programs.  
XX PS Claim 25; SEQ ID NO 50903; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of  
XX CC the 6213 antisense sequences given in the specification where expression  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid  
XX CC encoding a polypeptide whose expression is inhibited by the antisense  
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX CC polypeptide or its fragment whose expression is inhibited by the  
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding  
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX CC proliferation or the activity of a gene in an operon required for  
XX CC proliferation; (7) identifying a compound that influences the activity of  
XX CC the gene product or that has an activity against a biological pathway  
XX CC required for proliferation, or that inhibits cellular proliferation; (8)  
XX CC identifying a gene required for cellular proliferation or the biological  
XX CC pathway in which a proliferation-required gene or its gene product lies  
XX CC or a gene on which the test compound that inhibits proliferation of an  
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX CC compound's activity; (11) a culture comprising strains in which the gene  
XX CC product is overexpressed or underexpressed; (12) determining the extent  
XX CC to which each of the strains is present in a culture or collection of  
XX CC strains; or (13) identifying the target of a compound that inhibits the  
XX CC proliferation of an organism. The antisense nucleic acids are useful for  
XX CC identifying proteins or screening for homologous nucleic acids required  
XX CC for cellular proliferation to isolate candidate molecules for rational  
XX CC drug discovery programs, or for screening homologous nucleic acids  
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
XX CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
SQ Sequence 619 AA;

Query Match 16.4%; Score 99; DB 6; Length 619;  
Best Local Similarity 29.0%; Pred. No. 0.0088;  
Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG--HPDKASVLLAALLQIHDPDHOGGRRTLLVALLKOGEGEAAAHVDQLMQQGEAD 77  
DB 259 LEYGAKVDATRAQHQARAFINRNDARKLRLMLAGQADGGYDGLAELQAMRRSPED 318

QY 78 GPLWLCRSRACQLAGRLDEARFAYQOYLEEEQNE-STHP 116  
DB 319 FDLFMFMAQLAYKAGRLDQARGYLQYLDVQNRQMATAP 358

RESULT 5

AAAY35024  
ID AAY35024 standard; protein; 143 AA.

XX AC AAY35024;  
XX DT 17-OCT-2003 (revised)

XX DT 13-SEP-1999 (first entry)  
XX DE Chlamydia pneumoniae transmembrane protein sequence.

XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
XX KW neutralising epitope.

XX OS Chlamydothila pneumoniae.  
XX PN WO9927105-A2.

XX PD 03-JUN-1999.  
XX PF 20-NOV-1998; 98WO-IB001890.

XX PR 21-NOV-1997; 97FR-00014673.  
XX PR 04-NOV-1998; 98US-0107078P.

XX PA (GEST ) GENSET.  
XX PI Griffais R;

XX DR WPI; 1999-357842/30.  
XX PT Genome sequence of Chlamydia pneumoniae.

XX PS Page 921; Disclosure; 1912pp; English.  
XX CC AAY34584-Y35879 represent the proteins encoded by all the open reading

XX CC frames in the complete genome (see AAX9190) of Chlamydia pneumoniae. C.  
XX CC pneumoniae causes respiratory disease such as pneumonia and bronchitis  
XX CC and is thought to be a contributing factor in heart disease, sarcoidosis,  
XX CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
XX CC polypeptides encoded by the open reading frames of the C. pneumoniae  
XX CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as  
XX CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
XX CC be used as immunogenic compositions, especially where the vector directs  
XX CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
XX CC -OCT-2003 to standardise OS field)

XX SQ Sequence 143 AA;

Query Match 16.0%; Score 96.5; DB 2; Length 143;  
Best Local Similarity 33.3%; Pred. No. 0.0026;  
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYQCHDPDKASVLLAALLQTHP-----DHQGRRTLLVALLKQGEGERALAH 66  
Db 19 EEURISGYSFLRGHYSKAILFPEALVILDPISYDHH---TLGGLYLQIGENSQALAV 74  
QY 67 VDQLMQGGEADGSLPWICRSRACQLAGRLDEARFAYQQYL 105  
Db 75 LDQALRMQGDHPLTLLNKTKALFCLGRIEEAT-AIATYLL 112

RESULT 6	
ABO79661	
ID	ABO79661 standard; protein; 870 AA.
XX	
AC	ABO79661;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Pseudomonas aeruginosa polypeptide #11836.
KW	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX	
OS	Pseudomonas aeruginosa.
XX	
PN	US6551795-B1.
XX	
PD	22-APR-2003.
XX	
PF	18-FEB-1999; 99US-00252991.
XX	
PR	18-FEB-1998; 98US-0074788P.
XX	
PR	27-JUL-1998; 98US-0094190P.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX	
DR	WPI; 2003-615309/58.
DR	N-PSDB; ABD13232.
XX	
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
PT	
PS	Disclosure; SEQ ID NO 28407; 455pp; English.
XX	
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biopchip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX	
SQ	Sequence 870 AA;

Db	427	AQWQGLFGILLHCRGERGAADYLREALQLPEDAWSQ--LICRSALMQLATIEGRMDQA	484
Qy	98	RFAYQQVLEEEQNES 113	
Db	485	RLIGRDALRLAREHDS 500	
RESULT 7			
ADX89002			
ID	ADX89002	standard; protein; 719 AA.	
XX	AC	ADX89002;	
XX	DT	21-APR-2005 (first entry)	
XX	DE	Plant full length insert polypeptide seqid 51666.	
XX	KW	plant protectant; plant growth regulant; gene therapy; plant;	
XX	KW	recombinant DNA construct; physical array; plant breeding marker;	
XX	KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
XX	KW	extreme osmotic condition; pathogen tolerance; pest tolerance;	
XX	KW	growth rate; cell cycle pathway; disease resistance;	
XX	KW	galactomannan production; lignin production; plant growth regulator;	
XX	KW	yield; plant growth; plant development; seed oil; protein yield;	
XX	OS	protein content.	
XX	OS	Unidentified.	
XX	FN	US2004034888-A1.	
XX	PD	19-FEB-2004.	
XX	PF	28-APR-2003; 2003US-00425114.	
XX	PR	06-MAY-1999; 99US-00304517.	
XX	PR	05-NOV-2001; 2001US-00985678.	
XX	PA	(LTUJ/) LIU J.	
XX	PA	(ZHOU/) ZHOU Y.	
XX	PA	(KOVA/) KOVALIC D K.	
XX	PA	(SCRE/) SCREEN S E.	
XX	PA	(TABR/) TABASKA J E.	
XX	PA	(CAOY/) CAO Y.	
XX	PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
XX	DR	WPT; 2004-180133/17.	
XX	PT	New recombinant DNA construct, useful for improving plant tolerance to	
XX	PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
XX	PT	pests, for conferring increased resistance to plant disease, or for	
XX	PT	improving yield.	
XX	PS	Claim 1; SEQ ID NO 51666; 15pp; English.	
XX	CC	The invention describes a recombinant DNA construct comprising a	
XX	CC	polynucleotide consisting of a sequence encoding an amino acid sequence	
XX	CC	available in electronic form from the US patent office at	
XX	CC	ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide	
XX	CC	of the invention are also useful in physical arrays of molecules and as	
XX	CC	plant breeding markers. The recombinant DNA construct is useful for	
XX	CC	improving plant tolerance to cold, heat, drought, herbicides, extreme	
XX	CC	osmotic conditions, pathogens or pests, for manipulating growth rate in	
XX	CC	plant cells by modification of the cell cycle pathway, for conferring	
XX	CC	increased resistance to plant disease, for producing galactomannan,	
XX	CC	lignin or plant growth regulators, for increasing the rate of homologous	
XX	CC	recombination in plants, for improving yield by modification of	
XX	CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
XX	CC	or by providing improved plant growth and development under at least one	
XX	CC	stress condition or for modifying seed oil or protein yield and/or	
XX	CC	content. This is the amino acid sequence of a plant full length insert	
XX	CC	polypeptide that can be used in the recombinant DNA construct of the	

[illegible]









Result No.	Score	Query %			DB	ID	Description
		Match	Length	Length			
1	285	47.3	114	2	E35392	hypothetical prote	
2	285	47.3	114	2	T43590	hypothetical prote	
3	284	43.9	109	2	C83432	conserved hypothet	
4	96.5	16.0	142	2	E86543	CT274 hypothetical	
5	96.5	16.0	142	2	E74081	ct274 hypothetical	
6	88.5	14.7	827	2	H83217	probable transcrip	
7	86.5	14.4	384	2	S74806	hypothetical prote	
8	86	14.3	590	2	D83063	hypothetical prote	
9	84	14.0	698	2	A82593	hypothetical prote	
10	83	13.8	1193	2	F83264	hypothetical prote	
11	80.5	13.4	1334	2	T50568	probable multi-dom	
12	80	13.3	548	2	AH2962	cellulose biosynth	
13	80	13.3	553	2	F98320	hypothetical prote	
14	79.5	13.2	576	2	G43976	hypothetical prote	
15	78.5	13.0	139	2	S71534	hypothetical prote	
16	78	13.0	188	2	Q0180	CytB protein - Syn	
17	77	12.8	520	2	S27197	hydroxymethylgluta	
18	77	12.8	673	2	F87636	TPR domain protein	
19	76.5	12.7	1810	2	E88481	protein C16A3.2 [li	
20	76	12.6	320	2	H64332	hypothetical prote	
21	75.5	12.5	844	2	T05227	hypothetical prote	
22	75	12.5	400	2	B64733	protein transport	
23	75	12.5	593	2	AE3443	tetratricopeptide	
24	74.5	12.4	265	2	S31070	rpcE protein - Syn	
25	74.5	12.4	724	2	AG1971	hypothetical prote	
26	74	12.3	400	2	F90642	probable integral	
27	74	12.3	400	2	F85493	probable integral	
28	74	12.3	593	1	XY2ZFG	frzG protein - Myx	
29	73.5	12.2	172	2	B83696	hypothetical prote	

A;Molecule type: DNA  
A;Residues: 1-114 <PER>  
A;Cross-references: UNIPARC:UPI0000000246; EMBL:AF074612; NID:g3822037; PIDN:AAC69796.1;  
A;Experimental source: strain KIMS  
C;Genetics:  
A;Genome: plasmid pCD1  
A;Note: Y0046  
C;Superfamily: chaperrone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;  
Best Local Similarity 52.2%; Pred. No. 1.6e-22;  
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

QY 1 MTWLTSSQODALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRRTLIVALLKQGG 60  
DB 1 MNTLTWRQEFLLNGWLQCCGHAERACILDLALTLPNFEHAGRRCKLVALNNQG 60

QY 61 EAALAHVDLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEONES 113  
DB 61 ERAEKEAQLISHDPLQAGNWCLSLRAQQLNGDLDRKHAYQHYLEKOHNES 113

RESULT 3  
C83432  
conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aeruginosa  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: C83432  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: C83432  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-109 <STO>  
A;Cross-references: UNIPROT:Q91328; UNIPARC:UPI000000C5452; GB:AE004597; GB:AE004091; NID:10871362  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA1702

Query Match 43.9%; Score 264; DB 2; Length 109;  
Best Local Similarity 54.7%; Pred. No. 2.4e-20;  
Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

QY 3 MVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRRTLIVALLKQGEA 62  
DB 1 MTLKPTQRRLLMLGWLHLQCCGPRRAQVLLLEALLSVAPERRDGRALLLALIQQLGEP 60

QY 63 ALAHVDLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLELE 108  
DB 61 AVRLCRQLQDGBEPEPLWRLCLSRALQAGRLDAARAAHARALELE 106

RESULT 4  
E86543  
CT274 hypothetical protein [imported] - Chlamydomophila pneumoniae (strain J138)  
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E86543  
R;Shitai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise, N.  
Nucleic Acids Res. 28, 2311-2314, 2000  
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A;Reference number: A86491; MUID:20330349; PMID:10871362  
A;Accession: E86543  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-142 <STO>  
A;Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:BA000008; NID:g8978795; PIDN:10871362  
A;Experimental source: strain J138  
C;Genetics:

A;Gene: CPj0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;  
Best Local Similarity 33.3%; Pred. No. 0.0083;  
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPDKASVLLAALLQIHP----DHQGGRRRTLIVALLKQGEAALAH 66  
DB 18 EELRISGYSFLRQGHYSKAILFFELVILDPISYDHQ---TLGGLYLQIGENSQALAV 73

QY 67 VDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105  
DB 74 LQALRMQGDHLPTLLNKTALFCLGRIBEAT-AIATYL 111

RESULT 5  
A72081  
ct274 hypothetical protein - Chlamydomophila pneumoniae (strain CWL029)  
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: A72081  
R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999  
A;Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: A72081  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-142 <ARN>  
A;Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:AE001625; GB:AE001363; NID:10192388  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: CPn0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;  
Best Local Similarity 33.3%; Pred. No. 0.0083;  
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPDKASVLLAALLQIHP----DHQGGRRRTLIVALLKQGEAALAH 66  
DB 18 EELRISGYSFLRQGHYSKAILFFELVILDPISYDHQ---TLGGLYLQIGENSQALAV 73

QY 67 VDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105  
DB 74 LQALRMQGDHLPTLLNKTALFCLGRIBEAT-AIATYL 111

RESULT 6  
H83217  
probable transcription regulator PA3420 [imported] - Pseudomonas aeruginosa (strain PAO)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: H83217  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: H83217  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-827 <STO>  
A;Cross-references: UNIPROT:Q9HV15; UNIPARC:UPI000000C5A01; GB:AE004763; GB:AE004091; NID:10984043  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3420  
C;Superfamily: regulatory protein malt

Query Match 14.7%; Score 88.5; DB 2; Length 827;  
Best Local Similarity 26.5%; Pred. No. 0.38;  
Matches 36; Conservative 20; Mismatches 55; Indels 25; Gaps 5;

```
Qy 1 MTWLTSSQODALL-----LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLV 52
| | | | |
Db 354 MVLAIRDELPAALASTPRVLINAWTLTYAGRLAAEDCTGQARFLPMPFSASRQRVLL 413
| | | | |
Qy 53 A-----LLKQGEGEAALAH-----VDQLMQQGEADGFLWLCRSRACOLA---GRIDEA 97
| | | | |
Db 414 AQMQGLFGILLHCRGERGAADYLRALSLQEPEDAWSQG--LICKSALMQLAMIEGRMDQA 471
| | | | |
Qy 98 RFAYQOQYLEEQNES 113
| | | | |
Db 472 RLIGRDALRLAREHDS 487
| | | | |

RESULT 7
S74806
hypothetical protein sll1628 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
A:Accession: S74806
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74806
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <KAN>
A:Cross-references: UNIPROT:P73719; UNIPARC:UPI00000C10C7; EMBL:D90909; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
F:286-299/Domain: tetratricopeptide repeat homology <TT1>
F:300-333/Domain: tetratricopeptide repeat homology <TT2>
F:334-367/Domain: tetratricopeptide repeat homology <TT3>

Query Match 14.4%; Score 86.5; DB 2; Length 384;
Best Local Similarity 28.1%; Pred. No. 0.27;
Matches 27; Conservative 15; Mismatches 49; Indels 5; Gaps 1;

Qy 18 WL-----QLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHVDQLMQ 72
| | | | |
Db 269 WNLGIIQQAQGELETAIASHGEAISINPQWTSQWNGSALGVNGKLEALANFDEALA 328
| | | | |

Qy 73 QGEADGFLWLCRSRACQAGRLDEARFAYQOQYLE 108
| | | | |
Db 329 QNPDDAEVWLSRGLLEAMERKEAIPSYEKALTLE 364
| | | | |

RESULT 8
D83063
hypothetical protein PA4667 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83063
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83063
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: UNIPROT:P42810; UNIPARC:UPI000013A09A; GB:AE004880; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4667

Query Match 14.3%; Score 86; DB 2; Length 590;
Best Local Similarity 29.1%; Pred. No. 0.48;
Matches 30; Conservative 15; Mismatches 58; Indels 0; Gaps 0;
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Qy 13 LLLTGWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHVDQLMQ 72
| | | | |
Db 238 LLLRSRLQSMKRSDEALPLLKAGIKKEHPDDKRVLYARVLLVQENRLDDAKAEFAGLVQ 297
| | | | |
Qy 73 QGEADGFLWLCRSRACQAGRLDEARFAYQOQYLEEQNESTH 115
| | | | |
Db 298 QFPDDDDLRFSLALVCLCAQAWDEARLYLEELVERDSHVDAAH 340
| | | | |

RESULT 9
A82593
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
A:Accession: A82593
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82593
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-698 <SIM>
A:Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NI
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carret,
as-Neto, E.; Docena, C.; El-Dotry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2169

Query Match 14.0%; Score 84; DB 2; Length 698;
Best Local Similarity 28.6%; Pred. No. 0.92;
Matches 26; Conservative 13; Mismatches 50; Indels 2; Gaps 1;

Qy 15 LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHVDQLMQQ 74
| | | | |
Db 250 LTGEFELLAGHPDRALTHLRQVLATWPDPTLEALLTANKQLDMDDDARITLDAALDIK 309
| | | | |

Qy 75 EADGFLWLCRSRACQAGRLDEARFAYQOQYL 105
| | | | |
Db 310 PRNHDLWLARLAVPVGSG--DEARIVIERWL 338
| | | | |

RESULT 10
F83264
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83264
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83264
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1193 <STO>
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Qy 13 LLTTGWLQLOYCHPKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHVDQLMQ 72  
Db 223 LLRSRLQSMKRSDEALPLLKAGIKHEPDDKRVRLAYARLVQNRLLDDAKAFAGLVQ 282  
Qy 73 Q-GEADGPLWLCRSRACQACGLDEARFAYQOYLELEQNESTH 115  
Db 283 QFPDDDDLRFLSLALVCLCEAQAWDEARIYLEELVERDSHVDAAH 326

RESULT 15  
G71534  
hypothetical protein CT274 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: G71534  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,  
Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: G71534  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-139 <ARN>  
A:Cross-references: UNIPROT:O84276; UNIPARC:UPI00000C0B25; GB:AE001300; GB:AE001273; NID  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: CT274

Query Match 13.0%; Score 78.5; DB 2; Length 139;  
Best Local Similarity 28.6%; Pred. No. 0, 6;  
Matches 28; Conservative 20; Mismatches 49; Indels 1; Gaps 1;  
Qy 8 QQQDALLTGWLQYCHPKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHV 67  
Db 15 EELELRISGYSFLRQGHYQKAILFFEALVILDPVVDFTLGLGLYQISENTKALYVL 74  
Qy 68 DQLMQQGEADGPLWLCRSRACQACGLDEARFAYQOYL 105  
Db 75 DQALRMQGDHLPTLLNKTALFCLGRIBEAS-AIASYL 111

Search completed: June 16, 2006, 19:25:05  
Job time : 11.7886 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 91.1024 Seconds  
(without alignments)  
1177.815 Million cell updates/sec

Title: US-10-813-908A-4  
Perfect score: 602  
Sequence: 1 MTWVLTQQDALLTGWLQ.....ARFAYQYLSEEQNESTHP 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	100.0	116	Q8GA92_AERSA	Q8GA92 aeromonas s
2	547	90.9	116	Q5CCAL_AERSO	Q5ccal aeromonas s
3	537	89.2	116	Q699R4_AERHY	Q699r4 aeromonas h
4	483	80.2	116	Q6TLM6_AERHY	Q6tlm6 aeromonas h
5	467	77.6	116	Q5XL08_AERHY	Q5xl08 aeromonas h
6	338	56.1	109	Q84GV9_PHOLU	Q84gv9 photorhabdu
7	324	53.8	109	Q7N0W7_PHOLL	Q7n0w7 photorhabdu
8	285	47.3	114	YSCY_YEREN	Y93ku0 yersinia en
9	285	47.3	114	YSCY_YERPE	P61417 yersinia pe
10	270	44.9	109	Q663K5_YERPS	Q663k5 yersinia ps
11	264	43.9	109	Q30535_PSEAE	Q30535 pseudomonas
12	156.5	26.0	112	Q6QVR8_VIBHA	Q6qv8 vibrio harv
14	148.5	24.7	108	Q66PT9_PASPI	Q66pt9 pasteurella
15	140.5	23.3	112	Q48IR6_PSE14	Q48ir6 pseudomonas
16	138.5	23.0	114	Q87P55_VIBPA	Q87p55 vibrio para
17	126	20.9	700	Q2JHGS_9CYAN	Q2jhg5 cyanobacter
18	118	19.6	798	Q2W4R4_MAGSA	Q2w4r4 magnetospir
19	116	19.3	788	Q31S90_SYNPF	Q31s90 synechococc
20	116	19.3	788	Q5N228_SYNPE	Q5n228 synechococc
21	114.5	19.0	142	Q9AN16_BRAJA	Q9an16 bradyrhizob
22	107.5	17.9	467	Q5LTY9_SILPO	Q5lty9 silicibacte
23	107	17.8	955	Q34XX4_9GAMM	Q34xx4 alkalilimni
24	105.5	17.5	192	Q34XH6_9GAMM	Q34xh6 alkalilimni
25	105	17.4	1837	Q2RRU7_RHURU	Q2rru7 rhodospiril
26	104	17.3	313	Q39ZX0_PELCD	Q39zx0 pelobacter
27	99.5	16.5	530	Q4C0T9_CROWP	Q4c0t9 crocospahe
28	99	16.4	626	Q7W184_BORPA	Q7w184 bordetella
29	99	16.4	628	Q7VUG8_BORPE	Q7vug8 bordetella
30	99	16.4	628	Q7WNY7_BORBR	Q7wny7 bordetella
31	98	16.3	422	Q67NN9_SYNTH	Q67nn9 symbiobacte

32	97	16.1	443	2	Q40MR2_DESAC	Q40mr2 desulfuromo
33	96.5	16.0	142	2	Q9Z8C0_CHLPN	Q9z8c0 chlamydia p
34	95	15.8	774	2	Q2JSZ1_9CYAN	Q2jsz1 cyanobacter
35	94	15.6	582	2	Q5LPE5_SILPO	Q5lpe5 silicibacte
36	93.5	15.5	560	2	Q2ND56_9SPHN	Q2nd56 erythrobact
37	93	15.4	1138	2	Q46GI8_METEA	Q46gi8 methanosarc
38	93	15.4	1349	2	Q9L096_STRCO	Q9l096 streptomyce
39	92.5	15.4	161	2	Q3QHM9_9GAMM	Q3qhm9 shewanella
40	92.5	15.4	652	2	Q399P6_BURS3	Q399p6 burkholderi
41	92	15.3	718	2	Q2IFU6_9DELT	Q2ifu6 anaeromyxob
42	91	15.1	700	2	Q3XC2_2SETFL	Q3xc2 methylobaci
43	91	15.1	1198	2	Q4KCF4_PSEFS	Q4kcf4 pseudomonas
44	90	15.0	547	2	Q9X3W6_ZYMMO	Q9x3w6 zymomonas m
45	90	15.0	1129	2	Q8PTU5_METWA	Q8ptj5 methanosarc

ALIGNMENTS

RESULT 1  
Q8GA92\_AERSA  
ID Q8GA92\_AERSA PRELIMINARY; PRT; 116 AA.  
AC Q8GA92;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE ASCY protein.  
GN Name=ascY;  
OS Aeromonas salmonicida subsp. salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RX MEDLINE=22262111; PubMed=12374830;  
RX DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida.";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
CC -----  
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CC -----  
CC EMBL: AJ458292; CAD30217.1; -; Genomic DNA.  
CC EMBL: AJ616218; CAB83104.1; -; Genomic DNA.  
CC GO: GO:0005488; F:binding; IEA.  
CC DR InterPro: IPR011990; TPR-like\_helical.  
CC DR InterPro: IPR013105; TPR 2.  
CC DR InterPro: IPR013026; TPR region.  
CC DR PROSITE: PS50293; TPR\_REGION; 1.  
CC SEQUENCE 116 AA; 12945 MW; AC1273193B180CB1 CRC64;  
  
Query Match 100.0%; Score 602; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4.5e-51;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTWVLTQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG	60
Db	1	MTWVLTQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG	60
Qy	61	EALAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQYVLEEQNESTHP	116
Db	61	EALAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQYVLEEQNESTHP	116

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RESULT 2
Q5CCAL_AERSO
ID Q5CCAL_AERSO PRELIMINARY; PRT; 116 AA.
AC Q5CCAL;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Ascy protein.
GN Name=ascy;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca fluviatilis.";
RL J. Fish Dis. 28:141-150(2005).
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CC -----
CC EMBL: AJ749609; CAG44554.1; -; Genomic_DNA.
CC GO: GO:0005488; F.binding; IEA.
CC DR InterPro: IPR011990; TPR-like_helical.
CC DR InterPro: IPR013105; TPR.2.
CC SQ SEQUENCE 116 AA; 13033 MW; ECDSE1A5569E48A CRC64;

Query Match 90.9%; Score 547; DB 2; Length 116;
Best Local Similarity 92.4%; Pred. No. 1.1e-45;
Matches 107; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTWVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
DB 1 MTWVLSSQQDALLTGWLQYGHDPDRACVLLALLLHPAHQGGRRLLVALLKQEG 60

QY 61 EAALAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
DB 61 EAALAHVDQLMOQGEVDGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTLP 116

RESULT 3
Q699R4_AERHY
ID Q699R4_AERHY PRELIMINARY; PRT; 116 AA.
AC Q699R4;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ascy.
GN Name=ascy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
CC EMBL: AY528667; AAS91815.1; -; Genomic_DNA.
CC GO: GO:0005488; F.binding; IEA.
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DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR013105; TPR.2.
SQ SEQUENCE 116 AA; 13140 MW; FF798C42C5A104E9 CRC64;

Query Match 89.2%; Score 537; DB 2; Length 116;
Best Local Similarity 90.5%; Pred. No. 1.1e-44;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTWVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
DB 1 MTWVLSSQQDALLTGWLQYGHDPDRACVLLALLLHPSHQGGRRLLVALLKQEG 60

QY 61 EAALAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
DB 61 EAALAHVDQLMLERADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTFP 116

RESULT 4
Q6TLM6_AERHY
ID Q6TLM6_AERHY PRELIMINARY; PRT; 116 AA.
AC Q6TLM6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ascy.
GN Name=ascy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1 pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
CC EMBL: AY394563; AAR26335.1; -; Genomic_DNA.
CC GO: GO:0005488; F.binding; IEA.
CC DR InterPro: IPR005158; BTAD.
CC DR InterPro: IPR011990; TPR-like_helical.
CC DR InterPro: IPR013026; TPR_region.
CC Pfam: PF03704; BTAD; 1.
CC PROSITE: PS50293; TPR_REGION; 1.
CC SQ SEQUENCE 116 AA; 13174 MW; C8CBF54A5459863D CRC64;

Query Match 80.2%; Score 483; DB 2; Length 116;
Best Local Similarity 79.3%; Pred. No. 2.2e-39;
Matches 92; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MTWVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
DB 1 MTWVLSSQQDALLTGWLQYGHDPDRARTLLALLQHPGHESGRRLLVALLKLRG 60

QY 61 EAALAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
DB 61 EAALAHVDHLVSEGVTDALWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116

RESULT 5
Q5XL08_AERHY
ID Q5XL08_AERHY PRELIMINARY; PRT; 116 AA.
AC Q5XL08;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ascy.
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GN Name=ascY;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU; DOI=10.1128/IAI.73.10.6446-6457.2005;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RL Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
CC
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CC -----
CC EMBL; AY763611; AAV30229.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR_2.
DR InterPro; IPR013026; TPR_region.
DR PROSITE; PS0293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 12997 MW; 48E0C804287AB265 CRC64;

Query Match 77.6%; Score 467; DB 2; Length 116;
Best Local Similarity 78.1%; Pred. No. 8.2e-38;
Matches 89; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MTWLTQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 60
Db 1 MTMLTSQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 60

Qy 61 EAALAHVDLMOQGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEEEQNEST 114
Db 61 EEALAHVEQLVAEGEADGALWLCRSRACOLAGRLDEARFAYQHYLEEEQNEPT 114

RESULT 6
ID Q84GY9 PHOLU PRELIMINARY; PRT; 109 AA.
AC Q84GY9
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE 07-FEB-2006, entry version 9.
LSSC.
GN Name=IscC;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., French-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
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CC -----
CC EMBL; AY144116; AAO18049.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
SQ SEQUENCE 109 AA; 12103 MW; 3D6DBE6BD1B84FD2 CRC64;

Query Match 56.1%; Score 338; DB 2; Length 109;
Best Local Similarity 63.1%; Pred. No. 3.5e-25;
Matches 65; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Qy 3 MWLTQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 62
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Db 1 MTLSSAKQSQALLLTGWLQYGHDPDRARILLDALLALHPEHQERRALVSLLLKQEGSA 60
Qy 63 ALAHVDLMOQGEADGPLWLCRSRACOLAGRLDEARFAYQOYL 105
Db 61 AKEHCSLLQEGEQSAAALWLCVSRACQEQGNLEARSAYQYLL 103

RESULT 7
ID Q7NOW7 PHOLL PRELIMINARY; PRT; 109 AA.
AC Q7NOW7
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Type III secretion protein ScTy.
GN Name=ScTy; OrderedLocNames=plu3762;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyassinat G., Gaudriault S.,
RA Medigue C., Lanois K., Powell K., Siquier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RT Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
CC EMBL; BX571871; CAE16134.1; -; Genomic_DNA.
DR Photolist; plu3762; -.
DR BioCyc; PLUM243265:PLU3762-MONOMER; -.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12176 MW; 516493CB4A65312D CRC64;

Query Match 53.8%; Score 324; DB 2; Length 109;
Best Local Similarity 60.2%; Pred. No. 8.4e-24;
Matches 62; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 3 MWLTQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 62
Db 1 MTLSSAKQSQALLLTGWLQYGHDPDRARILLDALLALHPEHQERRALVSLLLKQGSM 60

Qy 63 ALAHVDLMOQGEADGPLWLCRSRACOLAGRLDEARFAYQOYL 105
Db 61 AKEHCTLLQEGEQSAAALWLCVSRACQEQGNLEARSAYQYLL 103

RESULT 8
ID YSCY YEREN STANDARD; PRT; 114 AA.
AC Q93KU0; F21209;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 2.
DE 07-MAR-2006, entry version 17.
DE Chapterone protein yscY (Yop proteins translocation protein Y).
GN Name=yscY;
OS Yersinia enterocolitica.
OS Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OS Plasmid pYval27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.  
 RC STRAIN=serotype O:3; PLASMID=pyv;  
 RX MEDLINE=90264308; PubMed=2160939;  
 RA Viitanen A.-M., Toivanen P., Skurnik M.;  
 RT "The lcrF gene is part of an operon in the lcr region of Yersinia  
 RL enterocolitica O:3.";  
 RL J. Bacteriol. 172:3152-3162(1990).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pyVe227;  
 RA Iriarte M., Lambermont I., Kerbouch C., Cornelis G.R.;  
 RT "Detailed genetic map of the pyVe227 plasmid of Yersinia  
 RL enterocolitica serotype O:9.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pyVe8081;  
 RX MEDLINE=21295118; PubMed=11402007;  
 RX DOI=10.1128/IAI.69.7.4627-4638.2001;  
 RA Snellings N.J., Popek M., Lindler L.E.;  
 RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-  
 RL calcium-response plasmid reveals a new virulence plasmid-associated  
 RL replicon.";  
 RL Infect. Immun. 69:4627-4638(2001).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pyVal27/90;  
 RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;  
 RA Foultier B., Cornelis G.R.;  
 RT "DNA sequence and analysis of the pyVal27/90 virulence plasmid of  
 RL Yersinia enterocolitica strain A127/90.";  
 RL Res. Microbiol. 154:553-557(2003).  
 RN [5]  
 RN PLASMID=pyv;  
 RC MEDLINE=99102236; PubMed=9882687;  
 RA Iriarte M., Cornelis G.R.;  
 RT "Identification of SyoN, YscX, and YscY, three new elements of the  
 RL Yersinia Yop virulon.";  
 RL J. Bacteriol. 181:675-680(1999).  
 CC -!- FUNCTION: Required for Yop secretion. Functions probably as a  
 CC chaperone which stabilizes yscX within the cell, before its  
 CC secretion (by similarity).  
 CC -!- SUBUNIT: Binds to yscX (by similarity).  
 CC -!- INDUCTION: Temperature ceptoms to play the major role in regulation  
 CC of transcription of the lcrF-containing operon of pyv, whereas  
 CC Ca(2+) concentration has only a moderate effect at 37 degrees  
 CC Celsius, and no effect at room temperature.  
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 CC -----  
 CC EMBL; M32097; AAA98432.1; -; Genomic DNA.  
 CC EMBL; AF102990; AAD16819.1; -; Genomic DNA.  
 CC EMBL; AF336309; AAK69217.1; -; Genomic DNA.  
 CC EMBL; AY150843; AAN37530.1; -; Genomic DNA.  
 CC PIR; E35392; E35392.  
 CC InterPro: IPR011950; TPR-like\_helical.  
 KW Chaperone; Plasmid.  
 FT CHAIN 1 114 Chaperone protein yscY.  
 FT FTID=PRO\_000066501.  
 FT VARIANT 38 38 T -> M (in plasmid pyVe8081).  
 FT VARIANT 114 114 P -> L (in plasmid pyVe8081).  
 SQ SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;  
 Query Match 47.3%; Score 285; DB 1; Length 114;  
 Best Local Similarity 52.2%; Pred. No. 5-9e-20;  
 Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;  
 CC

QY 61 EAALAHVDLMQGGADGPIWLCSRAQGLDEARFAYQOYLEEONES 113  
 DB 61 ERAEKAQWLISHDPLQAGNWLCLSRQAQLGDLKARHAYQHYLEKOHNES 113  
 RESULT 9  
 YSCY YERPE  
 ID YSCY\_YERPE STANDARD; PRT; 114 AA.  
 AC Pe1417; P21209;  
 DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 24-MAY-2004, sequence version 1.  
 DE Chaperone protein yscY (Yop proteins translocation protein Y).  
 GN Name=yscY; Ordered locus names=YPCD1.35c, Y5043, Y0046, pCD48;  
 OS Yersinia pestis.  
 OG Plasmid pCD1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 RN [1]\_TaxID=632;  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98427122; PubMed=9746557;  
 RA Ferry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,  
 RA Blattner F.R.;  
 RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of  
 RL Yersinia pestis KIM5.";  
 RL Infect. Immun. 66:4611-4623(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98422474; PubMed=9748454;  
 RA Hu P., Elliott J., McCreedy P., Skowronski E., Garnes J.,  
 RA Kobayashi A., Brubaker R.R., Garcia E.;  
 RT "Structural organization of virulence-associated plasmids of Yersinia  
 RL pestis.";  
 RL J. Bacteriol. 180:5192-5202(1998).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
 RL Nature 413:523-527(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=91001 / Biovar Mediaevalis;  
 RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;  
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,  
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,  
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,  
 RA Yang H., Wang J., Huang P., Yang R.;  
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate  
 RL avirulent to humans.";  
 RL DNA Res. 11:179-197(2004).  
 RN [5]  
 RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.  
 RC STRAIN=KIM8;  
 RX PubMed=10714987; DOI=10.1128/JB.182.7.1834-1843.2000;  
 RA Day J.B., Plano G.V.;  
 RT "The Yersinia pestis yscY protein directly binds YscX, a secreted  
 RL component of the type III secretion machinery.";  
 RL J. Bacteriol. 182:1834-1843(2000).  
 CC -!- FUNCTION: Required for Yop secretion. Functions probably as a  
 CC chaperone which stabilizes yscX within the cell, before its  
 CC secretion.  
 CC

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CC -!- SUBUNIT: Binds to yscY.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
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CC -----
DR EMBL: AF074612; AAC69796.1; -; Genomic_DNA.
DR EMBL: AF053946; AAC62570.1; -; Genomic_DNA.
DR EMBL: AL117189; CAB54912.1; -; Genomic_DNA.
DR EMBL: AE017043; AAS58567.1; -; Genomic_DNA.
DR PIR: T43590; T43590.
DR GenomeReviews: AE017043 GR; pCD48.
DR GenomeReviews: AL117189 GR; YPCD1.35C.
DR BioCyc: YPES229193:PCD48-MONOMER; -.
DR InterPro: IPR011990; TPR-like_helical.
KW Chaperone; Complete proteome; Plasmid.
FT CHAIN 1 114 Chaperone protein yscY.
FT /FTID=PRO.0000066502
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;

Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MTWVLTQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQEG 60
Db 1 MNITLTQRQEFLLNGWLQCCGHAERACILLDALTTLNPEHLAGRRCRLVALLNNQ 60
Qy 61 EALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEEONES 113
Db 61 ERAEKAQWLISHDPLQAGNWLCLSRQAQLNGDLDKARHAYQHYLELKHNES 113

RESULT 10
O663K5 YERPS PRELIMINARY; PRT; 114 AA.
ID O663K5 YERPS
AC O663K5
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE yscY; putative type III secretion protein.
GN OrderedLocNames=pYV0061;
OS Yersinia pseudotuberculosis.
OG Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -----
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CC -----
DR EMBL: BX936399; CAF25404.1; -; Genomic_DNA.
DR GO: GO:0005488; F-binding; IEA.
DR InterPro: IPR011990; TPR-like_helical.
KW Complete proteome; Plasmid.
FT CHAIN 1 114
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;

Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
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Qy 1 MTWVLTQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQEG 60
Db 1 MNITLTQRQEFLLNGWLQCCGHAERACILLDALTTLNPEHLAGRRCRLVALLNNQ 60
Qy 61 EALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEEONES 113
Db 61 ERAEKAQWLISHDPLQAGNWLCLSRQAQLNGDLDKARHAYQHYLELKHNES 113

RESULT 11
O30535 PSEAE PRELIMINARY; PRT; 109 AA.
ID O30535 PSEAE
AC O30535
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Pcr4.
GN Name=pcr4;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RX MEDLINE=98037517; PubMed=9371466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chaperone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
CC -----
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CC -----
DR EMBL: AF010150; AAC45943.1; -; Genomic_DNA.
DR EMBL: DQ000666; AAY17110.1; -; Genomic_DNA.
DR GO: GO:0005488; F-binding; IEA.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR013026; TPR region.
DR PROSITE: PS50293; TPR_REGION; 1.
DR SEQUENCE 109 AA; 12222 MW; 3C3F19535EB038C9 CRC64;

Query Match 44.9%; Score 270; DB 2; Length 109;
Best Local Similarity 55.7%; Pred. No. 1.7e-18;
Matches 59; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

Qy 3 MVLTSQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQGEA 62
Db 1 MTLKPTQRLMLGLWHLQCGQPRRAQVLLALLSVAPERRDGRALLALLQQQLGEP 60
Qy 63 ALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLELE 108
Db 61 AVLRCRQLQEDGEEPGWLCLSRQAQLNGDLDAARAHAHALELE 106

RESULT 12
Q91328 PSEAE PRELIMINARY; PRT; 109 AA.
ID Q91328 PSEAE
AC Q91328
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocNames=PA1702;
OS Pseudomonas aeruginosa.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 15692 / PAOI;  
 RX MEDLINE=2043737; PubMed=10984043; DOI=10.1038/35023079;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Misoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964 (2000).  
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 CC -----  
 CC EMBL: AE004597; AAG05091.1; -; Genomic\_DNA.  
 DR PR; C83432; C83432.  
 DR BIOCyc; PAER287:PAI702-MONOMER; -.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR011990; TPR-like helical.  
 DR InterPro; IPR013026; TPR region.  
 DR PROSITE; PS50293; TPR\_REGION, 1.  
 DR Complete proteome; Hypothetical protein.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 109 AA; 12265 MW; 3C3F19535EAFD937 CRC64;  
 Query Match 43.9%; Score 264; DB 2; Length 109;  
 Best Local Similarity 54.7%; Pred. No. 6.5e-18;  
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 DB 1 MTLKPTQRRLLMLGWLHLQCGPRAQVLEALLSVAPRRDGRALLLALLQCGLGP 60  
 OY 63 ALAHVDQLMOQGEADGPMWLCRSRACQLAGRLDEARFAVQOYLE 108  
 DB 61 AVRLCRQLQEDGEEPLMRLCLSRAEQLAGRLDAARAHAARALELE 106  
 Query Match 26.0%; Score 156.5; DB 2; Length 112;  
 Best Local Similarity 36.3%; Pred. No. 2.4e-07;  
 MATCHES 41; Conservative 22; Mismatches 45; Indels 5; Gaps 3;  
 OY 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEBA 63  
 DB 1 MLQSKDVELLLHAALQVQYQKPEQAITLLDALLEIEPQHQEVRQTLAVACLNSGRYTRS 60  
 OY 64 LAHVLDQLMOQGEADGPMWLCRSRACQLAGRLDEARFAVQOYLE-EEONE 112  
 DB 61 IELCESLLKTEHSNKAGLWFLCLSQARWKQDVEGARHARRHYLQSLNESNE 112  
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 Q66PT9\_PASPI PRELIMINARY; PRT; 108 AA.  
 ID Q66PT9\_PASPI PRELIMINARY; PRT; 108 AA.  
 AC Q66PT9;  
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 7.  
 DE Putative TTSS protein Y.  
 OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Photobacterium.  
 OX NCBI\_TaxID=38294;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;  
 RT "Photobacterium damsela subsp. piscicida encodes a functional type  
 RT three secretion system (TTSS) that is involved in pathogenesis.";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: AY647223; AAU11477.1; -; Genomic\_DNA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR011990; TPR-like helical.  
 DR InterPro; IPR013026; TPR region.  
 DR PROSITE; PS50293; TPR\_REGION, 1.  
 DR SEQUENCE 108 AA; 12478 MW; 75C85FDF70C1470C CRC64;  
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 Best Local Similarity 34.6%; Pred. No. 1.4e-06;  
 Matches 36; Conservative 24; Mismatches 43; Indels 1; Gaps 1;  
 OY 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEBA 63  
 DB 1 MLQTKDVELLLHAALQVQYQKPEQAITLLDALLEIEPQHQEVRQTLAVACLNSGRYTRS 60  
 OY 64 LAHVLDQLMOQGEADGPMWLCRSRACQLAGRLDEARFAVQOYLE 106  
 DB 61 IELCESLLKTEHSNKAGLWFLCLSQARWKQDVEGARHARRHYLQ 104  
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 ID Q48IR6\_PSE14 PRELIMINARY; PRT; 112 AA.  
 AC Q48IR6;  
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.  
 DT 13-SEP-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 7.  
 DE Type III secretion component, putative (EC 2.4.1.-).  
 GN OrderedLocName=PSPPH\_2519;  
 OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=264730;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;  
 RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,  
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,  
 RA Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,  
 RA Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar L., Zhou L.,

RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,  
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,  
RA Mansfield J., Collmer A., Buehl R.;  
RT "Whole-genome sequence analysis of *Pseudomonas syringae* pv.  
RT phaseolicola 1448A reveals divergence among pathovars in genes  
RT involved in virulence and transposition.";   
RL J. Bacteriol. 187:6488-6498(2005).  
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CC -----  
DR EMBL; CP000058; AA234406.1; -: Genomic\_DNA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
DR InterPro; IPR013026; TPR region.  
DR Pfam; PF07721; TPR\_4; 1.  
DR SMART; SM00028; TPR; 1.  
DR PROSITE; PS50005; TPR; 2.  
DR PROSITE; PS50293; TPR\_REGION; 1.  
KW Complete proteome; Glycosyltransferase; Transferase.  
SQ SEQUENCE 112 AA; 12534 MW; 1DACD78D6FAE2C59 CRC64;

Query Match 23.3%; Score 140.5; DB 2; Length 112;  
Best Local Similarity 34.0%; Pred. No. 9e-06;  
Matches 35; Conservative 23; Mismatches 42; Indels 3; Gaps 1;

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Db 4 SQDRECIELHGMGDLVRRSGOPQORALVMLLIAIQLAPTNSALLHSLVIAFTDSGDTDRA 63  
|| : : | : : | : : | : : | : : | : : | : : | : : | : : |  
Qy 64 LAHVDOLMQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLE 106  
|| : : | : : | : : | : : | : : | : : | : : | : : | : : |  
Db 64 IAAIDLRLVEQOGESAAALLLRSRALWKAGRKDDARQCFFRYLE 106  
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Job time : 91.1024 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 21.4081 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-4  
Perfect score: 602  
Sequence: 1 MTWLTSSQDALLLTGWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	45.2	231	2	US-09-252-991A-29962
2	111.5	18.5	470	2	US-09-902-540-12418
3	96.5	16.0	143	2	US-09-198-452A-442
4	96.5	16.0	143	2	US-09-438-185A-425
5	88.5	14.7	870	2	US-09-252-991A-28407
6	83	13.8	1219	2	US-09-252-991A-28840
7	81	13.5	953	2	US-09-902-540-14681
8	80	13.3	368	2	US-09-252-991A-30717
9	79.5	13.2	956	2	US-09-902-540-10395
10	78.5	13.0	169	2	US-08-833-167-58
11	78.5	13.0	169	2	US-08-344-837A-58
12	78	13.0	325	2	US-09-510-238A-273
13	78	13.0	390	2	US-09-902-540-16621
14	77.5	12.9	171	2	US-08-833-167-44
15	77.5	12.9	171	2	US-08-833-167-45
16	77.5	12.9	171	2	US-08-833-167-47
17	77.5	12.9	171	2	US-08-833-167-57
18	77.5	12.9	171	2	US-08-833-167-59
19	77.5	12.9	171	2	US-08-833-167-60
20	77.5	12.9	171	2	US-08-344-837A-44
21	77.5	12.9	171	2	US-09-344-837A-45
22	77.5	12.9	171	2	US-09-344-837A-47
23	77.5	12.9	171	2	US-09-344-837A-57
24	77.5	12.9	171	2	US-09-344-837A-59
25	77.5	12.9	171	2	US-09-344-837A-60
26	77.5	12.9	299	2	US-09-510-238A-193

27	77.5	12.9	302	2	US-09-510-238A-168	Sequence 168, App
28	77.5	12.9	302	2	US-09-510-238A-170	Sequence 170, App
29	77.5	12.9	302	2	US-09-510-238A-172	Sequence 172, App
30	77.5	12.9	302	2	US-09-510-238A-174	Sequence 174, App
31	77.5	12.9	302	2	US-08-957-610A-474	Sequence 474, App
32	77.5	12.9	302	2	US-08-957-610A-476	Sequence 476, App
33	77.5	12.9	302	2	US-08-957-610A-478	Sequence 478, App
34	77.5	12.9	302	2	US-08-957-610A-480	Sequence 480, App
35	77.5	12.9	317	2	US-09-510-238A-169	Sequence 169, App
36	77.5	12.9	317	2	US-09-510-238A-171	Sequence 171, App
37	77.5	12.9	317	2	US-09-510-238A-173	Sequence 173, App
38	77.5	12.9	317	2	US-09-510-238A-175	Sequence 175, App
39	77.5	12.9	317	2	US-08-957-610A-475	Sequence 475, App
40	77.5	12.9	317	2	US-08-957-610A-477	Sequence 477, App
41	77.5	12.9	317	2	US-08-957-610A-479	Sequence 479, App
42	77.5	12.9	317	2	US-08-957-610A-481	Sequence 481, App
43	77.5	12.9	319	2	US-09-510-238A-199	Sequence 199, App
44	77.5	12.9	319	2	US-09-510-238A-201	Sequence 201, App
45	77.5	12.9	319	2	US-08-957-610A-505	Sequence 505, App

ALIGNMENTS

RESULT 1  
US-09-252-991A-29962  
; Sequence 29962, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29962  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29962

Query Match 45.2% Score 272; DB 2; Length 231;  
Best Local Similarity 55.1%; Pred. No. 1.5e-26;  
Matches 59; Conservative 13; Mismatches 35; Indels 0; Gaps 0;  
Qy 2 TMVLTSSQDALLLTGWLQYGHDPDKASVLLAALQIHPDHQGRRTLLVALLKQGE 61  
Db 122 SMTLKQTQQRLLMLGWLHLQCGOPRAQVLLLEALLSVAPERRDGRALLLALLOQGLGE 181  
Qy 62 AALAHVDLMQOGEADGPLMCRSACQLAGRLDEARFAYQQYLELE 108  
Db 182 PAVRLCRLQOEDGEEPGLMWLCLSRARQLAGRLDARAARAHALELE 228

RESULT 2  
US-09-902-540-12418  
; Sequence 12418, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 12418  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-12418

Query Match 18.5%; Score 111.5; DB 2; Length 470;  
Best Local Similarity 36.6%; Pred. No. 1.5e-05;  
Matches 34; Conservative 8; Mismatches 44; Indels 7; Gaps 2;  
  
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Db LLLAGFLDCGYEDGRPGQGPVQAALLRELLRSHPDHAGVHHAWQAMLSGRPEAARD 115  
  
QY 66 HVQLMQGGEADGPMWLCRSRACQLAGRLDEAR 98  
Db 116 SAHRLVALAPRAGPALLSAGRLLRQVGLVAEAR 148

RESULT 3  
US-09-198-452A-442  
; Sequence 442, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Grifffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 442  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-442

Query Match 16.0%; Score 96.5; DB 2; Length 143;  
Best Local Similarity 33.3%; Pred. No. 0.00025;  
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;  
  
QY 11 DALLTGTWQLQYGHDPKASVLLAALLQIHP----DHQGRRTLLVALLKQGEAAALAH 66  
Db 19 EELRISGYSFLRQGHYSKAILFPEALVILDPLSIYDHQ-----TLGGYLQIGENSQALAV 74  
  
QY 67 VQOLMQGGEADGPMWLCRSRACQLAGRLDEARFAYQOYL 105  
Db 75 LQALRMQGDHPLTLNKTALFCLGRIBEAT-AIATYL 112

RESULT 4  
US-09-438-185A-425  
; Sequence 425, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 425  
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; OTHER INFORMATION: Cpn0423  
US-09-438-185A-425

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Best Local Similarity 33.3%; Pred. No. 0.00025;  
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;  
  
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QY 67 VQOLMQGGEADGPMWLCRSRACQLAGRLDEARFAYQOYL 105  
Db 75 LQALRMQGDHPLTLNKTALFCLGRIBEAT-AIATYL 112

RESULT 5  
US-09-252-991A-28407  
; Sequence 28407, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28407  
; LENGTH: 870  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28407

Query Match 14.7%; Score 88.5; DB 2; Length 870;  
Best Local Similarity 26.5%; Pred. No. 0.032;  
Matches 36; Conservative 20; Mismatches 55; Indels 25; Gaps 5;  
  
QY 1 MTWVLTSQQODALL-----LTGWLQYGHDPKASVLLAALLQIHPDHQGRRTLLV 52  
Db 367 MVLLALRDELPAALLASTPRLVILNAWTLTYAGRLAEAEDECIGQLARFLPMPASRQVLL 426  
  
QY 53 A-----LLKQGEAAALAH-----VDOLMQGGEADGPMWLCRSRACOLA---GRLEDA 97  
Db 427 AQWQGLFGILLHCRGERGAADYLRLEALQEPEDAWSQ---LICRSALMQLATIEGRMDQA 484  
  
QY 98 RFAYQOYLEERQNES 113  
Db 485 RLIGRDALRLAREHDS 500

RESULT 6  
US-09-252-991A-28840  
; Sequence 28840, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18







```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15774
; FILING DATE: 06-OCT-1996
; APPLICATION NUMBER: US 60/004,834
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 2910/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-510-238A-273

Query Match 13.0%; Score 78; DB 2; Length 325;
Best Local Similarity 28.2%; Pred. No. 0.18; Indels 24; Gaps 4;
Matches 31; Conservative 15; Mismatches 40; Indels 24; Gaps 4;

Qy 24 GHPDKASVLLAALQIHPDHQGRRTLLVALLK-----QGGEA-----ALAH 66
Db 120 GSPGPGPISTINPPSPKESKSPNMAFLKLSLEQVRKIQGDGAALQEKLCATYKLC 179

Qy 67 VDQLMQQGEADG----PLWLCRSRACQIAG---RLDEARFAYQVYLEEE 109
Db 180 PEELVLLGSLGIPWAPLSLSCPSQALQALAGLSQLHSLGLYQGLQALE 229

RESULT 13
US-09-902-540-16621
; Sequence 16621, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16621
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16621

Query Match 13.0%; Score 78; DB 2; Length 390;
Best Local Similarity 27.3%; Pred. No. 0.23; Indels 42; Gaps 8;
Matches 39; Conservative 17; Mismatches 17; Indels 42; Gaps 8;

Qy 10 QDALLLTGWLQYCHPDK--ASVLLAALQIHPDH-----QGGR--TLLV 52
Db 35 KDSALLGLARLRLAQHDETAARAVLQRLVALHPTPEALSHLARLDAEKGDARQLDLA 94

Qy 53 ALLKQ-----GGEAALAH-----VDQL-----MQQGEADGPLWLCRSRACQIAG 92
Db 95 ALAAQPKAGPFVFNHGRALLGHDRYAAAIPELERALALQPNQATLTTL--GNALQGDK 152

Qy 93 RLDEARFAYQVYLEEQNESTH 115
Db 153 QLDR---ALRRYLEAAEANKTEH 172
```

## RESULT 14

US-08-833-167-44  
; Sequence 44, Application US/08833167  
; Patent No. 6100070

## GENERAL INFORMATION:

APPLICANT: ZURFLUH, LINDA L  
APPLICANT: MCWHERTER, CHARLES A  
APPLICANT: MCKEARN, JOHN P  
APPLICANT: KLEIN, BARBARA K  
APPLICANT: FENG, YIQING  
APPLICANT: BRAFORD-GOLDBERG, SARAH R  
APPLICANT: LEE, STEPHEN C  
TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS  
NUMBER OF SEQUENCES: 129  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,  
ADDRESSEE: CORPORATE PATENT DEPT.  
STREET: P.O. BOX 5110  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60680

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,167  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US 96/15935  
FILING DATE: 04-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,382  
FILING DATE: 05-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BENNETT, DENNIS A  
REFERENCE/DOCKET NUMBER: 2907/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-694-5402  
TELEFAX: 314-694-9095

INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 171 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-167-44

Query Match 12.9%; Score 77.5; DB 2; Length 171;  
Best Local Similarity 32.6%; Pred. No. 0.088;  
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

Qy 45 GGRRTLLVALLK-----QGGEA-----ALAHVDQLMQQGEADG----PLWLCRSR 86  
Db 83 GGSQSFLLKSLQVRKIQGDGAALQEKLCATYKLCHPPEELVLLGSLGIPWAPLSLSCPSQ 142  
Qy 87 ACQIAG---RLDEARFAYQVYLEEE 109  
Db 143 ALQIAGCLSLQHSGLFLYQGLQALE 168

## RESULT 15

US-08-833-167-45  
; Sequence 45, Application US/08833167  
; Patent No. 6100070

GENERAL INFORMATION:  
APPLICANT: ZURFLUH, LINDA L

```

; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRADFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-167-45

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Query Match      12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

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QY 45 GGRRTLLVALLK-----QGEGEA-----ALAHVDQLMQOGEADG---PLWLCSR 86
Db 47 GGSQSFLLKLEQVRKIQGGGALQKLCATYKLCHPPELVLLGHSLGIPWAPLSSCP 106
QY 87 ACQLAG---RLDEARFAYQQYLEEE 109
Db 107 ALQLAGCLSQLHSGFLYQGLLQALE 132

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Search completed: June 16, 2006, 19:28:56
Job time : 22.4081 secs

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Result No.	Score			Query		Length	DB	ID	Description
	Score	Match	Query						
1	602	100.0	116	5	US-10-813-908-4	Sequence 4, Appli			
2	141.5	23.5	113	6	US-11-098-686-10792	Sequence 10792, A			
3	99	16.4	619	4	US-10-282-122A-50903	Sequence 50903, A			
4	96.5	16.0	143	4	US-10-289-762-442	Sequence 442, App			
5	86.5	14.4	713	4	US-10-425-115-201172	Sequence 201172,			
6	86.5	14.4	719	4	US-10-425-114-51666	Sequence 51666, A			
7	84.5	14.0	643	4	US-10-425-115-201174	Sequence 201174,			
8	84.5	14.0	737	4	US-10-425-114-57283	Sequence 57283, A			
9	83	13.8	1586	4	US-10-282-122A-49391	Sequence 49391, A			
10	83	13.8	1864	5	US-10-732-923-2391	Sequence 2391, Ap			
11	79.5	13.2	1743	5	US-10-732-923-18400	Sequence 18400, A			
12	79	13.1	107	6	US-11-096-568A-26393	Sequence 26393, A			
13	79	13.1	108	6	US-11-096-568A-26392	Sequence 26392, A			
14	79	13.1	124	6	US-11-097-143-32322	Sequence 32322, A			
15	78.5	13.0	1234	6	US-10-695-584A-273	Sequence 273, App			
16	78	13.0	325	4	US-10-695-584A-193	Sequence 3, Appli			
17	77.5	12.9	238	3	US-09-920-552-3	Sequence 193, App			
18	77.5	12.9	299	4	US-10-695-584A-168	Sequence 168, App			
19	77.5	12.9	302	4	US-10-695-584A-170	Sequence 170, App			
20	77.5	12.9	302	4	US-10-695-584A-172	Sequence 172, App			
21	77.5	12.9	302	4	US-10-695-584A-174	Sequence 174, App			
22	77.5	12.9	302	4	US-10-695-584A-169	Sequence 169, App			
23	77.5	12.9	317	4	US-10-695-584A-171	Sequence 171, App			
24	77.5	12.9	317	4	US-10-695-584A-173	Sequence 173, App			
25	77.5	12.9	317	4	US-10-695-584A-175	Sequence 175, App			
26	77.5	12.9	317	4	US-10-695-584A-199	Sequence 199, App			
27	77.5	12.9	319	4	US-10-695-584A-199	Sequence 199, App			



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QY      71 MQQGEADGPLWLCRSRACQLA-----GRLEDEARFAYOOYLEL-----EQNEST 114
           |||          |         :||| ||||| :   :   :|||
DB      405 SMSMVANGQETEVASVDCSIGDIYLSGLRYDEAVFYOKALT VFKTSKGENHAT 458
           |||          |         :||| ||||| :   :   :|||

RESULT 6
US-10-425-114-51666
; Sequence 51666, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51666
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700207818_FLI.pep
US-10-425-114-51666

Query Match              14.4%; Score 86.5; DB 4; Length 719;
Best Local Similarity    29.8%; Pred. No. 0.73; Indels 23; Gaps 4;
Matches 34; Conservative 15; Mismatches 42;

QY      19 LQLOYGHDPKASVLIAALLQIHPDHQ-----GGRETLIVALLKQGEGAALAHVDQL 70
           |||          |         :||| :   :   :||| :
DB      356 LQL-----DEAQRLCQIALDIHREHRETASLEETADRLMGLICTDKGHEALEHLVMA 410
           |||          |         :||| :   :   :||| :

QY      71 MQQGEADGPLWLCRSRACQLA-----GRLEDEARFAYOOYLEL-----EQNEST 114
           |||          |         :||| ||||| :   :   :|||
DB      411 SMSMVANGQETEVASVDCSIGDIYLSGLRYDEAVFYOKALT VFKTSKGENHAT 464
           |||          |         :||| ||||| :   :   :|||

RESULT 7
US-10-425-115-201174
; Sequence 201174, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 363326
; SEQ ID NO 201174
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_115056C.1.pep
US-10-425-115-201174

Query Match              14.0%; Score 84.5; DB 4; Length 643;
Best Local Similarity    30.7%; Pred. No. 1.1; Indels 23; Gaps 4;
Matches 35; Conservative 14; Mismatches 42;

QY      19 LQLOYGHDPKASVLIAALLQIHPDHQ-----GGRETLIVALLKQGEGAALAHVDQL 70
           |||          |         :||| :   :   :||| :

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Db 350 LQL-----DEAQRLCQIALDIHREHGCGTASLEETADRLMGLIYDTKGDHEAALEHLVMA 404

Qy 71 MQOGEADGPLWLCRSRACQLA-----GRLDEARFAYQQYLEL-----EEQNEST 114  
|: | | | | | | | | | | | | | | | | | | | | : | : | : | : | : |  
Db 405 GTAMIANGQETEVAUSDGSIIDIVLSLGRYDEAVFAYQKALTVPFKTSKGHNAT 458

RESULT 8  
US-10-425-114-57283  
; Sequence 57283, Application US/10425114  
; Publication No. US2004003488BA1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 57283  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZNFLMO17278G10\_FLI.ppep  
US-10-425-114-57283

Query Match 14.0%; Score 84.5; DB 4; Length 737;  
Best Local Similarity 30.7%; Pred. No. 1.3;  
Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

Qy 19 LQLOYGHDPDKASVLAAALLOHPDHOQ-----GRTLVALLLKQGEFAALAHVDOL 70  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 444 LQL-----DEAQRLCQIALDIHREHGCGTASLEETADRLMGLIYDTKGDHEAALEHLVMA 498

Qy 71 MQOGEADGPLWLCRSRACQLA-----GRLDEARFAYQQYLEL-----EEQNEST 114  
|: | | | | | | | | | | | | | | | | | | | | : | : | : | : | : |  
Db 499 GTAMIANGQETEVAUSDGSIIDIVLSLGRYDEAVFAYQKALTVPFKTSKGHNAT 552

RESULT 9  
US-10-282-122A-49391  
; Sequence 49391, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49391
; LENGTH: 1586
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49391
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Query Match 13.8%; Score 83; DB 4; Length 1586;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;

QY 3 MVLTSQQDALLTGMQLQYGHDPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 62
Db 391 IALNPSDVTVAQVLGEMLLANGDPVGAEQAYRMALRRQADNPDAVRLVGALAAQGRGDE 450
QY 63 ALAHVDQL--MQQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 451 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAEAGDLGARSILFEDAL 501
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```
RESULT 10
US-10-732-923-2391
; Sequence 2391, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2391
; LENGTH: 1864
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-732-923-2391
```

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Query Match 13.8%; Score 83; DB 5; Length 1864;
Best Local Similarity 28.8%; Pred. No. 5.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;

QY 3 MVLTSQQDALLTGMQLQYGHDPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 62
Db 669 IALNPSDVTVAQVLGEMLLANGDPVGAEQAYRMALRRQADNPDAVRLVGALAAQGRGDE 728
QY 63 ALAHVDQL--MQQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 729 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAEAGDLGARSILFEDAL 779
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RESULT 11
US-10-732-923-18400
; Sequence 18400, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
```

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; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18400
; LENGTH: 1743
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-732-923-18400
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Query Match 13.2%; Score 79.5; DB 5; Length 1743;
Best Local Similarity 23.8%; Pred. No. 14;
Matches 25; Conservative 21; Mismatches 40; Indels 19; Gaps 3;

QY 9 QODALLTGMQLQYGHDP--KASVLLAALLQIHPDHQGRRTLLVALLKQGEAALAH 66
Db 1627 QQHVLISKFAQLKFKHGDAERGRTLLGLVTAHPKKTDLWLVAEAVLK----HLGIEH 1682
QY 67 VQQLMQQGEADGGLWLCRSRACQLAGRLDEARFAYQQYLEBEQN 111
Db 1683 ARKVLSE-----RACNLGFSIHKMRPLYKKWLEMSKSH 1714
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RESULT 12
US-11-096-568A-26393
; Sequence 26393, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26393
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13564029
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: Xaa is any aa, unknown or other
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; NAME/KEY: misc feature
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; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26393
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Query Match 13.1%; Score 79; DB 6; Length 107;
Best Local Similarity 35.7%; Pred. No. 0.55;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

QY 49 TLLVALLKQGEAALAHVDQLMQ--QGEADGGLWLCRSRACQLAGRLDEARFAYQQYLE 106
Db 11 TWISGLAMHGHPQEAL----DLFQMDRDPDGATLLAVLRACSLAGRIDDARW---YFE 62
QY 107 LEEQNESTHP 116
Db 63 SMERVYGINP 72
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RESULT 13
US-11-096-568A-26392
; Sequence 26392, Application US/11096568A
; Publication No. US20060048240A1
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; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26392
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108)
; OTHER INFORMATION: Ceres Seq. ID no. 13564028
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (94)..(94)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26392

Query Match      13.1%; Score 79; DB 6; Length 108;
Best Local Similarity 35.7%; Pred. No. 0.56;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

Qy 49 TLLVALLKQGEAEALAHVDOLMQ--QGEADGPLWLCRSACOLAGRLDEARFAYQOYLE 106
Db 12 TWISGLAMHGHPQAL-----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 63

Qy 107 LEEQNESTHP 116
Db 64 SMERVYGINP 73

RESULT 14
US-11-096-568A-26391
; Sequence 26391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26391
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124)
; OTHER INFORMATION: Ceres Seq. ID no. 13564027
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (114)..(114)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26391

Query Match      13.1%; Score 79; DB 6; Length 124;
Best Local Similarity 35.7%; Pred. No. 0.66;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

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Qy 49 TLLVALLKQGEAEALAHVDOLMQ--QGEADGPLWLCRSACOLAGRLDEARFAYQOYLE 106
Db 28 TWISGLAMHGHPQAL-----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 79

Qy 107 LEEQNESTHP 116
Db 80 SMERVYGINP 89

RESULT 15
US-11-097-143-32322
; Sequence 32322, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32322
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32322

Query Match      13.0%; Score 78.5; DB 6; Length 1234;
Best Local Similarity 26.7%; Pred. No. 12;
Matches 36; Conservative 20; Mismatches 44; Indels 35; Gaps 7;

Qy 7 SQOODALLT-----LTGWLQVGHDPDKASVLLAALLQIHPDHQGGRRRTLLVALLKQGEAE 62
Db 1060 SQMENAVLRMRNLNSFLMVPVQVTKYPLLARLYKVTPSHLEGRE-----LLKQAQEKI 1114

Qy 63 ALAHVDOLMQGEADGP--LWL-----CRSRACQ-----LAGRLDEAR 98
Db 1115 EL-HLAHINQEAQ-DVPTKLWRRISSSPNRRASCEIDMINIKLRKMAIDVLEWNHDEV 1172

Qy 99 FAYQOYLEEEQNES 113
Db 1173 FAMEGRLLYTQPTDS 1187

Search completed: June 16, 2006, 20:24:54
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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(without alignments)  
523.484 Million cell updates/sec  
Title: US-10-813-908A-4  
Perfect score: 602  
Sequence: 1 MTWVLTQQDALLTGWLQ.....ARFAYQVLEEQNESTHP 116  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 96747 seqs, 22556637 residues  
Total number of hits satisfying chosen parameters: 96747  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA New:\*
- 1: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB.pbp:\*
  - 2: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pbp:\*
  - 3: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pbp:\*
  - 4: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pbp:\*
  - 5: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pbp:\*
  - 6: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pbp:\*
  - 7: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pbp:\*
  - 8: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pbp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	13.0	737	6	US-10-449-902-53938
2	74	12.3	599	6	US-10-449-902-47030
3	73.5	12.2	711	6	US-10-449-902-46399
4	73	12.1	457	7	US-11-221-332-32
5	71.5	11.9	570	6	US-10-953-349-4630
6	71.5	11.9	772	6	US-10-953-349-4629
7	71.5	11.9	802	6	US-10-953-349-4628
8	71	11.8	495	6	US-10-953-349-31757
9	71	11.8	530	6	US-10-953-349-31756
10	71	11.8	610	6	US-10-953-349-31755
11	70.5	11.7	228	7	US-11-289-102-381
12	70.5	11.7	804	6	US-10-449-902-38463
13	70	11.6	174	7	US-11-183-218-2
14	70	11.6	177	7	US-11-330-353-14
15	70	11.6	204	6	US-10-511-937-2461
16	70	11.6	787	7	US-11-330-353-16
17	69.5	11.5	599	6	US-10-449-902-53783
18	67	11.1	840	6	US-10-449-902-41113
19	66.5	11.0	469	6	US-10-953-349-24112
20	66.5	11.0	473	6	US-10-449-902-47334
21	66.5	11.0	876	6	US-10-449-902-44948
22	66	11.0	525	6	US-10-953-349-34744
23	66	11.0	699	6	US-10-449-902-45095
24	65	10.8	622	6	US-10-505-928-735
25	64.5	10.7	330	6	US-10-449-902-30918

26	64.5	10.7	626	6	US-10-449-902-46528	Sequence 46528, A
27	64.5	10.7	690	6	US-10-449-902-41502	Sequence 41502, A
28	64	10.6	272	6	US-10-449-902-37122	Sequence 37122, A
29	64	10.6	272	6	US-10-449-902-48530	Sequence 48530, A
30	64	10.6	711	6	US-10-449-902-48230	Sequence 48230, A
31	63.5	10.5	519	7	US-11-293-697-4747	Sequence 4747, Ap
32	63.5	10.5	842	7	US-11-266-446-68	Sequence 68, Appl
33	63.5	10.5	2364	7	US-11-289-102-242	Sequence 242, App
34	63	10.5	325	6	US-10-953-349-35099	Sequence 35099, A
35	63	10.5	515	6	US-10-449-902-37134	Sequence 37134, A
36	63	10.5	1011	6	US-10-449-902-36207	Sequence 36207, A
37	62.5	10.4	440	7	US-11-122-986-266	Sequence 266, App
38	62.5	10.4	440	7	US-11-122-986-268	Sequence 268, App
39	62.5	10.4	507	6	US-10-449-902-39176	Sequence 39176, A
40	62.5	10.4	794	6	US-10-449-902-42587	Sequence 42587, A
41	62.5	10.4	972	6	US-10-449-902-41157	Sequence 41157, A
42	62	10.3	235	6	US-10-449-902-34843	Sequence 34843, A
43	62	10.3	408	6	US-10-449-902-46992	Sequence 46992, A
44	62	10.3	587	6	US-10-449-902-40565	Sequence 40565, A
45	62	10.3	623	6	US-10-449-902-47699	Sequence 47699, A

ALIGNMENTS

RESULT 1  
US-10-449-902-53938  
; Sequence 53938, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-R0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53938  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-53938  
Query Match 13.0%; Score 78; DB 6; Length 737;  
Best Local Similarity 34.7%; Pred. No. 0.81;  
Matches 26; Conservative 17; Mismatches 20; Indels 12; Gaps 5;  
Qy 28 KASVLLAALQIHDPHOGGRRTLLVALLKQGEAALAHVDQLMQQGEADGP-----LWLC 83  
Db 289 KARLLKSVITQTPKPPG--WIAAARLEEVAGKLQVA--QLTIQGCCECTNEDVWL- 343  
Qy 84 RSRACOLAGRLDEAR 98  
Db 344 --KACRLASP-DEAK 355  
RESULT 2  
US-10-449-902-47030  
; Sequence 47030, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF



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; SEQ ID NO 4629
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4629

Query Match      11.9%; Score 71.5; DB 6; Length 772;
Best Local Similarity 22.9%; Pred. No. 4.3;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 378 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETBEAKRALKEA 437
Qy 63 -----ALAHVDQLMOQ-----GEADGPLWLCRSRACOLAG 92
Db 438 LKMTNRVELHDAVSHLKQLQKKKKVKKGNANSANEEGPFIVVSSKPKTVG 486

RESULT 7
US-10-953-349-4628
; Sequence 4628, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4628
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4628

Query Match      11.9%; Score 71.5; DB 6; Length 802;
Best Local Similarity 22.9%; Pred. No. 4.5;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 408 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETBEAKRALKEA 467
Qy 63 -----ALAHVDQLMOQ-----GEADGPLWLCRSRACOLAG 92
Db 468 LKMTNRVELHDAVSHLKQLQKKKKVKKGNANSANEEGPFIVVSSKPKTVG 516

RESULT 8
US-10-953-349-31757
; Sequence 31757, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31757

Query Match      11.8%; Score 71; DB 6; Length 495;
Best Local Similarity 25.4%; Pred. No. 2.9;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 121 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 177
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 178 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 228

RESULT 9
US-10-953-349-31756
; Sequence 31756, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match      11.8%; Score 71; DB 6; Length 530;
Best Local Similarity 25.4%; Pred. No. 3.2;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 156 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 212
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 213 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 263

RESULT 10
US-10-953-349-31755
; Sequence 31755, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31755

Query Match      11.8%; Score 71; DB 6; Length 610;
Best Local Similarity 25.4%; Pred. No. 3.7;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 236 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 292
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 293 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 343
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; SEQ ID NO 4629
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4629

Query Match      11.9%; Score 71.5; DB 6; Length 772;
Best Local Similarity 22.9%; Pred. No. 4.3;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 378 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETBEAKRALKEA 437
Qy 63 -----ALAHVDQLMOQ-----GEADGPLWLCRSRACOLAG 92
Db 438 LKMTNRVELHDAVSHLKQLQKKKKVKKGNANSANEEGPFIVVSSKPKTVG 486

RESULT 7
US-10-953-349-4628
; Sequence 4628, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4628
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4628

Query Match      11.9%; Score 71.5; DB 6; Length 802;
Best Local Similarity 22.9%; Pred. No. 4.5;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 408 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETBEAKRALKEA 467
Qy 63 -----ALAHVDQLMOQ-----GEADGPLWLCRSRACOLAG 92
Db 468 LKMTNRVELHDAVSHLKQLQKKKKVKKGNANSANEEGPFIVVSSKPKTVG 516

RESULT 8
US-10-953-349-31757
; Sequence 31757, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31757

Query Match      11.8%; Score 71; DB 6; Length 495;
Best Local Similarity 25.4%; Pred. No. 2.9;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 121 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 177
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 178 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 228

RESULT 9
US-10-953-349-31756
; Sequence 31756, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match      11.8%; Score 71; DB 6; Length 530;
Best Local Similarity 25.4%; Pred. No. 3.2;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 156 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 212
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 213 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 263

RESULT 10
US-10-953-349-31755
; Sequence 31755, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31755

Query Match      11.8%; Score 71; DB 6; Length 610;
Best Local Similarity 25.4%; Pred. No. 3.7;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 236 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 292
Qy 73 QGEADGPLWLCRSRACOLA-----GRLDEARFAYQOYLE-LEEQNESTHP 116
Db 293 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 343
```

```
RESULT 11
US-11-289-102-381
; Sequence 381, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-2

Query Match 11.6%; Score 70; DB 7; Length 174;
Best Local Similarity 34.8%; Pred. No. 1.1;
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;

QY 57 QGEGEA-----ALAHVDQLMQQGEADG----PLWLCRGRACOLAG---RLDEARFA 100
Db 25 QGDGAALQEKLCATYKLCHEPELVLLGHSGLGIPWAPLSSCPQALQACLSQLHSGFL 84
QY 101 YQYLELEE 109
Db 85 YQGLLQALE 93

RESULT 14
US-11-330-353-14
; Sequence 14, Application US/11330353
; Publication No. US20060105429A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guittton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; Sequence 381, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 381
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-381

Query Match 11.7%; Score 70.5; DB 6; Length 804;
Best Local Similarity 29.9%; Pred. No. 1.4;
Matches 26; Conservative 9; Mismatches 31; Indels 21; Gaps 4;

QY 3 MWLTSQDDALLTGMVLQYGHDPDKASVLLAALLQHPHQGRRTLLVALLKQGEA 62
Db 73 MILKQGTQEAIALNSL-----HPELDTNRYLYFHLQQOH-----LTLELRQRETEA 120
QY 63 ALAHVD-QLMQQGEADGSLWLCRSRAC 88
Db 121 ALFAQTQLAEQGE-----ESREC 139

RESULT 12
US-10-449-902-38463
; Sequence 38463, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MCA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38463
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38463

Query Match 11.7%; Score 70.5; DB 6; Length 804;
Best Local Similarity 30.4%; Pred. No. 5.8;
Matches 17; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 49 TLLVALLKQGEAALAHVDQLMQQGEADGSLWLCRSRACOLAGRLDEARFAYQQ 103
Db 503 SMIVALAQHQGEAEAVGLFEEMLRAGVEPDRTYVGVLSACSHAGFVNEGKRYDQ 558

RESULT 13
US-11-183-218-2
```

STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/330,353  
FILING DATE: 12-Jan-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/237,624  
FILING DATE: 10-Sep-2002  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-Jan-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-Jan-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-Jan-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-11-330-353-14

Query Match 11.6%; Score 70; DB 7; Length 177;  
Best Local Similarity 34.8%; Pred. No. 1.2;  
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;  
QY 57 QGEGEA-----ALAHVDQLMQQGEADG-----PLWLCSRACQLAG---RLDEARFA 100  
Db 28 QGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAPLSSCPSQLAGCLSQLHSGFL 87  
QY 101 YQYVLEEE 109  
Db 88 YQGLLQALE 96

RESULT 15  
US-10-511-937-2461  
Sequence 2461, Application US/10511937  
Publication No. US20060088836A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, MacDonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 50661200104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2461  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-511-937-2461  
Query Match 11.6%; Score 70; DB 6; Length 204;  
Best Local Similarity 34.8%; Pred. No. 1.4;  
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;  
QY 57 QGEGEA-----ALAHVDQLMQQGEADG-----PLWLCSRACQLAG---RLDEARFA 100  
Db 55 QGDGAALQEKLCATYKLCHEPELVLLGHSIGIPWAPLSSCPSQLAGCLSQLHSGFL 114  
QY 101 YQYVLEEE 109  
Db 115 YQGLLQALE 123  
Search completed: June 16, 2006, 20:25:53  
Job time : 5.99837 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 18:52:40 ; Search time 76.8618 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-5  
Perfect score: 602  
Sequence: 1 MTWLTSSQDALLTGWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8.\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	DB ID		
1	602	100.0	116	5	ABB80772	Abb80772 A. salmon
2	272	45.2	231	7	ABO81216	Abc81216 Pseudomon
3	111.5	18.5	470	9	ABM93219	Abm93219 M. xanthu
4	99	16.4	619	6	ABU22979	Abu22979 Protein e
5	96.5	16.0	143	2	AAV35024	Aay35024 Chlamydia
6	88.5	14.7	870	7	ABO79661	Abc79661 Pseudomon
7	86.5	14.4	719	8	ADK89002	Adk89002 Plant ful
8	84.5	14.0	122	3	AAH14133	Aab14133 Bordetell
9	84.5	14.0	737	8	ADK94619	Adx94619 Plant ful
10	83	13.8	1219	7	ABO80094	Abc80094 Pseudomon
11	83	13.8	1586	6	ABU21467	Abu21467 Protein e
12	81	13.5	953	9	ABM95482	Abm95482 M. xanthu
13	80	13.3	143	10	AAE60312	Aee60312 Cat chlam
14	80	13.3	368	7	ABO81971	Abc81971 Pseudomon
15	79.5	13.2	517	9	ABE49907	Aeb49907 P. aerugi
16	79.5	13.2	956	9	ABM91196	Abm91196 M. xanthu
17	79	13.1	2519	7	ABM88218	Abm88218 Rice abio
18	78.5	13.0	169	2	AAW15044	Aaw15044 G-CSF rec
19	78.5	13.0	1234	4	ABE68510	Abm68510 Drosophil
20	78	13.0	390	9	ABM97422	Abm97422 M. xanthu
21	78	13.0	577	9	ABE41002	Aeb41002 L. pneumo
22	78	13.0	587	9	ABE37691	Aeb37691 L. pneumo
23	77.5	12.9	171	2	AAW15045	Aaw15045 G-CSF rec

ALIGNMENTS

RESULT 1				
ABB80772	ID	ABB80772	standard; protein; 116 AA.	
XX	AC	ABB80772;		
XX	DT	23-SEP-2002	(first entry)	
XX	DE	A. salmonicida type III secretion protein acr4 sequence.		
XX	KW	Type III secretion protein; acrl; acr2; acr3; acr4; acrD; acrR; acrG; acrv; acrH; antibiotic; vaccine; fish.		
XX	OS	Aeromonas salmonicida.		
XX	PN	WO200240514-A2.		
XX	PD	23-MAY-2002.		
XX	PF	15-NOV-2001; 2001WO-CA001589.		
XX	PR	15-NOV-2000; 2000US-0248864P.		
XX	PA	(FREY/) FREY J.		
XX	PA	(STUB/) STUBER K.		
XX	PA	(THOR/) THORNTON J C.		
XX	PA	(KUZU/) KUZYSK M A.		
XX	PA	(BURI/) BURIAN J.		
XX	PI	Frey J, Stuber K, Thornton JC, Kuzysk MA, Burian J;		
XX	DR	WPI; 2002-537338/57.		
XX	DR	N-FSD; ABN86172.		
XX	PT	Novel protein from Aeromonas salmonicida and nucleic acid encoding the protein, useful for reducing susceptibility of fish to infection by a virulent strain of Aeromonas salmonicida.		
XX	PT	Claim 13; Page 27; 39pp; English.		
XX	PS	The invention relates to A. salmonicida type III secretion genes and encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.		
XX	CC	A. salmonicida type III secretion apparatus is useful for producing selected products, especially Aext. AcrV in vaccine, epitope or epitopic region of AcrV or any other protein of A. salmonicida type III secretion apparatus is useful for reducing the susceptibility of fish to infection		

24	77.5	12.9	171	2	AAW15046	Aaw15046 G-CSF rec
25	77.5	12.9	171	2	AAW15048	Aaw15048 G-CSF rec
26	77.5	12.9	171	2	AAW15050	Aaw15050 G-CSF rec
27	77.5	12.9	171	2	AAW15043	Aaw15043 G-CSF rec
28	77.5	12.9	171	2	AAW15049	Aaw15049 G-CSF rec
29	77.5	12.9	171	2	AAW15051	Aaw15051 G-CSF rec
30	77.5	12.9	238	2	AAV52089	Aay52089 Human ret
31	77.5	12.9	299	2	AAW17131	Aaw17131 Amino aci
32	77.5	12.9	302	2	AAW17108	Aaw17108 Amino aci
33	77.5	12.9	302	2	AAW17112	Aaw17112 Amino aci
34	77.5	12.9	302	2	AAW17106	Aaw17106 Amino aci
35	77.5	12.9	302	2	AAW17110	Aaw17110 Amino aci
36	77.5	12.9	302	2	AAW77845	Aaw77845 Multi-fun
37	77.5	12.9	302	2	AAW77839	Aaw77839 Multi-fun
38	77.5	12.9	302	2	AAW77841	Aaw77841 Multi-fun
39	77.5	12.9	302	2	AAW77843	Aaw77843 Multi-fun
40	77.5	12.9	317	2	AAW17113	Aaw17113 Amino aci
41	77.5	12.9	317	2	AAW17109	Aaw17109 Amino aci
42	77.5	12.9	317	2	AAW17111	Aaw17111 Amino aci
43	77.5	12.9	317	2	AAW17107	Aaw17107 Amino aci
44	77.5	12.9	317	2	AAW77842	Aaw77842 Multi-fun
45	77.5	12.9	317	2	AAW77840	Aaw77840 Multi-fun

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the A. salmonicida type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from A. salmonicida or its genes. The present  
CC sequence represents the A. salmonicida type III secretion protein acr4  
XX  
SQ Sequence 116 AA;

Query Match 100.0%; Score 602; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.1e-65;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWVLTQQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60  
DB 1 MTWVLTQQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60

QY 61 EALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLEEQNESTHP 116  
DB 61 EALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLEEQNESTHP 116

RESULT 2  
ABO81216  
ID ABO81216 standard; protein; 231 AA.  
XX  
AC ABO81216;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #13391.  
XX  
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
PF 18-FEB-1999; 99US-00252991.  
XX  
PR 18-FEB-1998; 98US-0074788P.  
XX  
PR 27-JUL-1998; 98US-0094190P.  
XX  
PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
DR WPI; 2003-615309/58.  
XX  
DR N-PSDB; ABD14787.

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 29962; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 231 AA;

Query Match 45.2%; Score 272; DB 7; Length 231;  
Best Local Similarity 55.1%; Pred. No. 1.2e-24;  
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 TMVLTQQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEGE 61  
DB 122 SMTLKQTQORLLMLGWLHLQCGPRRAQVLLLEALLSVAPERDGRALLALLQQGLGE 181  
QY 62 AALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLELE 108  
DB 182 PAVRLCRLQEDGEEBGLWLCLSRAEQLAGRLDAARAHAHALELE 228

RESULT 3  
ABM93219  
ID ABM93219 standard; protein; 470 AA.  
XX  
AC ABM93219;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE M. xanthus protein sequence, seq id 12418.  
XX  
KW Transgenic plant; DNA replication; gene regulation; gene expression.  
XX  
OS Myxococcus xanthus.  
XX  
PN US6833447-B1.  
XX  
PD 21-DEC-2004.  
XX  
PF 10-JUL-2001; 2001US-00902540.  
XX  
PR 10-JUL-2000; 2000US-0217883P.  
XX  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
XX  
DR WPI; 2005-028716/03.  
XX  
PT New substantially purified Myxococcus xanthus nucleic acid molecule  
PT encoding a nitrite reductase, useful for determining gene expression,  
PT identifying mutations in a gene of interest, and for constructing  
PT mutations in a gene of interest.

PS Example 2; SEQ ID NO 12418; 25pp; English.

CC The invention relates to a substantially purified nucleic acid molecule  
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
CC recombinant DNA construct for expression of a nitrite reductase gene in a  
CC plant cell, and a plant cell comprising the recombinant DNA construct.  
CC The nucleic acid is useful for determining gene expression, identifying  
CC mutations in a gene of interest, and for constructing mutations in a gene  
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent  
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO

SQ Sequence 470 AA;

Query Match 18.5%; Score 111.5; DB 9; Length 470;  
Best Local Similarity 36.6%; Pred. No. 0.00018;  
Matches 34; Conservative 8; Mismatches 44; Indels 7; Gaps 2;

QY 13 LLLTGWLQY---CHDPK----ASVLLAALQIHPDHQGGRTLLVALLKQEGEAAALA 65  
DB 56 LLLAGFLLDGYEPDGRPGQGPQAALLRELLRSHPDHAGVHVWQAMLSGRPEAARD 115

QY 66 HVDQLMOOGEADGPLWLCRSRACQLAGRLDEAR 98  
Db 116 SAHRLVALAPRAGPALLSAGRLQRLVGLVAEAR 148

RESULT 4

ABU22979  
ID ABU22979 standard; protein; 619 AA.

XX AC ABU22979;  
XX 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #8506.

XX DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX KW Bordetella pertussis.

XX OS WO200277183-A2.

XX PN 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA26849.

XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 50903; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 619 AA;

Query Match 16.4%; Score 99; DB 6; Length 619;  
Best Local Similarity 29.0%; Pred. No. 0.0088;  
Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG--HPDKASVLLAALLQIHDPDHOGGRRTLLVALLKKGEGEAAALAHVDQLMOOGEAD 77  
Db 259 LEYGAKVDATRAQHQARAFINRNPDKRLMLAGQADGGDYGALAELOAMGRSRSPD 318

QY 78 GPLWLCRSRACQLAGRLDEARFAYQOYLEEQNE-STHP 116

Db 319 FDLFMFQAQLAYKAGRLDQARGYLQOYLDVQNRQMATA 358

RESULT 5

AAV35024  
ID AAV35024 standard; protein; 143 AA.

XX AC AAV35024;

XX DT 17-OCT-2003 (revised)

XX DT 13-SEP-1999 (first entry)

XX DE Chlamydia pneumoniae transmembrane protein sequence.

XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
XX neutralising epitope.

XX OS Chlamydothiia pneumoniae.

XX PN WO9927105-A2.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-IB001890.

XX PR 21-NOV-1997; 97FR-00014673.

XX PR 04-NOV-1998; 98US-0107078P.

XX PA (GEST ) GENSET.

XX PI Griffais R;

XX DR WPI; 1999-357842/30.

XX PT Genome sequence of Chlamydia pneumoniae.

XX PS Page 921; Disclosure; 1912pp; English.

XX CC AAY34584-Y35879 represent the proteins encoded by all the open reading  
CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C.  
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis  
CC and is thought to be a contributing factor in heart disease, sarcoidosis,  
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
CC polypeptides encoded by the open reading frames of the C. pneumoniae  
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as  
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
CC be used as immunogenic compositions, especially where the vector directs  
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
CC -OCT-2003 to standardise OS field)

XX SQ Sequence 143 AA;

Query Match 16.0%; Score 96.5; DB 2; Length 143;  
Best Local Similarity 33.3%; Pred. No. 0.0026;

Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;



```
CC invention.
XX
SQ Sequence 719 AA;

Query Match      14.4%; Score 86.5; DB 8; Length 719;
Best Local Similarity 29.8%; Pred. No. 0.37;
Matches 34; Conservative 15; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQLQYGHDPKASVLLAALLQIHPDHQ-----GGRTLLVALLKQGEAAALAHVDQL 70
Db 356 LQL-----DEAQLRCQIALDIHREHRETASLEETADRLMLGLICDTKGDHEAALEHLVMA 410
QY 71 MQQGEADGPLWLCRSACOLA-----GRLEARFAYQOYLEL-----EEQNEST 114
Db 411 SMSWVANGQETEVASVDCISGDIYLSLGRYDEAFVQKALTVPFKTSKGENHAT 464

RESULT 8
AAB14133
ID AAB14133 standard; protein; 122 AA.
AC AAB14133;
XX
DT 02-FEB-2001 (first entry)
XX
DE Bordetella pertussis class II gene protein Orf2.
XX
KW Orf2; bacterial infection; anti-bacterial; vaccine; whooping cough;
KW type III secretion system; virulence factor; pathogenicity island.
XX
OS Bordetella pertussis.
XX
PN W0200037493-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-EP010297.
XX
PR 21-DEC-1998; 98GB-00028217.
XX
PA (ULBR ) UNIV LIBRE BRUXELLES.
XX
PI Bollen A, Fauconnier A, Godfroid E;
XX
DR WFI; 2000-452178/39.
DR N-PSDB; AAA64871, AAA64890.
XX
PT Novel polypeptides derived from Bordetella pertussis, useful for treating
PT and diagnosing Bordetella infection.
XX
PS Claim 1; Page 127; 165pp; English.
XX
CC Bordetella pertussis possesses a type III secretion system. Type III
CC secretion systems allow bacteria to target virulence factors directly at
CC host cells. The present sequence is the Orf2 protein of B. pertussis. The
CC present protein is encoded by a class II type gene and is an effector
CC protein involved in the type III secretion system of B. pertussis i.e. a
CC Bordetella pathogenicity protein. The gene of the present protein is
CC located within a pathogenicity island (see AAA64890). A pathogenicity
CC island is a compact, distinct genetic unit carrying virulence genes. The
CC present protein may be used to treat or diagnose B. pertussis infection.
CC e.g. as a vaccine. Whooping cough is a disease caused by infection by B.
CC pertussis
XX
SQ Sequence 122 AA;

Query Match      14.0%; Score 84.5; DB 3; Length 122;
Best Local Similarity 32.6%; Pred. No. 0.062;
Matches 29; Conservative 11; Mismatches 46; Indels 3; Gaps 1;

QY 19 LQLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAAALAHVDQLMQQGEADG 78
Db 26 LQROW---SKTVALLAALDALDAIDSQSLLALGALGYLHQGEPRMALVTLDRALRATPDA 82

OY 79 PLWLCRSACQLAGRLDEARFAYQOYLEL 107
Db 83 AGHLVRAQAMQALNRPDDARQAMRDYMAL 111

RESULT 9
ADX94619
ID ADX94619 standard; protein; 737 AA.
XX
AC ADX94619;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 57283.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 57283; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
```

Best Local Similarity 30.5%, Pred. NO. 2;  
Matches 25; Conservative 15; Mismatches 36; Indels 6; Gaps 2;







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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 11.7886 Seconds  
(without alignments)  
946.773 Million cell updates/sec

Title: US-10-813-908A-5  
Perfect score: 602  
Sequence: 1 MTWVLTSQQQDALLLTGWLQ.....ARFAYQQYLEBEQNESTHP 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	285	47.3	114	2 T35392	hypothetical prote
2	285	47.3	114	2 T43590	hypothetical prote
3	264	43.9	109	2 C83432	conserved hypot het
4	96.5	16.0	142	2 E86543	Ct274 hypothetical
5	96.5	16.0	142	2 A72081	ct274 hypothetical
6	88.5	14.7	827	2 H83217	probable transcrip
7	86.5	14.4	384	2 S74806	hypothetical prote
8	86	14.3	590	2 D83063	hypothetical prote
9	84	14.0	698	2 A82593	hypothetical prote
10	83	13.8	1193	2 R93264	hypothetical prote
11	80.5	13.4	1334	2 T50568	probable multi-dom
12	80	13.3	548	2 A82962	cellulose biosynth
13	80	13.3	553	2 F98320	hypothetical prote
14	79.5	13.2	576	2 S49376	hypothetical prote
15	78.5	13.0	139	2 G71534	hypothetical prote
16	78	13.0	188	2 P00180	CytB protein - Syn
17	77	12.8	520	2 S27197	hydroxymethylgluta
18	77	12.8	673	2 F87636	TPR domain protein
19	76.5	12.7	1810	2 E88481	protein Cl6A3.2 [i
20	76	12.6	320	2 H64332	hypothetical prote
21	75.5	12.5	844	2 T05227	hypothetical prote
22	75	12.5	400	2 B64733	protein transport
23	75	12.5	593	2 A83443	tetratricopeptide
24	74.5	12.4	265	2 S31070	tpcE protein - Syn
25	74.5	12.4	724	2 AG1971	hypothetical prote
26	74	12.3	400	2 F90642	probable integral
27	74	12.3	400	2 F95493	probable integral
28	74	12.3	593	1 XYVZFG	frzG protein - Myx
29	73.5	12.2	172	2 B83696	hypothetical prote

30	73.5	12.2	460	2	D75493	cell division cycl
31	73.5	12.2	990	2	H90703	bacteriophage N4 a
32	73.5	12.2	990	2	C85554	bacteriophage N4 a
33	73	12.1	187	2	G75273	conserved hypot het
34	73	12.1	457	2	JC5422	FK506-binding prot
35	73	12.1	559	2	T12680	peroxisomal target
36	72.5	12.0	990	2	E49351	bacteriophage N4 a
37	72	12.0	407	2	G83477	probable sigma-70
38	71.5	11.9	165	2	AG0619	probable bacteriop
39	71.5	11.9	267	2	E83858	hypothetical prote
40	71.5	11.9	460	2	T02544	hypothetical prote
41	71.5	11.9	802	2	C84733	probable O-GlcNAc
42	71	11.8	320	2	AB3630	taurine-binding pe
43	70.5	11.7	249	2	AI0350	probable fibrial
44	70.5	11.7	761	2	G70393	conserved hypot het
45	70	11.6	204	1	FQHUGL	granulocyte colony

ALIGNMENTS

RESULT 1

E35392

hypothetical protein 4 - Yersinia enterocolitica

C:Species: Yersinia enterocolitica

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Oct-2004

C:Accession: E35392

R:Viitainen, A.M.; Toivanen, P.; Skurnik, M.

J. Bacteriol. 172, 3152-3162, 1990

A:Title: The lcrE gene is part of an operon in the lcr region of Yersinia enterocolitica

A:Reference number: A35392; MUID:90264308; PMID:2160939

A:Accession: E35392

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 <VII>

A:Cross-references: UNIPROT:Q93KU0; UNIPARC:UPI0000000246; GB:M32097; NID:G155454; PID:1

C:Superfamily: chaperone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;

Best Local Similarity 52.2%; Pred. No. 1.6e-22;

Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

Oy 1 MTWVLTSQQQDALLLTGWLQYCHPDKASVLLAALLOIHPDHOGGRTLLVALLKQEG 60

Db 1 MNITLTKRQGEFLLLNGWLQCCHAERACILLDALTLNPEHLAGRRCRLVALLNNQ 60

Oy 61 EALAHVDQLMQQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLEEQNES 113

Db 61 ERAEKEAQLISHDPLOAGNWLCSRAQQLNGDLDRKHAYQHYLELKHNES 113

RESULT 2

T43590

hypothetical protein Y0046 - Yersinia pestis plasmid pCD1

C:Species: Yersinia pestis

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 05-Oct-2004

C:Accession: T43590; T42885

R:Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998

A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.

A:Reference number: 222578; MUID:98422474; PMID:9748454

A:Accession: T43590

A>Status: preliminary;

A:Molecule type: DNA

A:Residues: 1-114 <HUP>

A:Cross-references: UNIPROT:P61417; UNIPARC:UPI0000000246; EMBL:AF053946; NID:G2996222,

A:Experimental source: strain KIM

R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998

A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia

A:Reference number: 222273; MUID:98427122; PMID:9746557

A:Accession: T42885

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA  
A:Residues: 1-114 <PER>  
A:Cross-references: UNIPARC:UPI0000000246; EMBL:AF074612; NID:g3822037; PIDN:AAC69796.1;  
A:Experimental source: strain KIMS  
C:Genetics:  
A:Genome: plasmid pCD1  
A:Note: Y0046  
C:Superfamily: chaperone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;  
Best Local Similarity 52.2%; Pred. No. 1.6e-22;  
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MTWVLTQQQDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60  
Db 1 MNITLTTRQBFLLNGWLQCGHABRACILLDALLTLNPEHLAGRRCRLVALLNNQ 60  
Qy 61 EAALAHVDQLMOQGEADGPLWLCRRACQAGRLDEARFAYQOYLEEONES 113  
Db 61 ERAEKEAQLWLSHPDPLQAGNWLCRSRAQQNLGDLKARHAYQHYLELKOHNES 113

RESULT 3  
C83432  
conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: C83432  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Buchanan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: C83432  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109 <STO>  
A:Cross-references: UNIPROT:Q91328; UNIPARC:UPI000000C5452; GB:AE004597; GB:AE004091; NID:g8978795;  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1702

Query Match 43.9%; Score 264; DB 2; Length 109;  
Best Local Similarity 54.7%; Pred. No. 2.4e-20;  
Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

Qy 3 MVLTSQQDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 62  
Db 1 MTLKPTQQRLLMLGWLQCGQPRRAQVLEALLSVAPERRDRRRALLALLQQLGEP 60  
Qy 63 ALAHVDQLMOQGEADGPLWLCRRACQAGRLDEARFAYQOYLEE 108  
Db 61 AVRLCRQLQEDGEEPGPLWLCRSRAEQLAGRLDARAHARALELE 106

RESULT 4  
E86543  
CT274 hypothetical protein [imported] - Chlamydomophila pneumoniae (strain J138)  
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86543  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiguro, N.  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871362  
A:Accession: E86543  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-142 <STO>  
A:Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:BA000008; NID:g8978795;  
A:Experimental source: strain J138  
C:Genetics:

Qy 1 MTWLTSSQDALL-----LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLV 52  
Db 354 MVLALRDLPAALLASTPRVLINAWTLLYAGRLAEADCTGQGLARFLPMPASRQRVLL 413  
Qy 53 A-----LLKQGEAEALAH-----VDQLMQQGEADGPIWLCRSRACOLA---GRIDEA 97  
Db 414 AQWQGLFGILLHCRGERGAADYLRLEALEQLPEDAWSQG--LICRSALMQLAMIEGRMDQA 471  
Qy 98 RFAYQOQYLEBEQNES 113  
Db 472 RLIGRDALRLAREHDS 487

RESULT 7  
S74806  
hypothetical protein sll1628 - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 05-Oct-2004  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S74806  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-384 <KAN>  
A;Cross-references: UNIPROT:P73719; UNIPARC:UPI00000C10C7; EMBL:D90909; GB:AB001339; NID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
F;266-299/Domain: tetratricopeptide repeat homology <TT1>  
F;300-333/Domain: tetratricopeptide repeat homology <TT2>  
F;334-367/Domain: tetratricopeptide repeat homology <TT3>

Query Match 14.4%; Score 86.5; DB 2; Length 384;  
Best Local Similarity 28.1%; Pred. No. 0.27;  
Matches 27; Conservative 15; Mismatches 49; Indels 5; Gaps 1;

Qy 18 WL-----QLQVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQ 72  
Db 269 WNLGIIQQAQRGELETAIAGNGEAI SLNPQWTSNAQWNGSALGVNGKLEALANFDEALA 328

Qy 73 QGEADGPIWLCRSRACOLAGRLDEARFAYQOYLE 108  
Db 329 QNPDDAEVWLSRGLLLEAMERKEAIPSEYKALTLE 364

RESULT 8  
D83063  
hypothetical protein PA4667 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: D83063  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: D83063  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-590 <STO>  
A;Cross-references: UNIPROT:P42810; UNIPARC:UPI0000013A09A; GB:AE004880; GB:AE004091; NID  
A;Experimental source: strain PAO1  
C;Genetics:  
A;Gene: PA4667

Query Match 14.3%; Score 86; DB 2; Length 590;  
Best Local Similarity 29.1%; Pred. No. 0.48;  
Matches 30; Conservative 15; Mismatches 58; Indels 0; Gaps 0;

Qy 13 LLLTWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQ 72  
Db 238 LLLRSRLQSMKRSDEALPLLKAGIKHEPPDDKRVLYARVLLVQNRLDDAKAEFAGLVQ 297  
Qy 73 QGEADGPIWLCRSRACOLAGRLDEARFAYQOYLEBEQNES 115  
Db 298 QFPDDDDLRFLSLVLCLEAQAWDEARIYLELVERDHSVDAAH 340

RESULT 9  
A82593  
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: A82593  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: A82593  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-698 <SIM>  
A;Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NID  
A;Experimental source: strain 9a5c  
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carret, as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kutamae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF2169

Query Match 14.0%; Score 84; DB 2; Length 698;  
Best Local Similarity 28.6%; Pred. No. 0.92;  
Matches 26; Conservative 13; Mismatches 50; Indels 2; Gaps 1;

Qy 15 LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQ 74  
Db 250 LTGEFELLAGHPDRALTHLRQVLATWPDPTLEALLITANKQLDMDDDARITLDAALDIK 309

Qy 75 EADGPIWLCRSRACOLAGRLDEARFAYQOYL 105  
Db 310 PRNHDLWLARLAVPVGS--DEARIVIERWL 338

RESULT 10  
F83264  
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: F83264  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: F83264  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1193 <STO>



Qy	13	LLLLTGWLQLOVCHPPKASVLAALLQIHPDHOGGRTLLVALLKQGEAGAAAHVQDLQMQ	72
Db	223	LLLLSRLLQSMKRSDEALPLPKAGIKIEHPDVKRVLAVARLLVEQNRLDDAKAEFAGLVQ	282
Qy	73	Q-GEADGPLWLCRSACQLAGRLDEARFAYQOYLEEQNESTH	115
Db	283	QFPDDDDLRFSIALVLCLEAAQAWDEARYYLEELVERDSDHVAAH	326

RESULT 15

G71534  
hypotheical protein CT274 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: G71534  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, S.  
Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis CT274  
A:Reference number: A71570; MUID:9900809; PMID:9784136  
A:Accession: G71534  
A:Status: preliminary.  
A:Molecule type: DNA  
A:Residues: 1-139 <ARN>  
A:Cross-references: UNIPROT:O84276; UNIPARC:UPI00000C0B25; GB:AE001300; GB:AE001273; NID  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: CT274

Query Match 13.0%; Score 78.5; DB 2; Length 139;  
Best Local Similarity 28.6%; Pred. No. 0.6;  
Matches 28; Conservative 20; Mismatches 49; Indels 1; Gaps 1;

Qy		8 QQQDALLLTGWLQLQYGHDPDKASVLLAALLQHHPDHQGGRRTLIVALLKQGEGERAAAHV	67
	:	:	:
	:	:	:
	:	:	:
Dd	15 EEELRISGSFRLRGCHYOXAILFFPALVIDPLSVDFQTGLGGLYLQISENTKALYYL	74	

Qy	68	DQLMQQGEADG	PLWL	CRSRAC	QLAGRL	DEARFAYQYL	105
		:	:	:	:	:	
D <sub>b</sub>	75	DQALRMQGDH	PLTL	NKTKAL	FCLGR	EIASYL	111

Search completed: June 16, 2006, 19:25:05  
Job time : 13.7886 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 91.1024 Seconds  
(without alignments)  
1177.815 Million cell updates/sec

Title: US-10-813-908A-5  
Perfect score: 602  
Sequence: 1 MTWVLTSSQDDALLLTGWLQ.....ARFAYQOYLEBQNESTHP 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	2	Q8GA92 aeromonas s
2	547	90.9	116	2	Q5CCAL aeromonas s
3	537	89.2	116	2	Q699R4 aeromonas h
4	483	80.2	116	2	Q6TLM6 aeromonas h
5	467	77.6	116	2	Q5XL08 aeromonas h
6	338	56.1	109	2	Q84GV9 photorhabdu
7	324	53.8	109	2	Q7N0W7 photorhabdu
8	285	47.3	114	1	YSCY_YEREN
9	285	47.3	114	1	YSCY_YERPE
10	285	47.3	114	2	Q663K5 yersinia ps
11	270	44.9	109	2	Q30535 pseudomonas
12	264	43.9	109	2	Q91328 pseudomonas
13	156.5	26.0	112	2	Q6QVR8 vibrio harv
14	148.5	24.7	108	2	Q66PT9 pasteurella
15	140.5	23.3	112	2	Q48IR6 pseudomonas
16	138.5	23.0	114	2	Q87P55 vibrio para
17	126	20.9	700	2	Q2JHG5 cyanobacter
18	118	19.6	798	2	Q2W4R4 magnetospir
19	116	19.3	788	2	Q31890 synecococc
20	116	19.3	788	2	Q5N228 synecococc
21	114.5	19.0	142	2	Q9AN16 bradyrhizob
22	107.5	17.9	467	2	Q5LTY9 silicibacte
23	107	17.8	955	2	Q34XX4 alkalilimni
24	105.5	17.5	192	2	Q34XH6 9GAMM
25	105	17.4	1837	2	Q2RRU7 RHORU
26	104	17.3	313	2	Q39ZK0 PELCD
27	99.5	16.5	530	2	Q4C0T9 CROPT
28	99	16.4	626	2	Q7W184 BORPA
29	99	16.4	628	2	Q7VUG8 BORPE
30	99	16.4	628	2	Q7WNY7 BORER
31	98	16.3	422	2	Q67NN9_SYMTH

32	97	16.1	443	2	Q40MR2 DESAC	Q40mr2 desulfuromo
33	96.5	16.0	142	2	Q9Z8C0 CHLPN	Q9z8c0 chlamydia p
34	95	15.8	774	2	Q2JSZ1_9CYAN	Q2jsz1 cyanobacter
35	94	15.6	582	2	Q5LPE5_SILPO	Q5lpe5 silicibacte
36	93.5	15.5	560	2	Q2N556_SPHN	Q2nd56 erythroba
37	93	15.4	1138	2	Q46GI8_METHA	Q46gi8 methanosarc
38	93	15.4	1349	2	Q9L096_STRCO	Q9l096 streptomyce
39	92.5	15.4	161	2	Q3QHM9_9GAMM	Q3qhm9 shewanella
40	92.5	15.4	652	2	Q399P6_BURS3	Q399p6 burkholderi
41	92	15.3	718	2	Q2IFU6_9DELT	Q2ifub6 anaeromyxob
42	91	15.1	700	2	Q3X9C2_METEL	Q3x9c2 methylobaci
43	91	15.1	1198	2	Q4KCF4_PSEF5	Q4kcf4 pseudomonas
44	90	15.0	547	2	Q9X3W6_ZYMMO	Q9x3w6 zymomonas m
45	90	15.0	1129	2	Q8PTJ5_METWA	Q8ptj5 methanosarc

ALIGNMENTS

RESULT 1  
Q8GA92\_AERSA  
ID Q8GA92\_AERSA PRELIMINARY; PRT; 116 AA.  
AC Q8GA92  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE Ascy protein.  
GN Name=ascy;  
OS Aeromonas salmonicida subsp. salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RX MEDLINE=22262111; PubMed=12374830;  
RX DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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CC -----  
CC EMBL; AJ458292; CAD30217.1; -; Genomic\_DNA.  
CC EMBL; AJ616218; CAE83104.1; -; Genomic\_DNA.  
CC GO; GO:0005488; F:binding; IEA.  
CC DR InterPro; IPR011990; TPR-like\_helical.  
CC DR InterPro; IPR013105; TPR 2.  
CC DR InterPro; IPR013026; TPR\_region.  
CC DR PROSITE; PS50293; TPR\_REGION; 1.  
CC SEQUENCE 116 AA; 12945 MW; AC1273193B180CB1 CRC64;

Query Match	Score	602;	DB 2;	Length	116;
Best Local Similarity	100.0%;	Pred. No.	4.5e-51;		
Matches	116;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
QY	1	MTWVLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG	60		
Db	1	MTWVLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG	60		
QY	61	EALAHVDQIMQOGEADGPLWLCRSRACLAGRLDEARFAYQOYLEBQNESTHP	116		
Db	61	EALAHVDQIMQOGEADGPLWLCRSRACLAGRLDEARFAYQOYLEBQNESTHP	116		

```
RESULT 2
OSCCAL_AERSO PRELIMINARY; PRT; 116 AA.
ID Q5CCAL_AERSO
AC Q5CCAL;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acyl protein.
GN Name=acy;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca fluviatilis."
RL J. Fish Dis. 28:141-150(2005).
CC -----
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CC -----
DR EMBL; AJ749609; CAG4554.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR 2.
SQ SEQUENCE 116 AA; 13033 MW; ECD5E1A55569E48A CRC64;

Query Match 90.9%; Score 547; DB 2; Length 116;
Best Local Similarity 92.2%; Pred. No. 1.le-45;
Matches 107; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 3
Q699R4_AERHY PRELIMINARY; PRT; 116 AA.
ID Q699R4_AERHY
AC Q699R4;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acyl.
GN Name=acy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas hydrophila strain."
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91815.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR 2.
SQ SEQUENCE 116 AA; 13140 MW; FF798C42C5A104E9 CRC64;

Query Match 89.2%; Score 537; DB 2; Length 116;
Best Local Similarity 90.5%; Pred. No. 1.le-44;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 4
Q6TLM6_AERHY PRELIMINARY; PRT; 116 AA.
ID Q6TLM6_AERHY
AC Q6TLM6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acyl.
GN Name=acy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1 pathogenesis."
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL; AY394563; AAR26335.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR005158; BTAD.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF03704; BTAD; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 13174 MW; C8CBF54A5459863D CRC64;

Query Match 80.2%; Score 483; DB 2; Length 116;
Best Local Similarity 79.3%; Pred. No. 2.2e-39;
Matches 92; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTQQDALLLTGWLQYGHDPDKASVLLAALLQHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDLMQOGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 5
Q5XL08_AERHY PRELIMINARY; PRT; 116 AA.
ID Q5XL08_AERHY
AC Q5XL08;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acyl.
```





RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.  
 RC STRAIN=serotype O:3; PLASMID=pYV;  
 RX MEDLINE=90264308; PubMed=2160939;  
 RA Vilitanen A.-M., Toivanen P., Skurnik M.;  
 RT "The lcrE gene is part of an operon in the lcr region of Yersinia  
 J. Bacteriol. 172:3152-3162(1990).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RP STRAIN=22703 / Serotype O:9 / Biotype 2; PLASMID=pYve227;  
 RA Iriarte M., Lambert M., Kerbourn C., Cornelis G.R.;  
 RT "Detailed genetic map of the pYve227 plasmid of Yersinia  
 enterocolitica serotype O:9";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RP STRAIN=6081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;  
 RC MEDLINE=21295118; PubMed=11402007;  
 RX DOI=10.1128/JAI.69.7.4627-4638.2001;  
 RA Snellings N.J., Popek M., Lindler L.E.;  
 RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-  
 calcium-response plasmid reveals a new virulence plasmid-associated  
 replicon";  
 RL Infect. Immun. 69:4627-4638(2001).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RP STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYVal27/90;  
 RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;  
 RA Foulciet B., Cornelis G.R.;  
 RT "DNA sequence and analysis of the pYVal27/90 virulence plasmid of  
 Yersinia enterocolitica strain A127/90";  
 RL Res. Microbiol. 154:553-557(2003).  
 RN [5]  
 RP PLASMID=pYV;  
 RC MEDLINE=99102236; PubMed=9882687;  
 RX Iriarte M., Cornelis G.R.;  
 RA "Identification of SyncN, YscX, and YscY, three new elements of the  
 Yersinia Yop virulon";  
 RL J. Bacteriol. 181:675-680(1999).  
 CC -1- FUNCTION: Required for Yop secretion. Functions probably as a  
 chapterone which stabilizes yscX within the cell, before its  
 secretion (By similarity).  
 CC -1- SUBUNIT: Binds to yscX (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).  
 CC -1- INDUCTION: Temperature seems to play the major role in regulation  
 of transcription of the lcrE-containing operon of pYV, whereas  
 Ca(2+) concentration has only a moderate effect at 37 degrees  
 Celsius, and no effect at room temperature.  
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 CC -----  
 CC EMBL; M22097; AAA98432.1; -; Genomic DNA.  
 CC EMBL; AF102990; AAD16819.1; -; Genomic DNA.  
 CC EMBL; AF363609; AAK69217.1; -; Genomic DNA.  
 CC EMBL; AY150843; AAN37530.1; -; Genomic DNA.  
 CC PIR; E35392; E35392.  
 CC InterPro; IPR011990; TPR-like\_helical.  
 KW Chapterone; Plasmid.  
 FT CHAIN 1 114 Chapterone protein yscY.  
 FT VARIANT 38 38 /FTId=pYV 000006501.  
 FT VARIANT 114 114 T -> M (in plasmid pYve8081).  
 FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;  
 Query Match 47.3%; Score 285; DB 1; Length 114;  
 Best Local Similarity 52.2%; Pred. No. 5.9e-20;  
 Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;  
 QY 1 MTWVLTSSQDALLTGWLQVGHDPKASVLLAALQIHPDHQGRRTLLVALLKQGG 60  
 DB 1 MNITLTKROQEFLLNGWLQVGHDPKASVLLAALQIHPDHQGRRTLLVALLKQGG 60

QY 61 EAALAHVDLMQGGADGFLWLCRSRACOLACGLRDLDEARFAYQOYLELEQNES 113  
 DB 61 ERAEKEAQWLISHDPLQAGNWLCLSLRAQQLNGDLQKARHAYOHYLELKQHNES 113  
 RESULT 9  
 YSCY YERPE  
 ID YSCY YERPE STANDARD; PRT; 114 AA.  
 AC P61417; P21209;  
 DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 24-MAY-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 16.  
 DE Chapterone protein yscY [Yop proteins translocation protein Y].  
 GN Name=yscY; OrderedLocusNames=YPCD1.35c, y5043, y0046, pCD48;  
 OS Yersinia pestis.  
 OG Plasmid pCD1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 RN [1]\_TaxID=632;  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98427122; PubMed=9746557;  
 RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,  
 RA Blattner F.R.;  
 RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of  
 Yersinia pestis KIM5";  
 RL Infect. Immun. 66:4611-4623(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98422474; PubMed=9748454;  
 RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,  
 RA Kobayashi A., Brubaker R.R., Garcia E.;  
 RT "Structural organization of virulence-associated plasmids of Yersinia  
 pestis";  
 RL J. Bacteriol. 180:5192-5202(1998).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holoyston P.C.F., Quail M.A., Rutherford K.M.,  
 RA Leather S., Moule S., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague";  
 RL Nature 413:523-527(2001).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=91001 / Biovar Mediaevalis;  
 RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;  
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,  
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,  
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,  
 RA Yang H., Wang J., Huang P., Yang R.;  
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate  
 avirulent to humans";  
 RL DNA Res. 11:179-197(2004).  
 RN [5]  
 RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.  
 RC STRAIN=KIM5;  
 RX PubMed=10714987; DOI=10.1128/JB.182.7.1834-1843.2000;  
 RA Day J.B., Plano G.V.;  
 RT "The Yersinia pestis yscY protein directly binds YscX, a secreted  
 component of the type III secretion machinery";  
 RL J. Bacteriol. 182:1834-1843(2000).  
 CC -1- FUNCTION: Required for Yop secretion. Functions probably as a  
 chapterone which stabilizes yscX within the cell, before its  
 secretion.

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CC -!- SUBUNIT: Binds to yscY.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -----
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CC -----
DR EMBL: AF074612; AAC69796.1; -; Genomic_DNA.
DR EMBL: AF053946; AAC82570.1; -; Genomic_DNA.
DR EMBL: AL117189; CAB54912.1; -; Genomic_DNA.
DR EMBL: AE017043; AAS58567.1; -; Genomic_DNA.
DR PIR: T43590; T43590.
DR GenomeReviews: AE017043 GR; pCD48.
DR BioCyc: YPES229193:PCD48-MONOMER; -.
DR InterPro: IPR011990; TPR-like_helical.
DR Complete proteome; Plasmid.
KW CHAIN 1 114
FT CHAIN 1 114
FT FTId=PRO 0000066502.
FT FTId=PRO 0000066502.
SQ SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;

Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MTWVLTQQDALLTGWLOQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60
Db 1 MNITLTTRQQBFLLNGWLQCCGHAERACILLDALLTLNPEHLAAGRCRLVALLNNQ 60
Qy 61 EAALAHVDQLMQOGEADGPLWLCRSRACQLAGRLDEARFAYQOYLEEQNES 113
Db 61 ERAEKAQWLISHDPLOAGNWLCLSRAQQLNGDLDKARHAYQHYLELKHNES 113

RESULT 10
ID Q663K5 YERPS PRELIMINARY; PRT; 114 AA.
AC Q663K5
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE YscY; putative type III secretion protein.
GN OrderedLocusNames=pYV0061.
OS Versinia pseudotuberculosis.
OC Plasmid pIV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Versinia pestis through whole-genome
RT comparison with Versinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -----
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CC -----
DR EMBL: BX936399; CAF25404.1; -; Genomic_DNA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR011990; TPR-like_helical.
KW Complete proteome; Plasmid.
SQ SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;

Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
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Qy 1 MTWVLTQQDALLTGWLOQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60
Db 1 MNITLTTRQQBFLLNGWLQCCGHAERACILLDALLTLNPEHLAAGRCRLVALLNNQ 60
Qy 61 EAALAHVDQLMQOGEADGPLWLCRSRACQLAGRLDEARFAYQOYLEEQNES 113
Db 61 ERAEKAQWLISHDPLOAGNWLCLSRAQQLNGDLDKARHAYQHYLELKHNES 113

RESULT 11
ID O30535 PSEAE PRELIMINARY; PRT; 109 AA.
AC O30535
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Pcr4.
GN Name=pCr4;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RX MEDLINE=98037517; PubMed=9371466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon."
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Bröms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chaperone That Is
RT Required for Regulation of Yersinia Type III Secretion."
RL J. Bacteriol. 187:7738-7752(2005).
CC -----
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CC -----
DR EMBL: AF010150; AAC45943.1; -; Genomic_DNA.
DR EMBL: DQ000666; AAY17110.1; -; Genomic_DNA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR013026; TPR region.
DR PROSITE: PS0293; TPR_REGION; 1.
DR SEQUENCE 109 AA; 12222 MW; 3C3F19535EB038C9 CRC64;

Query Match 44.9%; Score 270; DB 2; Length 109;
Best Local Similarity 55.7%; Pred. No. 1.7e-18;
Matches 59; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

Qy 3 MVLTSQQDALLTGWLOQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA 62
Db 1 MTLKPTQORLLMLGWLHLQCGQPRRAQVLEALLSVAPERRDGRALLALLQQLGEP 60
Qy 63 ALAHVDQLMQOGEADGPLWLCRSRACQLAGRLDEARFAYQOYLELE 108
Db 61 AVRLCRLQDGEPEGPGWLCLSLRAEQLAGRLDRAARAHAALELE 106

RESULT 12
Q91328 PSEAE
ID Q91328 PSEAE PRELIMINARY; PRT; 109 AA.
AC Q91328
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocusNames=PA1702;
OS Pseudomonas aeruginosa.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
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CC -----
DR EMBL; AE004597; AAG05091.1; -; Genomic_DNA.
DR PIR; C83432; C83432.
DR BLOSCY; PAER287; PAI702-MONOMER; -.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
DR InterPro; IPR013026; TPR region.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 109 AA; 12265 MW; 3C3F19535EAFD937 CRC64;

Query Match 43.9%; Score 264; DB 2; Length 109;
Best Local Similarity 54.7%; Pred. No. 6.5e-18;
Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

Qy 3 MVLTSQQDALLTGWLQYQHPDKASVLLAALLQHPHQGRRTLLVALLKQGEAA 62
Db 1 MTLKPTQORLLMLGWLHLCQGPRAQVLLLEALLSVAPRRDGRALLLALQQLGEP 60
Qy 63 ALAHVDOLMGOOGADGFLWLCRSRACQLAGRLDEARFAYQOYLE 108
Db 61 AVRLCRLQDGEGBEPLWLCRSRACQLAGRLDEARFAYQOYLE 106

RESULT 13
Q6QVR8_VIBHA
ID Q6QVR8_VIBHA PRELIMINARY; PRT; 112 AA.
AC Q6QVR8
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Vacy.
GN Name=vacy;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY524044; AAS1313.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
DR InterPro; IPR013026; TPR region.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 112 AA; 12913 MW; BAB232661790D401 CRC64;

Query Match 26.0%; Score 156.5; DB 2; Length 112;
Best Local Similarity 36.3%; Pred. No. 2.4e-07;
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Matches 41; Conservative 22; Mismatches 45; Indels 5; Gaps 3;

Qy 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQHPHQGRRTLLVALLKQGEAA 63
Db 1 MLQSKDVELLLVHAALQVQYQKPEQAITLLDALLEPQHQEQVROTAVACLNSGRYTRS 60
Qy 64 LAHVDDOLM--QQGEADGFLWLCRSRACQLAGRLDEARFAYQOYLEL--EQNE 112
Db 61 IELCESLLKTEHSNKEG-LWFCLSQARWKOQDVEGARHARRYLQSLNESSE 112

RESULT 14
Q66PT9_PASPI
ID Q66PT9_PASPI PRELIMINARY; PRT; 108 AA.
AC Q66PT9
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Putative TTSS protein Y.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
RT three secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY647223; AAU11477.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like helical.
DR InterPro; IPR013026; TPR region.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 108 AA; 12478 MW; 75C85DF70C1470C CRC64;

Query Match 24.7%; Score 148.5; DB 2; Length 108;
Best Local Similarity 34.6%; Pred. No. 1.4e-06;
Matches 36; Conservative 24; Mismatches 43; Indels 1; Gaps 1;

Qy 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQHPHQGRRTLLVALLKQGEAA 63
Db 1 MLQTKDVELLLVHAALQVQYQKPEQAITLLDALLEPQHQEQVROTAVACLNSGRYTRS 60
Qy 64 LAHVDDOLMGOOGADGFLWLCRSRACQLAGRLDEARFAYQOYLE 106
Db 61 IELCESLLKTEHSNKAFLWLCRSRACQLAGRLDEARFAYQOYLE 104

RESULT 15
Q48IR6_PSEI4
ID Q48IR6_PSEI4 PRELIMINARY; PRT; 112 AA.
AC Q48IR6
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE Type III secretion component, putative (BC 2.4.1.-).
GN OrderedLocusNames=PSPPH_2519;
OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OX NCBI_TaxID=264730;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Winn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
RA Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar N., Zhou L.,
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RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,  
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,  
RA Mansfield J., Collmer A., Buehl R.;  
RT "Whole-genome sequence analysis of *Pseudomonas syringae* pv.  
RT phaseolicola 1448A reveals divergence among pathovars in genes  
RT involved in virulence and transposition.";  
RL J. Bacteriol. 187:6488-6498(2005).  
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CC -----  
DR EMBL; CP000058; AA234406.1; -; Genomic\_DNA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.  
DR InterPro; IPR013026; TPR\_region.  
DR Pfam; PF07721; TPR\_4; 1.  
DR SMART; SM00028; TPR; 1.  
DR PROSITE; PS50005; TPR; 2.  
DR PROSITE; PS50293; TPR\_REGION; 1.  
KW Complete proteome; Glycosyltransferase; Transferase.  
SQ SEQUENCE 112 AA; 12534 MW; 1DACD78D6FAE2C59 CRC64;  
  
Query Match 23.3%; Score 140.5; DB 2; Length 112;  
Best Local Similarity 34.0%; Pred. No. 9e-06;  
Matches 35; Conservative 23; Mismatches 42; Indels 3; Gaps 1;  
  
Qy 7 SQQDALL--TWLQLYGHPDKASVLLAALLQIHDPHQGRRTLLVALLKQGEAA 63  
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Db 4 SQDRECIELLHGMDLYRRSQPQKALVMLLIAQLAPTNSALLHSLVLAFTDSGDTDR 63  
| | : : | | : : | | : : | | : : | | : : | | : : | | : : |  
  
Qy 64 LAHVQDLMOQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLE 106  
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Db 64 IAAIDRLVEQQGESALLLLRSRALWKGAKRKDDARQCRRYLE 106  
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Search completed: June 16, 2006, 19:22:56  
Job time : 94.1024 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 21.4081 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-5  
Perfect score: 602  
Sequence: 1 MTWLTQQQDALLTGTWLQ.....ARFAYQQYLEEONESTHP 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /EMC\_Celerra\_SID3S/ptodata/2/iaa/5\_COMB.pep.\*
  - 2: /EMC\_Celerra\_SID3S/ptodata/2/iaa/6\_COMB.pep.\*
  - 3: /EMC\_Celerra\_SID3S/ptodata/2/iaa/7\_COMB.pep.\*
  - 4: /EMC\_Celerra\_SID3S/ptodata/2/iaa/H\_COMB.pep.\*
  - 5: /EMC\_Celerra\_SID3S/ptodata/2/iaa/PCITUS\_COMB.pep.\*
  - 6: /EMC\_Celerra\_SID3S/ptodata/2/iaa/RE\_COMB.pep.\*
  - 7: /EMC\_Celerra\_SID3S/ptodata/2/iaa/backfilesl.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	45.2	231	2	US-09-252-991A-29962
2	111.5	18.5	470	2	US-09-902-540-12418
3	96.5	16.0	143	2	US-09-198-452A-442
4	96.5	16.0	143	2	US-09-438-185A-425
5	88.5	14.7	870	2	US-09-252-991A-28407
6	83	13.8	1219	2	US-09-252-991A-28840
7	81	13.5	953	2	US-09-902-540-14681
8	80	13.3	368	2	US-09-252-991A-30717
9	79.5	13.2	956	2	US-09-902-540-10395
10	78.5	13.0	169	2	US-08-833-167-58
11	78.5	13.0	169	2	US-09-344-837A-58
12	78	13.0	325	2	US-09-510-238A-273
13	78	13.0	390	2	US-09-902-540-16621
14	77.5	12.9	171	2	US-08-833-167-44
15	77.5	12.9	171	2	US-08-833-167-45
16	77.5	12.9	171	2	US-08-833-167-47
17	77.5	12.9	171	2	US-08-833-167-57
18	77.5	12.9	171	2	US-08-833-167-59
19	77.5	12.9	171	2	US-08-833-167-60
20	77.5	12.9	171	2	US-09-344-837A-44
21	77.5	12.9	171	2	US-09-344-837A-45
22	77.5	12.9	171	2	US-09-344-837A-47
23	77.5	12.9	171	2	US-09-344-837A-57
24	77.5	12.9	171	2	US-09-344-837A-59
25	77.5	12.9	171	2	US-09-344-837A-60
26	77.5	12.9	299	2	US-09-510-238A-193

27	77.5	12.9	302	2	US-09-510-238A-168	Sequence 168, App
28	77.5	12.9	302	2	US-09-510-238A-170	Sequence 170, App
29	77.5	12.9	302	2	US-09-510-238A-172	Sequence 172, App
30	77.5	12.9	302	2	US-09-510-238A-174	Sequence 174, App
31	77.5	12.9	302	2	US-08-957-610A-474	Sequence 474, App
32	77.5	12.9	302	2	US-08-957-610A-476	Sequence 476, App
33	77.5	12.9	302	2	US-08-957-610A-478	Sequence 478, App
34	77.5	12.9	302	2	US-08-957-610A-480	Sequence 480, App
35	77.5	12.9	317	2	US-09-510-238A-169	Sequence 169, App
36	77.5	12.9	317	2	US-09-510-238A-171	Sequence 171, App
37	77.5	12.9	317	2	US-09-510-238A-173	Sequence 173, App
38	77.5	12.9	317	2	US-09-510-238A-175	Sequence 175, App
39	77.5	12.9	317	2	US-08-957-610A-475	Sequence 475, App
40	77.5	12.9	317	2	US-08-957-610A-477	Sequence 477, App
41	77.5	12.9	317	2	US-08-957-610A-479	Sequence 479, App
42	77.5	12.9	317	2	US-08-957-610A-481	Sequence 481, App
43	77.5	12.9	319	2	US-09-510-238A-199	Sequence 199, App
44	77.5	12.9	319	2	US-09-510-238A-201	Sequence 201, App
45	77.5	12.9	319	2	US-08-957-610A-505	Sequence 505, App

ALIGNMENTS

RESULT 1  
US-09-252-991A-29962  
; Sequence 29962, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29962  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29962

Query Match 45.2%; Score 272; DB 2; Length 231;  
Best Local Similarity 55.1%; Pred. No. 1.5e-26;  
Matches 59; Conservative 13; Mismatches 35; Indels 0; Gaps 0;  
Qy 2 TWLTSSQQDALLTGTWLQYGHDPKASVLLAALLQIHDPHOGGRRTLLVALIKQGE 61  
Db 122 SMTLKQTQORLLMLGLWHLQCCQPRRAQVLLLEALLSVAPERDRGRALLLALLOQSLGE 181  
Qy 62 AALAHVDQLMQQGEAGDGLMCLSRACQLAGRLDEARFAYQQYLE 108  
Db 182 PAVRLCRQLQEDGEEEPGLMCLSRAEQLAGRLDARAARAAHALELE 228

RESULT 2  
US-09-902-540-12418  
; Sequence 12418, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883





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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28840
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28840

Query Match      13.8%; Score 83; DB 2; Length 1219;
Best Local Similarity 30.5%; Pred. No. 0.26;
Matches 25; Conservative 15; Mismatches 36; Indels 6; Gaps 2;

Qy 1 MTWVLTSSQQDALLTGWLOQYGHDPKASVLLA-ALLQIHPDHQGGRRRTLLVALLKQGE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 LVLLWLTNSESEVFPSPG-----DGEPDASVNYAELLQAHPENDALRLTLIDLLVKLGD 110
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 GEAAALAHVDQLMQQGEADGGLW 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 FEQARHHLARLRGKDRLATPPY 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-902-540-14681
; Sequence 14681, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14681
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14681

Query Match      13.5%; Score 81; DB 2; Length 953;
Best Local Similarity 36.9%; Pred. No. 0.33;
Matches 31; Conservative 12; Mismatches 33; Indels 8; Gaps 5;

Qy 26 PDKASVLLAALLQIHPDHQGGRRRTLLVALLKQGEAALAHVDQLMQQGE-ADGPLWLCR 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 PERAERLLPALLN-HPD-VGLRCAAGALVKSTGSAVALDALRAMLSRGEGAPVPE---R 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 85 SRACQLAGRLDEARFA--YQOYLE 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 REVARLLGRIGNSRFAPEPLARYLE 503
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-252-991A-30717
; Sequence 30717, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
```

```
; SEQ ID NO 30717
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30717

Query Match      13.3%; Score 80; DB 2; Length 368;
Best Local Similarity 29.2%; Pred. No. 0.12;
Matches 26; Conservative 14; Mismatches 49; Indels 0; Gaps 0;

Qy 27 DKASVLLAALLQIHPDHQGGRRRTLLVALLKQGEAALAHVDQLMQQGEADGPLWLCRSR 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 30 DDALPLKAGIKKEHPDDKRVRLAYARLVLRQNRLDDAKAEFAGLVQQQFPDDDDDLRFLSAL 89
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 87 ACQAGLRDLEARFAYQOYLEEQNESTH 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 90 VCLEAQAWDEARIYLEELVERDSHVDAH 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-902-540-10395
; Sequence 10395, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10395
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10395

Query Match      13.2%; Score 79.5; DB 2; Length 956;
Best Local Similarity 33.8%; Pred. No. 0.52;
Matches 27; Conservative 10; Mismatches 24; Indels 19; Gaps 4;

Qy 21 LOYGHDPKASVLLAALLQIHPDH---QGRR-----TLVV-----ALLKQGE---GE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LEQGHPEQALLLDGVLRLQAPHAQAQWNRALVLRMGLTLLAAAEAFDAVVYKRGEPGWSE 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 AALAHVDQLMQQGEADGPLW 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 EARIRARALRQQTQARGRAW 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-08-833-167-58
; Sequence 58, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIONG
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
```

```

; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833.167
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; NAME: S. CHRISTOPHER BAUER
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-5095
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-167-58

Query Match      13.0%; Score 78.5; DB 2; Length 169;
Best Local Similarity 33.3%; Pred. No. 0.064;
Matches 28; Conservative 12; Mismatches 25; Indels 19; Gaps 4;

QY   45  GGRRTLLVALLK-----QGEGEA-----ALAHVDQLMQGGEADG---PLWLCSRAC 88
      |||::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db   54  GGSQSFLLSLEQVRKIQDGAALQEAKTYKLCHPELVLLGHSLGIPWAPLSSCPSQAL 113

QY   89  QLAG---RLDEARPAYQYLEEE 109
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db   114 QLAGCLSQLHSGFLYQGLLQALE 137

RESULT 11
US-09-344-837A-58
; Sequence 58, Application US/09344837A
; Patent No. 6358505
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. CHRISTOPHER BAUER
ADDRESSER: MONSANTO/G. D. SEARLE & CO.,
ADDRESSER: PATENT DEPARTMENT CENTRAL
STREET: P.O. BOX 5110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

QY   45  GGRRTLLVALLK-----QGEGEA-----ALAHVDQLMQGGEADG---PLWLCSRAC 88
      |||::||:||||:||||:||||:||||:||||:||||:||||:||||:
Db   54  GGSQSFLLSLEQVRKIQDGAALQEAKTYKLCHPELVLLGHSLGIPWAPLSSCPSQAL 113

QY   89  QLAG---RLDEARPAYQYLEEE 109
      ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db   114 QLAGCLSQLHSGFLYQGLLQALE 137

RESULT 12
US-09-510-238A-273
; Sequence 273, Application US/09510238A
; Patent No. 6730303
; GENERAL INFORMATION:
; APPLICANT: FENG, YIQING
; APPLICANT: BAUM, CHARLES M
; APPLICANT: CAPARON, MAIRE H
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: STATEN, NICHOLAS R
; APPLICANT: SUMMERS, NEENA L
; APPLICANT: BAUER, S C
; APPLICANT: LEE, STEPHEN C
TITLE OF INVENTION: MULTI-FUNCTIONAL HEMATOPOIETIC RECEPTOR
AGONISTS
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNIS A. BENNETT, G.D. SEARLE & CO.,
CORPORATE PATENT DEPT.
STREET: P.O. BOX 5110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/510,238A
FILING DATE: 22-Feb-2000

```

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US 96/15774
;   FILING DATE: 06-OCT-1996
;   APPLICATION NUMBER: US 60/004,834
;   FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: BENNETT, DENNIS A
;   REGISTRATION NUMBER: 34,547
;   REFERENCE/DOCKET NUMBER: 2910/1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 314-694-5402
;   TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 273:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 325 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-510-238A-273

Query Match      13.0%; Score 78; DB 2; Length 325;
Best Local Similarity 28.2%; Pred. No. 0.18; Indels 24; Gaps 4;
Matches 31; Conservative 15; Mismatches 40;

Qy 24 GHPDKASVLLAALQIHPDHQGGRTLLVALLK-----QGGEA-----ALAH 66
Db 120 GSPGSPGPISTINPSPSKESHKSPNNAFLKLSLEQVRKIQDGAALQEKLCATYKLC 179

Qy 67 VDQLMQQGEADG----PLWLCRSACQIAG---RLDEARFAYQVYLEEE 109
Db 180 PEELVLLGSLGIPWAPLSSCPSSQALQIAGCLSQLHSLGLYQGLQALE 229

RESULT 13
US-09-902-540-16621
; Sequence 16621, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16625
; SEQ ID NO 16621
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16621

Query Match      13.0%; Score 78; DB 2; Length 390;
Best Local Similarity 27.3%; Pred. No. 0.23; Indels 45; Gaps 8;
Matches 39; Conservative 17; Mismatches 45;

Qy 10 QDALLLTGWLQYGHDPK--ASVLLAALQIHPDH-----QGRR--TLLV 52
Db 35 KDASALLGLRLRLAQHDETAARAVLRLVALLPHTPEALSHLARLDAEKGDARQLDLA 94

Qy 53 ALLKQ-----GEGEAAALAH-----VDQL-----MQQGEADGPLWLCRSACQIAG 92
Db 95 ALAAQPKAGFFEVINHGSGALLGHDRYAAAIPERALARALQPGNAQTLYL--GMAIQGDK 152

Qy 93 RLDEARFAYQVYLEEONESTH 115
Db 153 QLDLR---ALRRYLEAAEANKTEH 172
```

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RESULT 14
US-08-833-167-44
; Sequence 44, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: PENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/833,167
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-167-44

Query Match      12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

Qy 45 GGRRTLLVALLK-----QGGEA-----ALAHVDQLMQQGEADG----PLWLCRSR 86
Db 83 GGSQFLKLSLEQVRKIQDGAALQEKLCATYKLCHELVLLGSLGIPWAPLSSCPSSQ 142

Qy 87 ACQIAG---RLDEARFAYQVYLEEE 109
Db 143 ALQIAGCLSQLHSLGLYQGLQALE 168

RESULT 15
US-08-833-167-45
; Sequence 45, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
```



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	602	100.0	116	5	US-10-813-908-4	Sequence 4, Appli
2	141.5	23.5	113	6	US-11-098-686-10792	Sequence 10792, A
3	99	16.4	619	4	US-10-282-122A-50903	Sequence 50903, A
4	96.5	16.0	143	4	US-10-289-762-442	Sequence 442, App
5	86.5	14.4	713	4	US-10-425-115-201172	Sequence 201172, App
6	86.5	14.4	719	4	US-10-425-114-51666	Sequence 51666, A
7	84.5	14.0	643	4	US-10-425-115-201174	Sequence 201174, A
8	84.5	14.0	737	4	US-10-425-114-57283	Sequence 57283, A
9	83	13.8	1586	4	US-10-282-122A-49391	Sequence 49391, A
10	83	13.8	1864	5	US-10-732-923-2391	Sequence 2391, Ap
11	79.5	13.2	1743	5	US-10-732-923-18400	Sequence 18400, A
12	79	13.1	107	6	US-11-096-568A-26393	Sequence 26393, A
13	79	13.1	108	6	US-11-096-568A-26392	Sequence 26392, A
14	79	13.1	124	6	US-11-097-143-32322	Sequence 26391, A
15	78.5	13.0	1234	6	US-11-097-143-32322	Sequence 2322, A
16	78	13.0	325	4	US-10-695-584A-273	Sequence 273, App
17	77.5	12.9	328	3	US-09-920-552-3	Sequence 3, Appli
18	77.5	12.9	299	4	US-10-695-584A-193	Sequence 193, App
19	77.5	12.9	302	4	US-10-695-584A-168	Sequence 168, App
20	77.5	12.9	302	4	US-10-695-584A-170	Sequence 170, App
21	77.5	12.9	302	4	US-10-695-584A-172	Sequence 172, App
22	77.5	12.9	302	4	US-10-695-584A-174	Sequence 174, App
23	77.5	12.9	317	4	US-10-695-584A-169	Sequence 169, App
24	77.5	12.9	317	4	US-10-695-584A-171	Sequence 171, App
25	77.5	12.9	317	4	US-10-695-584A-173	Sequence 173, App
26	77.5	12.9	317	4	US-10-695-584A-175	Sequence 175, App
27	77.5	12.9	319	4	US-10-695-584A-199	Sequence 199, App

```
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10792
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10792

Query Match      23.5%; Score 141.5; DB 6; Length 113;
Best Local Similarity 30.3%; Pred. No. 3.4e-08;
Matches 33; Conservative 28; Mismatches 43; Indels 5; Gaps 2;

QY 3 MVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQSGEA 62
Db 1 MLTSEQQRTLYILGYLYIRGLNDSAEERLFKTLISLFFPEDKWSHSLAVIAHRKGDSS 60

QY 63 ALAHVDLMQOGE-----ADGFLWLCRSRACOLAGRLDEARFAYQVYLEL 107
Db 61 CLAHYKAV-AGEHSIVKHAPLLLLQQAALWNLGRYSESRTSIQNVIKI 108

RESULT 3
US-10-282-122A-50903
; Sequence 50903, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsythe, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA 034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50903
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-50903

Query Match      16.4%; Score 99; DB 4; Length 619;
Best Local Similarity 29.0%; Pred. No. 0.022;
```

```
Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG---HPDKASVLLAALLQIHPDHQGGRRLLVALLKQSGEAAALAHVDQLMQQGEAD 77
Db 259 LEYGAKVDTATRAHQARAFINRNPDKRLMLAGQIADGGDYDALAEQLQAMSRSPED 318

QY 78 GPIWLCSRACOLAGRLDEARFAYQVYLEEEQNE-STHP 116
Db 319 FDLFWQAQLAYKAGRLDQARGYLQOYLVDVQNRQMATA 358

RESULT 4
US-10-289-762-442
; Sequence 442, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 442
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-442

Query Match      16.0%; Score 96.5; DB 4; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.0073;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPDKASVLLAALLQIHP-----DHQGGRRLLVALLKQSGEAAALAH 66
Db 19 EELRISGYSFLRQGHYSKAILFPEALVILDPLSIYDHQ----TLGGYLIQIGENSQALAV 74

QY 67 VDLMQOGEADGFLWLCRSRACOLAGRLDEARFAYQVYL 105
Db 75 LDAQLRMOGDHLPTLLNKTALFCLGRIBEAT-AIATYL 112

RESULT 5
US-10-425-115-201172
; Sequence 201172, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201172
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115054C.1.pap
US-10-425-115-201172

Query Match      14.4%; Score 86.5; DB 4; Length 713;
Best Local Similarity 29.8%; Pred. No. 0.72;
Matches 34; Conservative 15; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQSGEAAALAHVDQL 70
Db 350 LQL-----DEAQLCQIALDIHREHRETASLEETADRRMLGLICDTKGDHEAALEHVA 404
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Qy 71 MQQGEADGPLWLCRSACOLA-----GRLEARFAYQOYLEL-----EEQNEST 114  
Db 405 SMSVMANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPKTSKGHNAT 458

RESULT 6  
US-10-425-114-51666  
; Sequence 51666, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 51666  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700207818\_FLI.pep  
US-10-425-114-51666

Query Match 14.4%; Score 86.5; DB 4; Length 719;  
Best Local Similarity 29.8%; Pred. No. 0.73;  
Matches 34; Conservative 15; Mismatches 42; Indels 23; Gaps 4;

Qy 19 LQLOYGHPDKASVLLAALQIHPDHO-----GGRTLVALLKQGEAEALAHVDQL 70  
Db 356 LQL-----DEAQLCQIALDIHREHGTASLEETADRLMGLICTTKGDHEAALHLVMA 410

Qy 71 MQQGEADGPLWLCRSACOLA-----GRLEARFAYQOYLEL-----EEQNEST 114  
Db 411 SMSVMANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPKTSKGHNAT 464

RESULT 7  
US-10-425-115-201174  
; Sequence 201174, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 201174  
; LENGTH: 643  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_115056C.1.pep  
US-10-425-115-201174

Query Match 14.0%; Score 84.5; DB 4; Length 643;  
Best Local Similarity 30.7%; Pred. No. 1.1;  
Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

Qy 19 LQLOYGHPDKASVLLAALQIHPDHO-----GGRTLVALLKQGEAEALAHVDQL 70

Db 350 LQL-----DEAQLCQIALDIHREHGTASLEETADRLMGLICTTKGDHEAALHLVMA 404  
Qy 71 MQQGEADGPLWLCRSACOLA-----GRLEARFAYQOYLEL-----EEQNEST 114  
Db 405 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPKTSKGHNAT 458

RESULT 8  
US-10-425-114-57283  
; Sequence 57283, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 57283  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLM017278G10\_FLI.pep  
US-10-425-114-57283

Query Match 14.0%; Score 84.5; DB 4; Length 737;  
Best Local Similarity 30.7%; Pred. No. 1.3;  
Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

Qy 19 LQLOYGHPDKASVLLAALQIHPDHO-----GGRTLVALLKQGEAEALAHVDQL 70  
Db 444 LQL-----DEAQLCQIALDIHREHGTASLEETADRLMGLICTTKGDHEAALHLVMA 498

Qy 71 MQQGEADGPLWLCRSACOLA-----GRLEARFAYQOYLEL-----EEQNEST 114  
Db 499 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPKTSKGHNAT 552

RESULT 9  
US-10-282-122A-49391  
; Sequence 49391, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49391
; LENGTH: 1586
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49391
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Query Match 13.8%; Score 83; DB 4; Length 1586;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;
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QY 3 MVLTSQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA 62
Db 391 IALNPSDVTQAQVLGEMLLANGDPVGAQYRMAIRRDQNPDAVRGLVGALAAQGRGDE 450
QY 63 ALAHVDQL--MQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 451 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAEAGDLGARSJFEDAL 501
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RESULT 10
US-10-732-923-2391
; Sequence 2391, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2391
; LENGTH: 1864
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-732-923-2391
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Query Match 13.8%; Score 83; DB 5; Length 1864;
Best Local Similarity 28.8%; Pred. No. 5.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;
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```
QY 3 MVLTSQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA 62
Db 669 IALNPSDVTQAQVLGEMLLANGDPVGAQYRMAIRRDQNPDAVRGLVGALAAQGRGDE 728
QY 63 ALAHVDQL--MQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 729 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAEAGDLGARSJFEDAL 779
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RESULT 11
US-10-732-923-18400
; Sequence 18400, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
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; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18400
; LENGTH: 1743
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-732-923-18400
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Query Match 13.2%; Score 79.5; DB 5; Length 1743;
Best Local Similarity 23.8%; Pred. No. 14;
Matches 25; Conservative 21; Mismatches 40; Indels 19; Gaps 3;
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```
QY 9 QQDALLLTGWLQYGHDPD--KASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAH 66
Db 1627 QCHVQLISKFAQLQEFKXGDAERGRTLLGLVTAHPKKTDLWLVYAEAVLK---HLGIEH 1682
QY 67 VDQLMOQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLELEEQN 111
Db 1683 ARKVLK-----RACNLGFSIHKMRPLYKKWLEMSKH 1714
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RESULT 12
US-11-096-568A-26393
; Sequence 26393, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26393
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13564029
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (97)..(97)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26393
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Query Match 13.1%; Score 79; DB 6; Length 107;
Best Local Similarity 35.7%; Pred. No. 0.55;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;
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```
QY 49 TLLVALLKQGEAALAHVDQLMQ--QGEADGPLWLCRSRACQLAGRLDEARFAYQQYLE 106
Db 11 TWISGLAMVHGHPOEAL----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 62
QY 107 LEEQNESTHP 116
Db 63 SMERVYGINP 72
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RESULT 13
US-11-096-568A-26392
; Sequence 26392, Application US/11096568A
; Publication No. US20060048240A1
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; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26392
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108)
; OTHER INFORMATION: Ceres Seq. ID no. 13564028
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (94)..(94)
; OTHER INFORMATION: Xaa is any aa, unknown or other
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; NAME/KEY: misc_feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-096-568A-26392

Query Match      13.1%; Score 79; DB 6; Length 108;
Best Local Similarity 35.7%; Pred. No. 0.56;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

Qy 49 TLLVALLKQGEAEALAHVDQLMQ--QGEADGPIWLCRSRACQAGRLDEARFAYQOYLE 106
Db 12 TMISGLAMHGHPQEQAL-----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 63

Qy 107 LEEQNESTHP 116
Db 64 SMERVYGINP 73

RESULT 14
US-11-096-568A-26391
; Sequence 26391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26391
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124)
; OTHER INFORMATION: Ceres Seq. ID no. 13564027
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (114)..(114)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; US-11-096-568A-26391

Query Match      13.1%; Score 79; DB 6; Length 124;
Best Local Similarity 35.7%; Pred. No. 0.66;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

```

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Qy 49 TLLVALLKQGEAEALAHVDQLMQ--QGEADGPIWLCRSRACQAGRLDEARFAYQOYLE 106
Db 28 TMISGLAMHGHPQEQAL-----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 79

Qy 107 LEEQNESTHP 116
Db 80 SMERVYGINP 89

RESULT 15
US-11-097-143-32322
; Sequence 32322, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32322
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-32322

Query Match      13.0%; Score 78.5; DB 6; Length 1234;
Best Local Similarity 26.7%; Pred. No. 12;
Matches 36; Conservative 20; Mismatches 44; Indels 35; Gaps 7;

Qy 7 SQOODALL-----LTGWELOQVGHDPDKASVLLAALLQIHPDHQGGRRRTLLVALLKQGEAE 62
Db 1060 SQMENAVLRMRNLNSFLMVPQVQRTKYKYPILLARLYKVTSPHLEGRE-----LLKQAQEKI 1114

Qy 63 ALAHVDQLMQGEADGP--LWL-----CRSRACQ-----LAGRLDEAR 98
Db 1115 EL-HLNHINQEAQ-DVPTKLWRITSSSPNRRASCEIDMINIKLRKMAIDVLEWNHDEV 1172

Qy 99 FAYQOYLEEEQNES 113
Db 1173 FAMEGRLLYTOPTDS 1187

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Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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(without alignments)  
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Gapop 10.0 , Gapext 0.5  
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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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3: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.ppe:\*  
4: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.ppe:\*  
5: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.ppe:\*  
6: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.ppe:\*  
7: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.ppe:\*  
8: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.ppe:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	13.0	737	6	US-10-449-902-53938
2	74	12.3	599	6	US-10-449-902-47030
3	73.5	12.2	711	6	US-10-449-902-46399
4	73	12.1	457	7	US-11-221-332-32
5	71.5	11.9	570	6	US-10-953-349-4630
6	71.5	11.9	772	6	US-10-953-349-4629
7	71.5	11.9	802	6	US-10-953-349-4628
8	71	11.8	495	6	US-10-953-349-31757
9	71	11.8	530	6	US-10-953-349-31756
10	71	11.8	610	6	US-10-953-349-31755
11	70.5	11.7	228	7	US-11-289-102-381
12	70.5	11.7	804	6	US-10-449-902-38463
13	70	11.6	174	7	US-11-183-218-2
14	70	11.6	177	7	US-11-330-353-14
15	70	11.6	204	6	US-10-511-937-2461
16	70	11.6	787	7	US-11-330-353-16
17	69.5	11.5	599	6	US-10-449-902-53783
18	67	11.1	840	6	US-10-449-902-41113
19	66.5	11.0	469	6	US-10-953-349-24172
20	66.5	11.0	473	6	US-10-449-902-47334
21	66.5	11.0	876	6	US-10-449-902-44948
22	66	11.0	525	6	US-10-953-349-34744
23	66	11.0	699	6	US-10-449-902-45095
24	65	10.8	622	6	US-10-505-928-735
25	64.5	10.7	330	6	US-10-449-902-30918

ALIGNMENTS

RESULT 1  
US-10-449-902-53938  
; Sequence 53938, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53938  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-53938  
Query Match 13.0%; Score 78; DB 6; Length 737;  
Best Local Similarity 34.7%; Pred. No. 0.81;  
Matches 26; Conservative 17; Mismatches 20; Indels 12; Gaps 5;  
Qy 28 KASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQGEADGP----LWLC 83  
Db 289 KARLLKSVITQPKPPG--WIAARLEEVACKLQVA--QLIQRCCECPNTDVL- 343  
Qy 84 RSPACOLAGRLDEAR 98  
Db 344 --KACRLASP-DEAK 355  
RESULT 2  
US-10-449-902-47030  
; Sequence 47030, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF



```
; SEQ ID NO 4629
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4629

Query Match
Best Local Similarity 11.9%; Score 71.5; DB 6; Length 772;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 378 DALYNLGGLYMDLGRFQASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETEAKRALKEA 437
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRACQLAG 92
Db 438 LKMTNRVELHDVAHSLKQLQKKKKVKGNSANEKGFIVVSSKFTVG 486

RESULT 7
US-10-953-349-4628
; Sequence 4628, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4628
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4628

Query Match
Best Local Similarity 11.9%; Score 71.5; DB 6; Length 802;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 408 DALYNLGGLYMDLGRFQASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETEAKRALKEA 467
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRACQLAG 92
Db 468 LKMTNRVELHDVAHSLKQLQKKKKVKGNSANEKGFIVVSSKFTVG 516

RESULT 8
US-10-953-349-31757
; Sequence 31757, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31757

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 495;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;
```

```
Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLVALLKQGEAALAHVDQLMQ 72
Db 121 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 177
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEARFAYQOYLE-LEEQNESTHP 116
Db 178 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 228

RESULT 9
US-10-953-349-31756
; Sequence 31756, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 530;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLVALLKQGEAALAHVDQLMQ 72
Db 156 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 212
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEARFAYQOYLE-LEEQNESTHP 116
Db 213 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 263

RESULT 10
US-10-953-349-31755
; Sequence 31755, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31755

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 610;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLVALLKQGEAALAHVDQLMQ 72
Db 236 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 292
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEARFAYQOYLE-LEEQNESTHP 116
Db 293 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 343
```



STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/330,353  
FILING DATE: 12-Jan-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/237,624  
FILING DATE: 10-Sep-2002  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-11-330-353-14

Query Match 11.6%; Score 70; DB 7; Length 177;  
Best Local Similarity 34.8%; Pred. No. 1.2; Indels 16; Gaps 3;  
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;  
Qy 57 QGGEA-----ALAHVDQLMQOGEADG-----PLWLCSRACQLAG---RLDEARFA 100  
Db 28 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPQALQAGCLSLQHSGLFL 87  
Qy 101 YQYVLEEE 109  
Db 88 YQGLLOALE 96

RESULT 15  
US-10-511-937-2461  
Sequence 2461, Application US/10511937  
Publication No. US20060088836A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, MacDonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 50661200104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2461  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-511-937-2461  
Query Match 11.6%; Score 70; DB 6; Length 204;  
Best Local Similarity 34.8%; Pred. No. 1.4; Indels 16; Gaps 3;  
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;  
Qy 57 QGGEA-----ALAHVDQLMQOGEADG-----PLWLCSRACQLAG---RLDEARFA 100  
Db 55 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPQALQAGCLSLQHSGLFL 114  
Qy 101 YQYVLEEE 109  
Db 115 YQGLLOALE 123  
Search completed: June 16, 2006, 20:25:52  
Job time : 4.99837 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 61.622 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-6  
Perfect score: 483  
Sequence: 1 MLVREGGERAGLANPFAALY.....ATEQVCLRDMDRKQKGLA 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 8: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*  
9: Geneseqp2005s: \*  
10: Geneseqp2006s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	93	5 ABB80774	Abb80774 A. salmon
2	258	53.4	875	7 ABO81310	AbO81310 Pseudomon
3	72	14.9	929	4 ABG05766	Abg05766 Novel hum
4	72	14.9	2301	6 ABUS2379	Abu52379 Human GPC
5	72	14.9	2301	8 ADL24093	Adl24093 Human NOV
6	71	14.7	298	7 ADM66546	Adm26546 Hyperther
7	70.5	14.6	240	2 AAY35351	Aay35351 Amino aci
8	70	14.5	211	7 ABO74225	AbO74225 Pseudomon
9	69	14.3	236	7 ABM86863	Abm86863 Rice abio
10	69	14.3	441	6 ABM69700	Abm69700 Photorhab
11	68	14.1	76	4 AAM81462	Aam81462 Human hae
12	67.5	14.0	168	6 ABR43312	AbR43312 Human lip
13	67	13.9	378	7 ABO78198	AbO78198 Pseudomon
14	67	13.9	381	4 AAU33703	Aau33703 Pseudomon
15	67	13.9	381	6 ABUI5637	Abui5637 Protein e
16	67	13.9	395	7 ABM88963	Abm88963 Rice abio
17	66.5	13.8	369	7 ADD14092	Add14092 Human src
18	66.5	13.8	427	5 ABP63531	Abp63531 KRAA 0751
19	66.5	13.8	4201	7 ADD12210	Add12210 PBZ domai
20	66.5	13.8	1201	8 ADN21296	Adn21296 Bacterial
21	66.5	13.8	1333	6 ABO07123	AbO07123 Novel hum
22	66	13.7	374	8 ADX93170	Adx93170 Plant ful
23	65.5	13.6	202	2 AAU09385	Aau09385 S-recepto

24	65.5	13.6	375	6 ADA34975	Ada34975 Acinetoba
25	65.5	13.6	433	2 AAU09384	Aau09384 S-sugar p
26	65.5	13.6	1590	4 AAB73488	Aab73488 Mouse Rim
27	65	13.5	378	6 ABU49755	Abu49755 Protein e
28	65	13.5	2023	8 ABM84980	Abm84980 Human dia
29	64.5	13.4	197	8 ADX55891	Adx55891 Plant ful
30	64.5	13.4	468	8 ADN24975	Adn24975 Bacterial
31	64.5	13.4	468	8 ADN22215	Adn22215 Bacterial
32	64.5	13.4	469	6 ABU21852	Abu21852 Protein e
33	64	13.3	440	9 ABM96571	Abm96571 M. xanthu
34	63.5	13.1	133	4 ABG05180	Abg05180 Novel hum
35	63.5	13.1	420	2 AAW20266	Aaw20266 H. pylori
36	63.5	13.1	424	2 AAW20977	Aaw20977 H. pylori
37	63	13.0	472	8 AED27779	Aed27779 Bacterial
38	63	13.0	475	5 AED28479	Aed28479 Phospholi
39	62.5	12.9	57	5 ABP06256	Abp06256 Human ORF
40	62.5	12.9	220	7 ABO81436	AbO81436 Pseudomon
41	62.5	12.9	252	3 AAG07105	Aag07105 Arabidops
42	62.5	12.9	316	8 ADR09962	Adr09962 Human pro
43	62.5	12.9	391	3 AAG20311	Aag20311 Arabidops
44	62.5	12.9	391	3 AAG61061	Aag61061 Arabidops
45	62.5	12.9	397	3 AAG61060	Aag61060 Arabidops

ALIGNMENTS

RESULT 1  
ABB80774  
ID ABB80774 standard; protein; 93 AA.  
XX AC ABB80774;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE A. salmonicida type III secretion protein acrR sequence.  
XX  
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
KW acrv; acrH; antibiotic; vaccine; fish.  
XX  
OS Aeromonas salmonicida.  
XX  
PN WO2002040514-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 15-NOV-2001; 2001WO-CA001589.  
XX  
PR 15-NOV-2000; 2000US-0248864P.  
XX  
(FREY/) FREY J.  
(STUB/) STUBER K.  
(THOR/) THORNTON J C.  
(KUZV/) KUZYK M A.  
(BURI/) BURIAN J.  
XX  
Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;  
WPI: 2002-537338/57.  
N-PSDB; ABN86172.  
XX  
Novel protein from Aeromonas salmonicida and nucleic acid encoding the  
PT protein, useful for reducing susceptibility of fish to infection by a  
virulent strain of Aeromonas salmonicida.  
XX  
Claim 13; Page 28; 39pp; English.  
XX  
The invention relates to A. salmonicida type III secretion genes and  
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.  
CC A. salmonicida type III secretion apparatus is useful for producing  
CC selected products, especially hexT. AcrV in vaccine, epitope or epitopic  
CC region of AcrV or any other protein of A. salmonicida type III secretion  
CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the A. salmonicida type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from A. salmonicida or its genes. The present  
CC sequence represents the A. salmonicida type III secretion protein acr  
XX  
SQ Sequence 93 AA;

Query Match 100.0%; Score 483; DB 5; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSRLGRFYLRW 60  
DB 1 MLVRRGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSRLGRFYLRW 60

QY 61 TGASEPEPGWFMFLATEQVCSLRDMRKQKHGLA 93  
DB 61 TGASEPEPGWFMFLATEQVCSLRDMRKQKHGLA 93

RESULT 2  
ABO81310  
ID ABO81310 standard; protein; 875 AA.

AC ABO81310;

XX 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #13485.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD14881.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 30056; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
XX polynucleotides encoding them. The sequences are useful in diagnosis and  
XX therapy of pathological conditions, as molecular targets for diagnostics,  
XX prophylaxis and treatment of pathological conditions resulting from a  
XX bacterial infection, for evaluating a compound, such as a polypeptide,  
XX for the ability to bind a P. aeruginosa nucleic acid, as components of  
XX effective antibacterial targets, as targets for antibacterial drugs,  
XX including anti-P. aeruginosa drugs, as templates for recombinant  
XX production of P. aeruginosa-derived peptides or polypeptides, as target  
XX components for diagnosis and/or treatment of P. aeruginosa-caused  
XX infection, and in detection of P. aeruginosa sequences or other sequences  
XX of Pseudomonas species using biochip technology. Sequences ABO67826-  
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 875 AA;

Query Match 53.4%; Score 258; DB 7; Length 875;  
Best Local Similarity 58.4%; Pred. No. 6.6e-24;  
Matches 52; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSRLGRFYLRW 60  
DB 783 VMLRRRQARSGLANPFAALYLLAEATLDTLGPRLYKVLALAGSLPFGEMARFYRRW 842

QY 61 TGASEPEPGWFMFLATEQVCSLRDMRKROK 89

DB 843 TGABPADGWFELEAGRVTQSLRKROK 871

RESULT 3  
ABG05766  
ID ABG05766 standard; protein; 929 AA.

XX AC ABG05766;

XX 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #5757.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS69953.

XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.

XX Claim 20; SEQ ID NO 36125; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX sequences. (I) is useful as hybridisation probes, polymerase chain  
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX and in recombinant production of (II). The polynucleotides are also used  
XX in diagnostics as expressed sequence tags for identifying expressed  
XX genes. (I) is useful in gene therapy techniques to restore normal  
XX activity of (II) or to treat disease states involving (II). (II) is  
XX useful for generating antibodies against it, detecting or quantitating a  
XX polypeptide in tissue, as molecular weight markers and as a food  
XX supplement. (II) and its binding partners are useful in medical imaging  
XX of sites expressing (II). (I) and (II) are useful for treating disorders  
XX involving aberrant protein expression or biological activity. The  
XX polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
XX amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 929 AA;  
Query Match 14.9%; Score 72; DB 4; Length 929;  
Best Local Similarity 36.7%; Pred. No. 10;  
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;  
Oy 17 AALYLLAETLAVLPGHFYGNV--DVFRRSSLSRLG--RFYLWWTGASEPEPGWFM 72  
Db 128 AGYIFLQEASL----PGHQLYAVVIDTGFAPAPAQGLLRKIRLWHDGRGSPGWFI 183  
RESULT 4  
ABU52379  
ID ABU52379 standard; protein; 2301 AA.  
XX  
AC ABU52379;  
XX  
DT 03-MAR-2003 (first entry)  
XX  
DE Human GPCR related protein NOV29a.  
XX  
KW Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200279398-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 08-MAR-2002; 2002WO-US007355.  
XX  
PR 08-MAR-2001; 2001US-0274194P.  
PR 08-MAR-2001; 2001US-0274281P.  
PR 08-MAR-2001; 2001US-0274322P.  
PR 09-MAR-2001; 2001US-0274849P.  
PR 13-MAR-2001; 2001US-0275578P.  
PR 13-MAR-2001; 2001US-0275579P.  
PR 13-MAR-2001; 2001US-0275601P.  
PR 14-MAR-2001; 2001US-0276000P.  
PR 16-MAR-2001; 2001US-0276776P.  
PR 19-MAR-2001; 2001US-0276994P.  
PR 20-MAR-2001; 2001US-0277239P.  
PR 20-MAR-2001; 2001US-0277327P.  
PR 20-MAR-2001; 2001US-0277338P.  
PR 21-MAR-2001; 2001US-0277751P.  
PR 22-MAR-2001; 2001US-0277833P.  
PR 23-MAR-2001; 2001US-0278152P.  
PR 26-MAR-2001; 2001US-0278894P.  
PR 27-MAR-2001; 2001US-0278999P.  
PR 27-MAR-2001; 2001US-0279036P.  
PR 30-MAR-2001; 2001US-0280233P.  
PR 02-APR-2001; 2001US-0280802P.  
PR 02-MAY-2001; 2001US-0288052P.  
PR 02-MAY-2001; 2001US-0288056P.  
PR 02-MAY-2001; 2001US-0288228P.  
PR 17-MAY-2001; 2001US-0291266P.  
PR 07-JUN-2001; 2001US-0296693P.  
PR 08-JUN-2001; 2001US-0296856P.  
PR 05-JUL-2001; 2001US-0303230P.  
PR 05-JUL-2001; 2001US-0303237P.  
PR 05-JUL-2001; 2001US-0303237P.  
PR 08-AUG-2001; 2001US-0310913P.  
PR 13-AUG-2001; 2001US-0311978P.  
PR 14-AUG-2001; 2001US-0312191P.  
PR 16-AUG-2001; 2001US-0312916P.  
PR 17-AUG-2001; 2001US-0313182P.  
PR 20-AUG-2001; 2001US-0313626P.  
PR 21-AUG-2001; 2001US-0314018P.  
PR 27-AUG-2001; 2001US-0315227P.  
PR 10-SEP-2001; 2001US-0318403P.

PR 10-SEP-2001; 2001US-0318510P.  
PR 14-SEP-2001; 2001US-0322296P.  
PR 14-SEP-2001; 2001US-0322360P.  
PR 27-SEP-2001; 2001US-0325378P.  
PR 09-NOV-2001; 2001US-0332486P.  
PR 09-NOV-2001; 2001US-0345399P.  
PR 07-MAR-2002; 2002US-00094886.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;  
PI Guo X, Vernet CM, Li L, Gorman L, Malyankar UM, Boldog FL;  
PI Guo X, Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ;  
PI Pena CE, Gangoli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;  
PI PoChart PF, Fernandes ER, Shinkets RA, Rastelli L, Spaderna SK;  
PI Larochelle WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;  
XX  
DR WPI; 2003-058423/05.  
DR N-PSDB; ABX70470.  
XX  
PT NOVX polypeptides and polynucleotides, useful for treating a syndrome  
PT related to a human disease associated with the NOVX polypeptide e.g.,  
PT cancer.  
XX  
PS Claim 1; Page 182-183; 413pp; English.  
XX  
CC The present invention relates to the isolation of novel human  
CC polypeptides referred to as NOVX (NOV1-NOV44), variants of these  
CC proteins, and the polynucleotide sequences encoding them. The NOVX  
CC proteins of the invention are G-protein coupled receptor (GPCR) related  
CC proteins. The sequences of the invention are useful in the manufacture  
CC of a medicament for treating a syndrome related to a human disease  
CC associated with the polypeptides e.g. cancer. ABU52311-ABU52408 represent  
CC the human NOVX proteins of the invention  
XX  
SQ Sequence 2301 AA;  
Query Match 14.9%; Score 72; DB 6; Length 2301;  
Best Local Similarity 36.7%; Pred. No. 33;  
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;  
Oy 17 AALYLLAETLAVLPGHFYGNV--DVFRRSSLSRLG--RFYLWWTGASEPEPGWFM 72  
Db 1592 AGYIFLQEASL----PGHQLYAVVIDTGFAPAPAQGLLRKIRLWHDGRGSPGWFI 1647  
RESULT 5  
ADL24093  
ID ADL24093 standard; protein; 2301 AA.  
XX  
AC ADL24093;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human NOVX polypeptide #69.  
XX  
KW Human; NOVX; G protein-coupled receptor; GPCR; cardiomyopathy;  
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
KW arial septal defect; ASD; atrioventricular canal defect;  
KW ductus arteriosus; pulmonary stenosis; subaortic stenosis;  
KW ventricular septal defect; VSD; tuberosus sclerosis; scleroderma; obesity;  
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
KW neoplasm; adenocarcinoma; lymphoma; uterine cancer; haemophilia;  
KW hypercoagulability; idiopathic thrombocytopenia purpura;  
KW immunodeficiency; graft-versus-host disease; AIDS; bronchial asthma;  
KW Crohn's disease; multiple sclerosis;  
KW Albright's hereditary osteodystrophy; diabetes; infectious diseases;  
KW anorexia; neurodegenerative disorder; Alzheimer's disease;  
KW Parkinson's disease; haematopoietic disorder; metabolic disorder;  
receptor.  
XX  
OS Homo sapiens.  
XX

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PN US2004002120-A1.
XX 01-JAN-2004.
XX 07-MAR-2002; 2002US-00094886.
XX 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277933P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278994P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-MAY-2001; 2001US-0288052P.
PR 02-MAY-2001; 2001US-0288066P.
PR 02-MAY-2001; 2001US-0288228P.
PR 17-MAY-2001; 2001US-0291766P.
PR 07-JUN-2001; 2001US-0296693P.
PR 08-JUN-2001; 2001US-0296856P.
PR 05-JUL-2001; 2001US-0303230P.
PR 05-JUL-2001; 2001US-0303237P.
PR 08-AUG-2001; 2001US-0310913P.
PR 13-AUG-2001; 2001US-0311978P.
PR 14-AUG-2001; 2001US-0312191P.
PR 16-AUG-2001; 2001US-0312916P.
PR 17-AUG-2001; 2001US-0313182P.
PR 20-AUG-2001; 2001US-0313626P.
PR 21-AUG-2001; 2001US-0314018P.
PR 27-AUG-2001; 2001US-0315227P.
PR 10-SEP-2001; 2001US-0318403P.
PR 10-SEP-2001; 2001US-0318510P.
PR 14-SEP-2001; 2001US-0322296P.
PR 14-SEP-2001; 2001US-0322360P.
PR 27-SEP-2001; 2001US-0325378P.
PR 09-NOV-2001; 2001US-0332486P.
PR 09-NOV-2001; 2001US-0345399P.
XX (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENNA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.

(ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
XX
Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
PI Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
PI Guo X, Shenoy SG, Padigaru M, Tauquier RJ, Miller CE, Casman SJ;
PI Pena CEA, Gangolli EA, Gusev VY, Smithson G, Zerhusen BD, Gerlach V;
PI Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;
PI Larochelle WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;
XX
WPI: 2004-212692/20.
DR N-PSDB; ADL24092.
XX
Novel isolated G protein-coupled receptor polypeptides, referred as NOVX,
PT useful for treating scleroderma, obesity, congenital adrenal hyperplasia,
PT prostate cancer, hemophilia, AIDS, bronchial asthma, Crohn's disease.
XX
Claim 1; SEQ ID NO 138; 287pp; English.
XX
The invention relates to human G protein-coupled receptor-related (GPCR-
related) polypeptides (designated NOVX) and the polynucleotides encoding
them. The polypeptides and polynucleotides are useful as therapeutics in
the manufacture of medicaments for treating syndromes associated with
human diseases. The sequences are useful for treating a disorder
associated with aberrant NOVX expression or activity such as
cardiomyopathy, atherosclerosis, hypertension, congenital heart defects,
aortic stenosis, atrial septal defect (ASD), atrioventricular canal
defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis,
ventricular septal defect (VSD), tuberosus sclerosis, scleroderma,
obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate
cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, haemophilia,
hypercoagulability, idiopathic thrombocytopenia purpura,
immunodeficiencies, graft-versus-host disease, AIDS, bronchial asthma,
Crohn's disease, multiple sclerosis, Albright's hereditary
osteodystrophy, diabetes, infectious diseases, anorexia,
neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
immune disorders, haematopoietic disorders and metabolic disorders. This
sequence represents a human NOVX polypeptide of the invention.
XX
SQ Sequence 2301 AA;

Query Match 14.9%; Score 72; DB 8; Length 2301;
Best Local Similarity 36.7%; Pred. No. 33;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

QY 17 AALYLLAEATLAVLPGHPLYGNV--DVFSSSLSSERLG--RFVLRWTGASEPEPGWFM 72
Db 1592 AGYIFLQEASL---PGHLYAVVDTGTFRASAPAQGLGLRLKIRLWHDSRGPSFGWFI 1647

RESULT 6
ADM26546
ID ADM26546 standard; protein; 298 AA.
XX
AC ADM26546;
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE Hyperthermophile Methanopyrus kandleri protein #1152.
XX
KW hyperthermophile; protein stability enhancement;
XX protein activity enhancement.

```





CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
XX  
SQ Sequence 441 AA;

Query Match 14.3%; Score 69; DB 6; Length 441;  
Best Local Similarity 27.1%; Pred. No. 10;  
Matches 29; Conservative 15; Mismatches 43; Indels 20; Gaps 4;  
Qy 5 REGERAGLANPFAALYLIAE-----ATLAVLPGHFLYGNVDVFRSSLSSESLGRF 56  
Db 44 RIGELCHLRNPDTNLSLLAEVIGFQQHQALLTPGEMFGISSNTEVPTGMHGVGDY 103  
Qy 57 YL-----RWGASEPEP-GWFMFLATEQVCSLRDMRKRQKHGLA 93  
Db 104 LLQGVLDGLGNPFSGGQLPEQAWVYVRDAPAM--SRKRIEHPLS 148

RESULT 11  
AAM81462  
ID AAM81462 standard; protein; 76 AA.  
XX  
AC AAM81462;  
XX  
DT 13-NOV-2001 (first entry)  
XX  
DE Human haematological malignancy-related antigen #1160.  
XX  
KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;  
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;  
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200164886-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 01-MAR-2001; 2001WO-US007272.  
XX  
PR 01-MAR-2000; 2000US-0186126P.  
PR 17-MAR-2000; 2000US-0190479P.  
PR 27-APR-2000; 2000US-0200545P.  
PR 28-APR-2000; 2000US-0200303P.  
PR 28-APR-2000; 2000US-0200779P.  
PR 01-MAY-2000; 2000US-0200999P.  
PR 04-MAY-2000; 2000US-0202084P.  
PR 22-MAY-2000; 2000US-0206201P.  
PR 14-JUL-2000; 2000US-0218950P.  
PR 03-AUG-2000; 2000US-0222903P.  
PR 04-AUG-2000; 2000US-0223416P.  
PR 07-AUG-2000; 2000US-0223378P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Gaiger A, Algate PA, Mannion J;  
XX WPI; 2001-514842/56.  
XX  
XX

PT Compositions and methods for the detection of hematological malignancies,

PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and  
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.  
XX  
PS Claim 1; Page 974; 1252pp; English.  
XX  
CC The present invention relates to compositions and methods for the  
CC detection, diagnosis and therapy of haematological malignancies. The  
CC present sequence is the protein sequence of a human haematological  
CC malignancy related antigen. The methods of the present invention comprise  
CC detecting the presence of haematological malignancy related antigen(s) in  
CC a sample obtained from the patient (an increased level of the  
CC polypeptide, compared to an unaffected individual, is indicative of an  
CC increased risk). Haematological malignancies which can be treated using  
CC the present invention are chronic lymphocytic leukaemia, lymphoma,  
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B  
CC cell non-Hodgkin's lymphoma  
XX  
SQ Sequence 76 AA;

Query Match 14.1%; Score 68; DB 4; Length 76;  
Best Local Similarity 40.9%; Pred. No. 1.5;  
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;  
Qy 16 FAALYLIAEATLAVLPGHF-----LYGNVDVFRSSLSSESLGRFVLRWTGASEPE 67  
Db 13 FVSLPTMQEASLAVLFYHYHVISPCNKVLYRQVRSMLSLSLPRRL---RLRYRGNs-PV 68  
Qy 68 PGWFMFL 73  
Db 69 QSLFML 74

RESULT 12  
ABR43312  
ID ABR43312 standard; protein; 168 AA.  
XX  
AC ABR43312;  
XX  
DT 10-JUL-2003 (first entry)  
XX  
DE Human lipid-associated molecule LIPAM-17 protein SEQ ID NO:17.  
XX  
KW Human; lipid-associated molecule; LIPAM; cytostatic; cerebroprotective;  
KW antiarteriosclerotic; anti-HIV; antiallergic; antiparkinsonian; cardiant;  
KW anticonvulsant; nootropic; antiinflammatory; antitumor; hepatotropic;  
KW antibacterial; virucide; protozoacide; antiparasitic; antilipemic; AIDS;  
KW gene therapy; cell proliferative disease; cancer; atherosclerosis; ulcer;  
KW autoimmune disease; inflammatory disease; allergy; neurological disorder;  
KW stroke; Parkinson's disease; epilepsy; gastrointestinal disorder;  
KW cirrhosis; cardiovascular disorder; myocardial infarction; obesity;  
KW metabolic disorder; developmental disorder; endocrine disorder;  
KW pulmonary disorder; infection; lipid metabolism disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025150-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 19-SEP-2002; 2002WO-US029980.  
XX  
PR 21-SEP-2001; 2001US-0324039P.  
PR 26-OCT-2001; 2001US-0346197P.  
PR 02-NOV-2001; 2001US-0343876P.  
PR 30-NOV-2001; 2001US-0334211P.  
PR 14-DEC-2001; 2001US-0340223P.  
PR 18-DEC-2001; 2001US-0342166P.  
PR 22-JAN-2002; 2002US-0351262P.  
PR 03-MAY-2002; 2002US-0377576P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Warren BA, Emerling BM, Lee EA, Chang H, Forsythe JI, Griffin JA;

PI Baughn MR, Chawla NK, Khare R, Reddy R, Lee S, Bulloch SA, Lee SY;  
PI Tran UK, Elliott VS, Tang YT, Bhatia U, Burrill JD, Blake JJ, Ho A;  
XX Zheng W;

XX WPI; 2003-363142/34.  
DR N-PSDB; ACC49794.

XX New human lipid-associated molecules (LIPAM) useful for diagnosing,  
PT treating and preventing diseases or conditions associated with aberrant  
PT LIPAM expression, e.g. cancer, AIDS, atherosclerosis or infections.

XX Claim 1; Page 209; 225pp; English.

XX ACC49778 to ACC49794 encode the human lipid-associated molecule proteins  
CC given in ABR43296 to ABR43312, designated LIPAM-1 to LIPAM-17 (I). (I)  
CC have cytostatic, antiarteriosclerotic, anti-HIV, antiallergic, nootropic,  
CC cerebroprotective, antiparkinsonian, anticonvulsant, antiinflammatory,  
CC anticulcer, hepatotropic, antibacterial, virucide, protozoacide, cardiant,  
CC antiparasitic and antilipemic activities, and can be used in gene  
CC therapy. The LIPAM polypeptides and polynucleotides are useful in  
CC diagnosing, treating and preventing diseases or conditions associated  
CC with decreased expression or overexpression of LIPAM, such as cell  
CC proliferative diseases (e.g. cancer or atherosclerosis), autoimmune/  
CC inflammatory diseases (e.g. AIDS or allergies), neurological disorders  
CC (e.g. stroke, Parkinson's disease or epilepsy), gastrointestinal disorders  
CC (ulcer or cirrhosis), cardiovascular (e.g. myocardial infarction),  
CC metabolic (e.g. obesity), developmental, endocrine, or pulmonary  
CC disorders, infections (e.g. bacterial, viral, parasitic or protozoal),  
CC and disorders of lipid metabolism. They are also useful in assessing the  
CC effects of exogenous compounds on the expression of nucleic acid and  
CC amino acid sequences of LIPAM. The LIPAMs or their fragments are useful  
CC in screening compounds for effectiveness as agonist or antagonist of the  
CC polypeptides, or in altering the expression of the target polynucleotide  
CC and compounds that specifically bind to or modulate the activity of the  
CC polypeptide

XX Sequence 168 AA;

Query Match 14.0%; Score 67.5; DB 6; Length 168;  
Best Local Similarity 34.8%; Pred. No. 4.6;  
Matches 27; Conservative 12; Mismatches 28; Indels 11; Gaps 5;

QY 8 ERAGLANPFAALYLLAEATLVLG-PCGFLYGNVDVFRSSLSLSSRLGR- 64

DB 83 ERLTLRSPQLPLSLCEAPSPQLQPG- - -GNVTITYAGARAPMGQGFLLSYSQASL 138

QY 65 EPEPGWFMATEQVCSLR 82

DB 139 PRSPGWRL- - -RLCSSR 152

RESULT 13

ABO78198

ID ABO78198 standard; protein; 378 AA.

XX AC ABO78198;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #10373.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD11769.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 26944; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html

XX Sequence 378 AA;

Query Match 13.9%; Score 67; DB 7; Length 378;

Best Local Similarity 26.3%; Pred. No. 15;

Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;

QY 4 REGERAGLANPFAALYLLAE- - - - -TLAVLPGPHFLYGNVDVFRSSLSLSSRLGR 55

DB 191 RYRDAHSGMSGPYAPRRLQAWTHPAWMDVGLGKXPHDL-GNISAYRGNPTGLD- - - 246

QY 56 FYLRWTGAS-EPEPGW 70

DB 247 -YIGLGNFDPISW 261

RESULT 14

AAU33703

ID AAU33703 standard; protein; 381 AA.

XX AC AAU33703;

XX 14-FEB-2002 (first entry)

XX Pseudomonas aeruginosa cellular proliferation protein #147.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;  
KW antibacterial; drug design.

XX Pseudomonas aeruginosa.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206849P.

XX 26-MAY-2000; 2000US-0207272P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.



```
PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselebeck R, Ohlseen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS51562.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5199; Slipp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes,
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence represents an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 381 AA;
XX
XX Query Match 13.9%; Score 67; DB 4; Length 381;
XX Best Local Similarity 26.3%; Pred. No. 15;
XX Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
XX
XX Qy 4 RREGERAGLANPFAALYLLAEA-----TLAVLGPGHFLYGNVDVFRSSLSERLGR 55
XX Db 164 RYDAHSGMSGPYAAPRRILQAMTHPAWWDVGLLGPDKDL-GNISAYRGNPTGLE--- 219
XX
XX Qy 56 FYLRWTGAS-EPEPGW 70
XX Db 220 -YIGWLGANFDPISW 234
XX
XX RESULT 15
XX ABU15637
XX ID ABU15637 standard; protein; 381 AA.
XX XX
XX AC ABU15637;
XX
XX DT 19-JUN-2003 (first entry)
XX
XX DE Protein encoded by prokaryotic essential gene #1164.
XX
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX OS Pseudomonas aeruginosa.
XX
XX PN WO200277183-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 21-MAR-2002; 2002WO-US0009107.
XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX
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PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselebeck R, Ohlseen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX DR N-PSDB; ACA19507.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43561; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 381 AA;
XX
XX Query Match 13.9%; Score 67; DB 6; Length 381;
XX Best Local Similarity 26.3%; Pred. No. 15;
XX Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
XX
XX Qy 4 RREGERAGLANPFAALYLLAEA-----TLAVLGPGHFLYGNVDVFRSSLSERLGR 55
XX Db 164 RYDAHSGMSGPYAAPRRILQAMTHPAWWDVGLLGPDKDL-GNISAYRGNPTGLE--- 219
XX
XX Qy 56 FYLRWTGAS-EPEPGW 70
XX Db 220 -YIGWLGANFDPISW 234
XX
XX Search completed: June 16, 2006, 19:06:52
XX Job time : 63.622 secs
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RESULT 9  
G83050  
L-lactate dehydrogenase P44771 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: G83050  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: G83050

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-338 <KAW>  
A;Cross-references: UNIPROT:Q9YD07; UNIPARC:UPI000005DCEJ; DDBJ:AP000060; NID:q5104188;

A;Experimental source: strain K1  
C;Gene: APE0860  
C;Superfamily: Aeropyrum pernix hypothetical protein APE0860

Query Match 13.6%; Score 66.5; DB 2; Length 338;  
Best Local Similarity 35.9%; Pred. No. 5; 9;  
Matches 23; Conservative 2; Mismatches 24; Indels 15; Gaps 2;

QY 12 LANPFAALYLLAEATLAVLPGHFLYGNVDVFR-----SSLSSERLGRFYLRWT 61  
DB 14 LALPLLALVAGAEAPTLVGSQPF-----DVRVGGFYVALIDDGFFDEVGRGRFYLYWA 68  
QY 62 GASE 65  
DB 69 GSPE 72

RESULT 12  
GEO  
osteocalcin precursor - bovine  
N;Alternate names: BGP; bone Gla protein; gamma-carboxyglutamic acid-containing protein  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Apr-1984 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: S12653; A03303; S08693  
R;Kiefer, M.C.; Saphire, A.C.S.; Bauer, D.M.; Barr, P.J.  
Nucleic Acids Res. 18, 1909, 1990  
A;Title: The cDNA and derived amino acid sequences of human and bovine bone Gla protein.  
A;Reference number: S12652; MUID:90245603; PMID:2336375  
A;Accession: S12653  
A;Molecule type: mRNA  
A;Residues: 1-100 <KIE>  
A;Cross-references: UNIPROT:P02820; UNIPARC:UPI0000130ED9; EMBL:X53699; NID:g719; PIDN:C  
A;Note: alternative splicing may produce a sequence lacking residues 33-34  
R;Price, P.A.; Poser, J.W.; Raman, N.  
Proc. Natl. Acad. Sci. U.S.A. 73, 3374-3375, 1976  
A;Title: Primary structure of the gamma-carboxyglutamic acid-containing protein from bo  
A;Reference number: A03303; MUID:77036749; PMID:1068450  
A;Accession: A03303  
A;Molecule type: protein  
A;Residues: 52-100 <PRI>  
A;Cross-references: UNIPARC:UPI0000174545  
C;Comment: This protein, isolated from bone, binds strongly to apatite.  
C;Superfamily: osteocalcin  
C;Keywords: bone; calcium binding; carboxyglutamic acid; hydroxyproline  
F;1-51/Domain: signal sequence #status predicted <SIG>  
F;52-100/Product: osteocalcin #status experimental <WAT>  
F;60/Modified site: 4-hydroxyproline (Pro) #status experimental  
F;68,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
F;74-80/Disulfide bonds: #status experimental

Query Match 13.6%; Score 65.5; DB 1; Length 100;  
Best Local Similarity 36.6%; Pred. No. 2;  
Matches 26; Conservative 4; Mismatches 32; Indels 9; Gaps 3;

QY 19 LYLLAEATLAVLG-----PGHFLYGNVDVFRSSLSSE---RLGRFYLRWTGASBPFCW 70  
DB 7 LALLALATLCLAGRAKFDGAEKGAAFVSKQEGSEVVKRLRYLDHNLGAPADYPD- 65  
QY 71 FMLATEQVCSL 81  
DB 66 PLEPKREVCEL 76

RESULT 13  
T14392  
S-luciferase  
C;Species: Braggia rapa (turnip)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C;Accession: T14392  
R;Watanabe, M.; Takasaki, T.; Toriyama, K.; Yamakawa, S.; Isogai, A.; Suzuki, A.; Hinata  
Plant Cell Physiol. 35, 1221-1229, 1994  
A;Title: A high degree of homology exists between the protein encoded by SRK in self-ind

A;Reference number: Z18026; MUID:95211381; PMID:7697295  
A;Accession: T14392  
A;Status: Preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-433 <WAT>  
A;Cross-references: UNIPROT:Q39282; UNIPARC:UPI00000ACE55; EMBL:D30050; NID:g633030; P1;  
A;Experimental source: strain S9-homozygote; stigma  
C;Superfamily: S-locus glycoprotein; S-locus-specific glycoprotein homology  
C;Keywords: glycoprotein  
F;38-427/Domain: S-locus-specific glycoprotein homology <SSG>

Query Match 13.6%; Score 65.5; DB 2; Length 433;  
Best Local Similarity 28.2%; Pred. No. 10;  
Matches 20; Conservative 9; Mismatches 33; Indels 9; Gaps 2;

QY 9 RAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSSERLG-----RFYLRW 60  
DB 120 RENVSPVVA-ELLANGNFVVRDPGFLWQSGFDYDTLLPEMKLGYDLKTGLNRFVSW 178  
QY 61 TCASEPEPCWF 71  
DB 179 RSSDDPSSGDF 189

RESULT 14  
T14398  
S-receptor kinase (EC 2.7.1.1) - turnip  
C;Species: Brassica rapa (turnip)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C;Accession: T14398  
R;Suzuki, G.; Watanabe, M.; Isogai, A.; Hinata, K.  
Gene 191, 123-126, 1997  
A;Title: Highly conserved 5'-flanking regions of two self-incompatibility genes, SLG9 a  
A;Reference number: Z18032; MUID:97354304; PMID:9210598  
A;Accession: T14398  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-841 <SUZ>  
A;Cross-references: UNIPROT:O23745; UNIPARC:UPI00000AC8A5; EMBL:D88193; NID:g2251113; P;  
C;Genetics:  
A;Gene: SRK9 (B.c)  
A;Introns: 428/1; 471/1; 534/3; 604/1; 683/2; 730/3  
C;Function:  
A;Description: involved in preventing fertilization between plants having the same S-loc  
C;Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-speci  
C;Keywords: ATP; phosphotransferase; receptor; serine/threonine-specific protein kinase  
F;38-426/Domain: S-locus-specific glycoprotein homology <SSG>  
F;516-799/Domain: protein kinase homology <KIN>

Query Match 13.6%; Score 65.5; DB 2; Length 841;  
Best Local Similarity 28.2%; Pred. No. 21;  
Matches 20; Conservative 9; Mismatches 33; Indels 9; Gaps 2;

QY 9 RAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSSERLG-----RFYLRW 60  
DB 120 RENVSPVVA-ELLANGNFVVRDPGFLWQSGFDYDTLLPEMKLGYDLKTGLNRFVSW 178  
QY 61 TCASEPEPCWF 71  
DB 179 RSSDDPSSGDF 189

RESULT 15  
B23392  
L-lactate dehydrogenase VCA0984 [imported] - Vibrio cholerae (strain N16961 serogroup O:  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: B82392  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: B82392  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-378 <HEI>  
A:Cross-references: UNIPROT:O9KKW6; UNIPARC:UPI00000C3700; GB:AE004425; GB:AE003853; NID  
A:Experimental source: serogroup O1, strain N16961; biotype E1 Tor  
C:Genetics:  
A:Gene: VCA0984  
A:Map position: 2  
C:Superfamily: alpha-hydroxy acid dehydrogenase, FMN-dependent; (S)-2-hydroxy-acid oxid  
Query Match 13.5%; Score 65; DB 2; Length 378;  
Best Local Similarity 28.6%; Pred. No. 10;  
Matches 20; Conservative 13; Mismatches 23; Indels 14; Gaps 4;  
Qy 10 AGLAMPFAALYLLAEA-----TLAVLPGHFLYGNVDVFRSSSLSSERLGRFYLRWT 61  
Db 170 SGMSGPNAMRRVLQAMAHPSWANDVGLLGKPHDL-GNISKYRGSPTKLED----YIGWL 224  
Qy 62 GAS-EPEFGW 70  
Db 225 GANFDPSTSW 234

Search completed: June 16, 2006, 19:25:10  
Job time : 11.4512 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 18:53:15 ; Search time 73.039 Seconds  
(without alignments)  
1177.815 Million cell updates/sec  
Title: US-10-813-908A-6  
Perfect score: 483  
Sequence: 1 MLVRRERAGLANPFAALY.....ATEQVCSLRDMRKQKHGLA 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2849598 seqs, 92501592 residues  
Total number of hits satisfying chosen parameters: 2849598  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	100.0	93	2 Q8GA90_AERSA	Q8GA90 aeromonas s
2	439	90.9	151	2 Q699R2_AERHY	Q699R2 aeromonas h
3	426	88.2	93	2 Q5CC99_AERSO	Q5CC99 aeromonas s
4	418	86.5	151	2 Q5XL06_AERHY	Q5XL06 aeromonas h
5	282	58.4	146	1 LCRR_YEREN	O68549 yersinia en
6	282	58.4	146	1 LCRR_YERPE	P69959 yersinia pe
7	282	58.4	146	1 LCRR_YERPS	P69960 yersinia ps
8	276	57.1	144	2 Q84GY7_PHOLU	Q84GY7 photorhabdu
9	275	56.9	146	2 Q5TLM4_AERHY	Q5TLM4 aeromonas h
10	264	54.7	144	2 Q7N0W9_PHOLL	O7N0W9 photorhabdu
11	258	53.4	144	2 Q30537_PSEAE	O30537 pseudomonas
12	179	37.1	137	2 Q6QV80_VIBHA	Q6QV80 vibrio harv
13	175	36.2	137	2 Q66PT6_PASPI	Q66PT6 pasteurilla
14	164	34.0	137	2 Q87P57_VIBPA	Q87P57 vibrio para
15	76.5	15.8	1872	2 Q4Q2V5_LEIMA	Q4Q2V5 leishmania
16	75.5	15.6	612	2 Q2W001_MAGSA	Q2W001 magnetospir
17	75	15.5	500	2 Q446S7_SOLUS	Q446S7 solibacter
18	74	15.3	247	2 Q415P2_KINRA	Q415f2 kinococcus
19	73.5	15.2	938	2 Q7NUX4_CHRVO	Q7Nux4 chromobacte
20	73	15.1	383	1 LDDP_BARQU	Q690J2 bartonella
21	73	15.1	538	2 Q2RPL6_RHORU	Q2Rpl6 rhodospiril
22	72.5	15.0	234	2 Q3X3V1_9ACTN	Q3X3v1 rubrobacter
23	72.5	15.0	595	2 Q3WZG9_9ACTN	Q3wzg9 rubrobacter
24	72.5	15.0	1189	2 Q4DH02_TRYCR	Q4dh02 trypanosoma
25	71.5	14.8	272	2 Q3JZS7_RHIET	Q3jzs7 rhizobium e
26	71	14.7	191	2 Q93171_CAEEL	Q93171 caenorhabdi
27	71	14.7	286	2 Q3J390_RHOS4	Q3j390 rhodobacter
28	71	14.7	298	2 Q8TW84_METKA	O8tw84 methanopyru
29	70.5	14.6	240	2 Q92712_CHLPN	Q92712 chlamydia p
30	70.5	14.6	272	2 Q3PEU5_PARDE	Q3pel5 paracoccus
31	70.5	14.6	306	2 Q6P2G8_HUMAN	Q6p2g8 homo sapien

32 70.5 14.6 307 2 Q69YZ2\_HUMAN Q69yz2 homo sapien  
33 70.5 14.6 327 2 Q6P2Q5\_HUMAN Q6p2q5 homo sapien  
34 70.5 14.6 492 2 Q4NGZ7\_9MICC Q4ngz7 arthrobacte  
35 70.5 14.6 901 2 Q4Q3F6\_LEIMA Q4q3f6 leishmania  
36 70 14.5 372 2 Q391Z3\_BURS3 Q391z3 burkholderi  
37 70 14.5 377 2 Q4MLD7\_9BURK Q4mld7 burkholderi  
38 70 14.5 381 2 Q4ZZ10\_PSE02 Q4zz10 pseudomonas  
39 70 14.5 469 2 Q35LP6\_9BRAD Q35lp6 bradyrhizob  
40 70 14.5 909 2 Q31PL3\_SYNP7 Q31pl3 synechococc  
41 70 14.5 909 2 Q5N4L1\_SYNP6 Q5n4l1 synechococc  
42 69.5 14.4 309 2 Q72JN5\_THET2 Q72jn5 thermus the  
43 69.5 14.4 501 2 Q55LZ3\_CRYNE Q55lz3 cryptococcu  
44 69.5 14.4 501 2 Q5K8S5\_CRYNE Q5k8s5 cryptococcu  
45 69.5 14.4 885 2 Q4H6M1\_9DEIO Q4h6m1 deinococcus

ALIGNMENTS

RESULT 1  
Q8GA90\_AERSA  
ID Q8GA90\_AERSA PRELIMINARY; PRT; 93 AA.  
AC Q8GA90;  
DT 01-MAR-2003, integrated into UniprotKB/TREMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Acrr protein.  
GN Name:acrr;  
OS Aeromonas salmonicida subsp. salmonicida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RX MEDLINE=2262111; PubMed=12374830;  
RX DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RT "Evidence for a type III secretion system in Aeromonas salmonicida  
subsp. salmonicida.";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida  
type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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CC -----  
DR EMBL; AJ458292; CAD30219.1; -; Genomic DNA.  
DR EMBL; AJ616218; CAB83106.1; -; Genomic DNA.  
SQ SEQUENCE 93 AA; 10429 MW; 1A5CS91CD0D79460 CRC64;  
Query Match 100.0%; Score 483; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 4.2e-47;  
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLW 60  
Db 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLW 60  
Qy 61 TGASEPPGFWFLATEQVCSLRDMRKQKHGLA 93  
Db 61 TGASEPPGFWFLATEQVCSLRDMRKQKHGLA 93

RESULT 2  
Q699R2\_AERHY  
ID Q699R2\_AERHY PRELIMINARY; PRT; 151 AA.  
AC Q699R2;

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DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acrr.
GN Name=acrr;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919 (2004).
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CC -----
DR EMBL; AY282667; AA991817.1; -; Genomic DNA.
SQ SEQUENCE 151 AA; 16928 MW; 2B28207206E1B147 CRC64;

Query Match          90.9%; Score 439; DB 2; Length 151;
Best Local Similarity 89.2%; Pred. No. 7.9e-42;
Matches 83; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 LLVRRQGAQGLVNPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 TGASEPEPGWFLAEQVCSLRDMRKQKHGLA 151
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Q5CC99 AERSO
ID Q5CC99_AERSO PRELIMINARY; PRT; 93 AA.
AC Q5CC99;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acrr protein.
GN Name=acrr;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burt S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150 (2005).
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CC -----
DR EMBL; AJ749609; CAG44556.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10214 MW; D1F527554037FE6F CRC64;

Query Match          88.2%; Score 426; DB 2; Length 93;
Best Local Similarity 86.0%; Pred. No. 1.4e-40;
Matches 80; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLVRRQGAQGLVNPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
QY 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TGASEPEPGWFLAEQVCSLRDMRKQKHGLA 93
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q5XL06 AERHY
ID Q5XL06_AERHY PRELIMINARY; PRT; 151 AA.
AC Q5XL06;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acrr.
GN Name=acrr;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457 (2005).
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CC -----
DR EMBL; AY763611; AAV30231.1; -; Genomic DNA.
SQ SEQUENCE 151 AA; 17032 MW; BBDf211C884E20B6 CRC64;

Query Match          86.5%; Score 418; DB 2; Length 151;
Best Local Similarity 87.1%; Pred. No. 2e-39;
Matches 81; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 LLVRRHAELPGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSGERLGRFLRW 118
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 TGASEPEPGWFLAEQVCSLRDMRKQKHGLA 151
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RESULT 5
LCRR YEREN
ID LCRR_YEREN STANDARD; PRT; 146 AA.
AC O68549; Q93KU2;
DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1999, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Low calcium response locus protein R.
GN Name=lcrr;
OS Versinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYVe227;
RA Irtarte M., Lambrmont I., Kerbouch C., Cornelis G.R.;
RT "Detailed genetic map of the pYVe227 plasmid of Versinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYVe8081;
RX MEDLINE=21295118; PubMed=11402007;
DOI=10.1128/IAI.69.7.4627-4638.2001;
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RESULT 7
LCRR_YERPS STANDARD; PRT; 146 AA.
AC P69960; P19393; P31486; Q663K7;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 7.
DE Low calcium response locus protein R.
DS Name: lcrR; Ordered locus names: pYV0059;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RA Bergman T., Forsberg A., Backman A., Wolf-Watz H.;
RT "The lcrD protein of Yersinia pseudotuberculosis belongs to a novel
RT protein family involved in surface presentation of virulence
RT determinants.";
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP2953 / Serotype I; PLASMID=pYV;
RX PubMed=1535858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lemerlin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis";
RT Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 88-146.
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakanson S., Forsberg A., Norlander L., Macellaro A.,
RA Backman A., Boelin I., Wolf-Watz H.;
RT "Analysis of the V antigen lcrGVH-yopBD operon of Yersinia
RT pseudotuberculosis: evidence for a regulatory role of lcrH and lcrV.";
RL J. Bacteriol. 173:1607-1616 (1991).
CC -!- FUNCTION: Involved in the down-regulation of lcrGVH transcription
CC in the presence or absence of calcium and is necessary for lcrG
CC protein expression in the absence of calcium. Plays an important
CC role in the regulation of the low-calcium response.
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CC
DR EMBL; M96850; AAA27648.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25402.1; -; Genomic DNA.
DR EMBL; M57893; -; NOT_ANNOTATED_CDS; Genomic DNA.
DR PIR; D37314; D37314.
DR GenomeReviews; BX936399 GR; pYV0059.
KW Calcium; Complete proteome; Plasmid.
FT CHAIN 1 146 Low calcium response locus protein R.
FT /FTID=PRO_0000084375.
FT
FT SEQUENCE 146 AA; 16454 MW; 611A80CB2A2FF2F9 CRC64;
Query Match 58.4%; Score 282; DB 1; Length 146;
Best Local Similarity 58.1%; Pred. No. 7e-24;
Matches 54; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
QY 1 MLVRRGERAGLANPFAALYLAEATLAVLPGGHFLYGNVDVFRSSLSLSERLGRFYLRW 60
Db 54 VLTQRVEQRGLKNPFAALYMLANAARAVLGPDYLYLGNVDVLAGSSLSLSTQRLAIFYRRW 113
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQKHGLA 93
Db 114 TGAKELSTGWFLSKVQSIVTLTSLNKKRQNGFPA 146
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RESULT 8
Q84GY7_PHOLU PRELIMINARY; PRT; 144 AA.
AC Q84GY7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LssR.
DS Name=lssR;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545 (2002).
CC
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CC
DR EMBL; AY144116; AAO18051.1; -; Genomic DNA.
SQ SEQUENCE 144 AA; 16873 MW; A60908CC50676B8A CRC64;
Query Match 57.1%; Score 276; DB 2; Length 144;
Best Local Similarity 62.9%; Pred. No. 3.3e-23;
Matches 56; Conservative 8; Mismatches 25; Indels 0; Gaps 0;
QY 1 MLVRRGERAGLANPFAALYLAEATLAVLPGGHFLYGNVDVFRSSLSLSERLGRFYLRW 60
Db 52 IMLRRTQRRGLANPFAPLYLLATATMAVLGPGSLYQQVTLVDSPLNDRLARFYHRW 111
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQK 89
Db 112 TGASIEFGWFELEASCVISLHQMRRQK 140
RESULT 9
Q6TLM4_AERHY PRELIMINARY; PRT; 146 AA.
AC Q6TLM4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE AcrR.
DS Name=acrR;
OS Aeromonas hydrophila
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256 (2004).
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CC
DR EMBL; AY394563; AAR26337.1; -; Genomic DNA.
SQ SEQUENCE 146 AA; 16205 MW; FBD8A6D417A70279 CRC64;
Query Match 56.9%; Score 275; DB 2; Length 146;
Best Local Similarity 60.9%; Pred. No. 4.4e-23;
Matches 56; Conservative 9; Mismatches 27; Indels 0; Gaps 0;
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QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
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Db 54 VFIERVHERAGLSNPFALYLLASAGFSLGSGVLYGNVCLGSLSSDLRSLRFFYRCW 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQK 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 AGASEPQPGWFSLDVAKVISLTSMRKQNSDL 145

RESULT 10
Q7N0W9_PHOLL
ID Q7N0W9_PHOLL PRELIMINARY; PRT; 144 AA.
AC Q7N0W9;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Similar to transcription regulator proteins LcrR and PcrR.
GN OrderedLocusNames=plu3760;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok K., Frangeul E., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Bouraux-Lude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boenare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313 (2003).
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CC -----
CC EMBL; BX571871; CAB16132.1; -; Genomic_DNA.
DR Photolista; plu3760; -.
DR BioCyc; PLUM243265:PLU3760-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 16934 MW; 3C81F7EA0B53B083 CRC64;

Query Match 54.7%; Score 264; DB 2; Length 144;
Best Local Similarity 59.6%; Pred. No. 7.9e-22;
Matches 53; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
: : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 VMLRRTRQRGLANPFAPLYLATATWMLGPGSRLYGQVNTLVDSPLNDRLARFYHRW 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQK 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 TGANEVVPGWFELEASCVISLHOMRKQK 140

RESULT 11
Q30537_PSEAE
ID Q30537_PSEAE PRELIMINARY; PRT; 144 AA.
AC Q30537; Q7DCF0;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Transcriptional regulator protein PcrR.
GN Name=PcrR; OrderedLocusNames=PA1704;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

```
RC STRAIN=388;
RX MEDLINE=98037517; PubMed=93711466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7163-7168 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Wesbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.H., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.N., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -----
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CC -----
CC EMBL; AF010150; AAC45945.1; -; Genomic_DNA.
DR EMBL; AE004597; AAG05093.1; -; Genomic_DNA.
DR PIR; E83432; E83432.
DR BioCyc; PAER287:PA1704-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 16266 MW; 305F197EB33DE171 CRC64;

Query Match 53.4%; Score 258; DB 2; Length 144;
Best Local Similarity 58.4%; Pred. No. 3.8e-21;
Matches 52; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
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Db 52 VMLRRQARSGLANPFAALYLLAEATLDTLGPQRLYGKVLALAGSLPGRMARFYRRW 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQK 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 TGAEPADGWFLEAGRVVTVQSLRKQK 140

RESULT 12
Q6QVSO_VIBHA
ID Q6QVSO_VIBHA PRELIMINARY; PRT; 137 AA.
AC Q6QVSO;
DT 03-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE VcrR.
GN Name=vcrR;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; AY524044; AAS13311.1; -; Genomic_DNA.
DR EMBL; AY524044; AAS13311.1; -; Genomic_DNA.
SQ SEQUENCE 137 AA; 15912 MW; AEBD4CBF8657AF08 CRC64;

Query Match 37.1%; Score 179; DB 2; Length 137;
Best Local Similarity 43.3%; Pred. No. 4e-12;
Matches 39; Conservative 19; Mismatches 28; Indels 4; Gaps 2;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
: : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy 45 SSSLSSELGRFYLRWTCASE-PEPGWFMLATEOVCS---LRDMRKQKHG 91  
Db 1344 -----YLRDTRASDGVRAWCTLGNRVVCASLQLMAYVHRGQHG 1382

Search completed: June 16, 2006, 19:23:03  
Job time : 76.039 secs

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; LENGTH: 240
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-769

Query Match      14.6%; Score 70.5; DB 2; Length 240;
Best Local Similarity 32.0%; Pred. No. 0.31;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY 7 GERAGLANP-----FAALYLLAEATLAVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 29 GEIVGLLGNPGAGKTTAFYL-----TVGLRPDSGKIIFKNVDVTKTMDHRLGLGIL- 83
QY 60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKRQKH 90
Db 84 -----AQEPTIFKELTVQDNLICILEIIVKARKQOSH 115

RESULT 3
US-09-438-185A-725
; Sequence 725, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 725
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0723
US-09-438-185A-725

Query Match      14.6%; Score 70.5; DB 2; Length 242;
Best Local Similarity 32.0%; Pred. No. 0.31;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY 7 GERAGLANP-----FAALYLLAEATLAVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 31 GEIVGLLGNPGAGKTTAFYL-----TVGLRPDSGKIIFKNVDVTKTMDHRLGLGIL- 85
QY 60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKRQKH 90
Db 86 -----AQEPTIFKELTVQDNLICILEIIVKARKQOSH 117

RESULT 4
US-09-252-991A-22971
; Sequence 22971, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22971
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22971

Query Match      14.5%; Score 70; DB 2; Length 211;
Best Local Similarity 31.2%; Pred. No. 0.3;
Matches 24; Conservative 5; Mismatches 24; Indels 24; Gaps 3;

QY 5 REGERA-----GLANPFAALYLLAEATLAVLGPGHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 67 ROGERAGDDPTGRTGPGA-----LPGQRRWG-----AFAEHLGRHSCR 107
QY 60 WTGASEPEPGWFMLATE 76
Db 108 QPGRGVYPFGWPPARTE 124

RESULT 5
US-09-252-991A-26944
; Sequence 26944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26944
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26944

Query Match      13.9%; Score 67; DB 2; Length 378;
Best Local Similarity 26.3%; Pred. No. 1.8;
Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;

QY 4 RREGERAGLANPFAALYLLAE-----TLAVLGPGHFLYGNVDVFRSSLSLSSERLGR 55
Db 191 RYRDAHSGMSGPYAAPRRILQAMTHPAWADVGLLGKPHDL-GNISAYRGNPTGLE--- 246
QY 56 FYLRWTGAS-EPEPGW 70
Db 247 -YIGWLGANFDPISIW 261

RESULT 6
US-09-328-352-6262
; Sequence 6262, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6262
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6262
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Query Match 13.6%; Score 65.5; DB 2; Length 375;  
Best Local Similarity 42.9%; Pred. No. 2.9;  
Matches 15; Conservative 6; Mismatches 11; Indels 3; Gaps 1;  
Qy 57 YLRWTGASEPFGWFMFLATEQVCSLRDMRKQKHG 91  
Db 307 YLHWGDSQCEQD---LSAEQIQALQDQFKKQKTG 338

RESULT 7  
US-09-617-0998-1  
; Sequence 1, Application US/09617099B  
; Patent No. 6790949  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu  
; APPLICANT: Shibasaki, Tadao  
; APPLICANT: Ozaki, No. 6790949uaki  
; TITLE OF INVENTION: Protein Rim2  
; FILE REFERENCE: P19771  
; CURRENT APPLICATION NUMBER: US/09/617,099B  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: JP 288372/99  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1590  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-617-0998-1

Query Match 13.6%; Score 65.5; DB 2; Length 1590;  
Best Local Similarity 25.7%; Pred. No. 21;  
Matches 29; Conservative 8; Mismatches 41; Indels 35; Gaps 4;  
Qy 14 NPFAALYLL-----AEATLAVLPGHFLYGNV-----DVFRS 45  
Db 851 NPYVKIYFLPDRSDKNKRTTKVKTLEPKNQTFIYSPVHRRFRERMLEITLWDQARV 910  
Qy 46 SSLSSERLGRFYLRW-TGASEPEFGWFMFLATEQVCSLRDMR-----KROKHG 91  
Db 911 REESEFLGLIELETAALLDDEPHWYKLTQHDVSSLPPLRPPSYLPRQLHG 963

RESULT 8  
US-10-180-326A-1  
; Sequence 1, Application US/10180326A  
; Patent No. 6956104  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu  
; APPLICANT: Shibasaki, Tadao  
; APPLICANT: Ozaki, No. 6956104uaki  
; TITLE OF INVENTION: Protein Rim2  
; FILE REFERENCE: P21573  
; CURRENT APPLICATION NUMBER: US/10/180,326A  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: JP 288372/99  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1590  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-180-326A-1

Query Match 13.6%; Score 65.5; DB 2; Length 1590;  
Best Local Similarity 25.7%; Pred. No. 21;  
Matches 29; Conservative 8; Mismatches 41; Indels 35; Gaps 4;  
Qy 14 NPFAALYLL-----AEATLAVLPGHFLYGNV-----DVFRS 45

Query Match 13.3%; Score 64; DB 2; Length 440;  
Best Local Similarity 29.7%; Pred. No. 5.8;  
Matches 35; Conservative 11; Mismatches 40; Indels 32; Gaps 7;  
Qy 4 RREGER-AGLANP-FAALYLLAEATLAVLPGH-FLYGNV--DVFRSSLSSERLGRFYL 58  
Db 32 RREIRYAGFPPRWWSLLFFIPVLAVLSVGHVLYRRLVRDVKRKLRTAQLGFAV 91  
Qy 59 RWTGASE-----PEPG-----W-----FMLATEQVCSLRDMRKROK 89  
Db 92 GFVGALSARAIGSVLPSEGRRLGIVFLWLGVLVLLMFTLAVDMVRAAAWFERRK 149

RESULT 9  
US-09-902-540-15770  
; Sequence 15770, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 15770  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-15770

Query Match 12.9%; Score 62.5; DB 2; Length 220;  
Best Local Similarity 31.3%; Pred. No. 3.5;  
Matches 21; Conservative 8; Mismatches 25; Indels 13; Gaps 3;  
Qy 24 EATLAVLPGHFLYGNVDVFRSSLSSERLGRFYLRWTGASEPEPGWFMFLATEQVCSLRD 83  
Db 119 EGTLLRGLGPGCGRWRVHVTRADGLRRRLG-----TQSGN-QP-----AHQLRPARD 165  
Qy 84 MRKQKH 90

Db 166 RRRPDRH 172

RESULT 11

US-09-252-991A-21336

; Sequence 21336, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 21336

; LENGTH: 1520

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21336

Query Match 12.9%; Score 62.5; DB 2; Length 1520;

Best Local Similarity 26.3%; Pred. No. 53; Mismatches 38; Indels 37; Gaps 5;

Matches 31; Conservative 12; Mismatches 38; Indels 37; Gaps 5;

QY 3 VRRE-GERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSSL-----SSERL 53

Db 1022 LRDDWGSEGIAAAVAALDRACLASLAANLAGSGLFASATPLDPLATLQRLGTAERQRL 1081

QY 54 GRFYLR-----WTGASE-----PEPGWFMLA-----TEQVCSLRD 83

Db 1082 LRHLWRLQLEGGYLRAGEGWLGCARPAQSPEDAWTAFAGCAPAALWPAELVAYLRD 1139

RESULT 12

US-10-324-967-32

; Sequence 32, Application US/10324967

; Patent No. 6974680

; GENERAL INFORMATION:

; APPLICANT: Cossou, Pierre

; APPLICANT: Kohler, Thilo

; APPLICANT: Benghezal, Mohammed

; APPLICANT: Marchetti, Anna

; APPLICANT: van Delden, Christian

; TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE

; FILE REFERENCE: 25421-502

; CURRENT APPLICATION NUMBER: US/10/324,967

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 32

; LENGTH: 1809

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-10-324-967-32

Query Match 12.9%; Score 62.5; DB 2; Length 1809;

Best Local Similarity 26.3%; Pred. No. 67; Mismatches 38; Indels 37; Gaps 5;

Matches 31; Conservative 12; Mismatches 38; Indels 37; Gaps 5;

QY 3 VRRE-GERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSSL-----SSERL 53

Db 981 LRDDWGSEGIAAAVAALDRACLASLAANLAGSGLFASATPLDPLATLQRLGTAERQRL 1040

QY 54 GRFYLR-----WTGASE-----PEPGWFMLA-----TEQVCSLRD 83

Db 1041 LRHLWRLQLEGGYLRAGEGWLGCARPAQSPEDAWTAFAGCAPAALWPAELVAYLRD 1098

RESULT 13

US-08-673-789-7

; Sequence 7, Application US/08673789

; Patent No. 5814479

; GENERAL INFORMATION:

; APPLICANT: ZHOU, REMPING; SCHULZ, NICHOLAS,

; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,

; APPLICANT: GEORGE, F.

; TITLE OF INVENTION: BSK RECEPTOR LIKE

; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR

; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/673,789

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/177,812

; FILING DATE: 04-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4105

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 751-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970

; TYPE: AMINO ACID

; STRANDEDNESS: UNKNOWN

; TOPOLOGY: UNKNOWN

US-08-673-789-7

Query Match 12.8%; Score 62; DB 1; Length 970;

Best Local Similarity 34.0%; Pred. No. 33; Mismatches 15; Indels 12; Gaps 2;

Matches 18; Conservative 8; Mismatches 15; Indels 12; Gaps 2;

QY 46 SSLSSERLGRFYLRWTGASEPEPGWFMLA-----TEQVCSLRDMRKQ 89

Db 12 SSRSSRRRGVTSELAWT--THPETGWEVSGYDEAMQPIRTYQVCVREAQQQ 62

RESULT 14

US-09-252-991A-25773

; Sequence 25773, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25773
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25773

Query Match      12.7%; Score 61.5; DB 2; Length 386;
Best Local Similarity 28.2%; Pred.No.11;
Matches 20; Conservative 10; Mismatches 26; Indels 15; Gaps 1;

QY   33 GHFLYGNDVFRSSLSRSLGRYLRLWTGASEPEPCGWMLA-----TEQ 77
     |.|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|.:|
Db    96 GPFVAVNCGAPAESLSELFGHEKGAFGTALQSAGWFEAAANGTILFLDEIGDLPPSIQ 155
     |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   78 VCSLRDMRKQ 88
     ||||:|||||:
Db    156 VKLLRVLQERE 166
           :|||:

RESULT 15
US-09-107-532A-4866
; Sequence 4866, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4866:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...289
; SEQUENCE DESCRIPTION: SEQ ID NO: 4866:
US-09-107-532A-4866

Query Match      12.6%; Score 61; DB 2; Length 289;
Best Local Similarity 31.2%; Pred.No. 8.3;

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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 52.0195 Seconds  
(without alignments)  
828.131 Million cell updates/sec

Title: US-10-813-908A-6  
Perfect score: 483  
Sequence: 1 MLVRRGERAGLANPFAALY.....ATEQVCSLRDMRKQKHGLA 93

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pap.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	93	US-10-813-908-6	Sequence 6, Appli
2	72	14.9	929	US-10-450-763-36125	Sequence 36125, A
3	72	14.9	2301	US-10-094-886-138	Sequence 138, App
4	71	14.7	298	US-10-506-454-1151	Sequence 1151, Ap
5	70.5	14.6	240	US-10-289-762-769	Sequence 769, App
6	69	14.3	980	US-10-437-963-128383	Sequence 128383,
7	68.5	14.2	917	US-10-732-923-12941	Sequence 12941, A
8	68.5	14.2	917	US-10-732-923-12942	Sequence 12942, A
9	68	14.1	76	US-09-796-692-1826	Sequence 1826, Ap
10	68	14.1	76	US-10-040-862-1826	Sequence 1826, Ap
11	68	14.1	76	US-10-057-475B-1826	Sequence 1826, Ap
12	68	14.1	76	US-10-154-884B-1826	Sequence 1826, Ap
13	68	14.1	76	US-10-764-324-1826	Sequence 1826, Ap
14	67	13.9	381	US-09-815-242-5199	Sequence 5199, Ap
15	67	13.9	381	US-10-282-122A-43561	Sequence 43561, A
16	66.5	13.8	369	US-10-501-035-281	Sequence 281, App
17	66.5	13.8	427	US-10-938-249-467	Sequence 467, App
18	66.5	13.8	427	US-10-485-788A-503	Sequence 503, App
19	66.5	13.8	1200	US-10-756-149-5235	Sequence 5235, Ap
20	66.5	13.8	1201	US-10-369-493-3949	Sequence 3949, Ap
21	66.5	13.8	1333	US-10-161-927-24	Sequence 24, Appl
22	66	13.7	268	US-10-425-115-187933	Sequence 187933,
23	66	13.7	374	US-10-425-114-55834	Sequence 55834, A
24	66	13.7	661	US-10-425-115-187929	Sequence 187929,
25	65.5	13.6	433	US-11-087-099-3764	Sequence 3764, Ap
26	65.5	13.6	597	US-10-437-963-168169	Sequence 168169,
27	65.5	13.6	804	US-10-156-761-8615	Sequence 8615, Ap

28	65.5	13.6	839	6	US-11-087-099-2713	Sequence 2713, Ap
29	65.5	13.6	841	6	US-11-087-099-10714	Sequence 10714, A
30	65.5	13.6	1590	4	US-10-180-326-1	Sequence 1, Appli
31	65	13.5	378	4	US-10-282-122A-77679	Sequence 77679, A
32	65	13.5	502	4	US-10-437-963-168918	Sequence 168918, A
33	64.5	13.4	163	4	US-10-767-701-31909	Sequence 31909, A
34	64.5	13.4	197	4	US-10-425-114-36734	Sequence 36734, A
35	64.5	13.4	357	6	US-11-188-298-814	Sequence 814, App
36	64.5	13.4	377	4	US-10-369-493-4868	Sequence 33648,
37	64.5	13.4	468	4	US-10-369-493-4868	Sequence 4868, Ap
38	64.5	13.4	468	4	US-10-369-493-7628	Sequence 7628, Ap
39	64.5	13.4	468	4	US-10-282-122A-49776	Sequence 49776, A
40	64.5	13.4	579	4	US-10-437-963-140815	Sequence 140815,
41	64	13.3	220	5	US-10-732-923-16837	Sequence 16837, A
42	64	13.3	220	6	US-11-188-298-9826	Sequence 9826, Ap
43	64	13.3	243	4	US-10-425-115-292119	Sequence 292119,
44	64	13.3	555	4	US-10-413-943-65	Sequence 65, Appl
45	64	13.3	712	4	US-10-413-943-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-10-813-908-6

; Sequence 6, Application US/10813908

; Publication No. US20050058662A1

; GENERAL INFORMATION:

; APPLICANT: Frey, Joachim Stuber

; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and U

; FILE REFERENCE: MIC01/2315/WO

; CURRENT APPLICATION NUMBER: US/10/813,908

; CURRENT FILING DATE: 2004-03-26

; PRIOR APPLICATION NUMBER: US/10/416,902

; PRIOR FILING DATE: 2003-05-15

; PRIOR APPLICATION NUMBER: PCT/CA01/01589

; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Aeromonas salmonicida

; US-10-813-908-6

Query Match 100.0%; Score 483; DB 5; Length 93;

Best Local Similarity 100.0%; Pred. No. 5,9e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSLSERLGRFYLRW 60

Db 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSLSERLGRFYLRW 60

Qy 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93

Db 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93

RESULT 2

US-10-450-763-36125

; Sequence 36125, Application US/10450763

; Publication No. US20050196754A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

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/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 36125
/ LENGTH: 929
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (852)..(895)
/ OTHER INFORMATION: Envelope Polyprotein GP41 domain identified by eMATRIX,
/ accession number PF00517B, p-value=6.654e-09, raw score of 22.57
US-10-450-763-36125

Query Match 14.9%; Score 72; DB 5; Length 929;
Best Local Similarity 36.7%; Pred. No. 15;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

QY 17 AALYLLAEATLAVLPGHFHLYGNV--DVFRSSSLSSERLG--RFYLRWTGASEPEPGWPM 72
Db 128 AGYIFLQEASL-----FGHQLYAVVDTGFRAPASAPAQGLGLLRKIRLWHDSRGSPSGWFI 183

RESULT 3
US-10-094-886-138
/ Sequence 138, Application US/10094886
/ Publication No. US20040002120A1
/ GENERAL INFORMATION:
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Vernet, Corine A.
/ APPLICANT: Li, Li
/ APPLICANT: Gorman, Linda
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Taupier, Raymond J., Jr.
/ APPLICANT: Miller, Charles
/ APPLICANT: Casman, Stacie
/ APPLICANT: Pena, Carol
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Zerhusen, Bryan
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Pochart, Pascal
/ APPLICANT: Fernandez, Eima
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Spaderna, Steven
/ APPLICANT: LaRoche, William
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-290 B
/ CURRENT APPLICATION NUMBER: US/10/094,886
/ CURRENT FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: 60/274,322
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: 60/313,182
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 60/288,052
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/318,510
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/274,281
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: 60/314,018
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/ PRIOR FILING DATE: 2001-08-21
/ PRIOR APPLICATION NUMBER: 60/274,194
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: 60/274,849
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/296,693
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/313,626
/ PRIOR FILING DATE: 2001-08-21
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 298
/ SOFTWARE: PatentIn 2.1
/ SEQ ID NO 138
/ LENGTH: 2301
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-094-886-138

Query Match 14.9%; Score 72; DB 4; Length 2301;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

QY 17 AALYLLAEATLAVLPGHFHLYGNV--DVFRSSSLSSERLG--RFYLRWTGASEPEPGWPM 72
Db 1592 AGYIFLQEASL-----FGHQLYAVVDTGFRAPASAPAQGLGLLRKIRLWHDSRGSPSGWFI 1647

RESULT 4
US-10-506-454-1151
/ Sequence 1151, Application US/10506454
/ Publication No. US20060068386A1
/ GENERAL INFORMATION:
/ APPLICANT: Mezheva, Alexi I
/ APPLICANT: Polushin, Nikolai N
/ APPLICANT: Shcherbinina, Olga V
/ APPLICANT: Shakhova, Vera V
/ APPLICANT: Malykh, Andrei G
/ APPLICANT: Kozyavkin, Sergei A
/ TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophilic
/ TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
/ FILE REFERENCE: FID001
/ CURRENT APPLICATION NUMBER: US/10/506,454
/ CURRENT FILING DATE: 2004-08-31
/ PRIOR APPLICATION NUMBER: PCT/US03/06664
/ PRIOR FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: 60/361,742
/ PRIOR FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 1722
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1151
/ LENGTH: 298
/ TYPE: PRT
/ ORGANISM: Methanopyrus kandleri
/ US-10-506-454-1151

Query Match 14.7%; Score 71; DB 5; Length 298;
Best Local Similarity 30.9%; Pred. No. 5.2;
Matches 29; Conservative 8; Mismatches 33; Indels 24; Gaps 5;

QY 3 VRREGERAGLANPFAALYLLAEATL---AVLQPG-HFLYGNVDVFRSSSLSSERLGRFY 58
Db 50 VFRVCKR-----LYLVSLGYCEGETILEPGVEVELSGQVLAEPFLSEYHGRLWI 100

QY 59 R-----WTGASEPEPGWFMATEQVCSLRD 83
Db 101 RIGYFPFGIHW--VELPERGFFFLTRGVCAIRD 132

RESULT 5
US-10-289-762-769
/ Sequence 769, Application US/10289762
```



```
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffaie, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; FILE REFERENCE: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 769
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-769

Query Match      14.6%; Score 70.5; DB 4; Length 240;
Best Local Similarity 32.0%; Pred. No. 4.6;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY  7 GERAGLANP-----FAALLAEATLAVLGP--GHFLYGNVDVFRSSLSERLGRFYLR 59
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  29 GEIVGLGPGAGKTTAFYL-----TVGLIRPDSGKIIFKNVDVTKTMDHRARLIGYLV- 83
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKQKH 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  84 -----AQEPTIFKELTVQDNLICILEIYKARKQKQSH 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-10-437-963-128383
; Sequence 128383, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128383
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30741C.1.pep
US-10-437-963-128383

Query Match      14.3%; Score 69; DB 4; Length 980;
Best Local Similarity 28.6%; Pred. No. 39;
Matches 34; Conservative 13; Mismatches 26; Indels 46; Gaps 8;

QY  4 RREGER--AGLANPFAALLAEATLAVLGPCHP-----LYGNVDVFRSSSL----- 48
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  148 KREGKRVKAGLT-----ADLSVGPAPHLAGLTGAFGRSDRWKSSLTGIQRFD 196
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  49 -----SSERLGR--FYLRWTCASPEPGWF---MLATE--QVCSLRDMRKQKH 89
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  197 RRFASSVVRASSSSNRLNRGHYL---PPRTBPKRWMPKDLMATQRRRLQRLRAQIREK 253
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-10-732-923-12941
; Sequence 12941, Application US/10732923
; Publication No. US20050108791A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 12941
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-732-923-12941

Query Match      14.2%; Score 68.5; DB 5; Length 917;
Best Local Similarity 30.0%; Pred. No. 41;
Matches 27; Conservative 12; Mismatches 32; Indels 19; Gaps 4;

QY  6 EGERAGLANPFAAL--YLLAEATLAVLGPCHFLYGNVDVFRSSLSERLGRFYLRWTG- 62
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  736 ESEHGTPLPIVALTAHANANEKRALQSG-----MDDYLTKPISERQLAQVVLKWTGL 789
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  63 -----ASE-PEPGWFMLATEQVCSLR 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  790 ALRNQGPASERPELGLLEQLVLDQDEGLR 819
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-10-732-923-12942
; Sequence 12942, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 12942
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-732-923-12942

Query Match      14.2%; Score 68.5; DB 5; Length 917;
Best Local Similarity 30.0%; Pred. No. 41;
Matches 27; Conservative 12; Mismatches 32; Indels 19; Gaps 4;

QY  6 EGERAGLANPFAAL--YLLAEATLAVLGPCHFLYGNVDVFRSSLSERLGRFYLRWTG- 62
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  736 ESEHGTPLPIVALTAHANANEKRALQSG-----MDDYLTKPISERQLAQVVLKWTGL 789
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  63 -----ASE-PEPGWFMLATEQVCSLR 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  790 ALRNQGPASERPELGLLEQLVLDQDEGLR 819
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-796-692-1826
; Sequence 1826, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
```

```
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1826
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1826
```

```
Query Match 14.1%; Score 68; DB 3; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

QY 16 FAALYLLAEATLAVLPGHF-----LYGNVDVFRSSSLSSERLGRFYLRTWTGASEPE 67
Db 13 FVSLPTMQEASLAVLFYHYIISPICKNVLYQVRSMLSSLSLSPRRL---RLRYRGNs-PV 68

QY 68 PGWFML 73
Db 69 QSLFML 74
```

```
RESULT 10
US-10-040-862-1826
; Sequence 1826, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
```

```
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1826
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1826
```

```
Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

QY 16 FAALYLLAEATLAVLPGHF-----LYGNVDVFRSSSLSSERLGRFYLRTWTGASEPE 67
Db 13 FVSLPTMQEASLAVLFYHYIISPICKNVLYQVRSMLSSLSLSPRRL---RLRYRGNs-PV 68

QY 68 PGWFML 73
Db 69 QSLFML 74
```

```
RESULT 11
US-10-057-475B-1826
; Sequence 1826, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-475B-1826

Query Match 14.1%; Score 68; DB 4; Length 76;  
Best Local Similarity 40.9%; Pred. No. 2.4;  
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAAYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSRSLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYISPICKVKLYRQVRSMSSLSPPRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 12

US-10-154-884B-1826

; Sequence 1826, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; PRIOR FILING DATE: 2002-05-23

; PRIOR FILING DATE: 2000-03-01

; PRIOR FILING DATE: 2000-03-17

; PRIOR FILING DATE: 2000-03-17

; PRIOR FILING DATE: 2000-04-27

; PRIOR FILING DATE: 2000-04-28

; PRIOR FILING DATE: 2000-04-28

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 2000-05-04

; PRIOR FILING DATE: 2000-05-22

; PRIOR FILING DATE: 2000-07-14

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-1826

Query Match 14.1%; Score 68; DB 4; Length 76;  
Best Local Similarity 40.9%; Pred. No. 2.4;  
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAAYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSRSLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYISPICKVKLYRQVRSMSSLSPPRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 13

US-10-764-324-1826

; Sequence 1826, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; PRIOR FILING DATE: 2004-01-23

; PRIOR FILING DATE: 2001-11-06

; PRIOR FILING DATE: 2000-03-01

; PRIOR FILING DATE: 2000-03-17

; PRIOR FILING DATE: 2000-04-27

; PRIOR FILING DATE: 2000-04-28

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 2000-05-04

; PRIOR FILING DATE: 2000-05-22

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-764-324-1826

Query Match 14.1%; Score 68; DB 4; Length 76;  
Best Local Similarity 40.9%; Pred. No. 2.4;  
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAAYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSRSLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYISPICKVKLYRQVRSMSSLSPPRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 14

US-09-815-242-5199

; Sequence 5199, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.







```
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-501-834-26

Query Match      12.7%; Score 61.5; DB 6; Length 1871;
Best Local Similarity 27.5%; Pred. No. 42;
Matches 25; Conservative 5; Mismatches 24; Indels 37; Gaps 4;

Qy 11 GLANPEAA-----LYLLA---EATLAVLGGHLYGNVDVFRSSLSLSSERLGRFYLRWT 61
Db 1493 GVINVFAEARHILPLLYFVGNIERYVPAGPAHL-----QLASTAAG----- 1534

Qy 62 GASEPEPGWFMLATEQVCSLRDMRKQKHGL 92
Db 1535 -----CLATEPLGLNDTRVKHSNKL 1555

RESULT 7
US-10-449-902-48431
; Sequence 48431, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48431
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48431

Query Match      12.6%; Score 61; DB 6; Length 466;
Best Local Similarity 32.9%; Pred. No. 9.3;
Matches 24; Conservative 7; Mismatches 24; Indels 18; Gaps 4;

Qy 22 LABATLAVLGP-----GHFLYGNVDVFRSSLSLSSERLGRFYLRWTGASEPEPGW-----FM 72
Db 358 LAHAATAIMGFWETLGNPCVGGNDIFRSTTFFSQ--STFVL-----PIPLGLSGSFIM 408

Qy 73 LATEQVCSLRDMR 85
Db 409 ADRWSPSELDRSR 421

RESULT 8
US-10-953-349-25312
; Sequence 25312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25312
```

```
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25312

Query Match      12.5%; Score 60.5; DB 6; Length 185;
Best Local Similarity 34.3%; Pred. No. 3.5;
Matches 23; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

Qy 45 SSSLSE-----RLGRFYLRWTGASEPEPGWF-----MLATQVCSLRDMRK 86
Db 63 SESESEEEQDQQRVETVXRAGVARLGVGAARP-PRWRSRRPAAAAATLQVVVLRDQR 121

Qy 87 RQKHGLA 93
Db 122 AREGVA 128

RESULT 9
US-10-953-349-25311
; Sequence 25311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25311
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (209)..(209)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25311

Query Match      12.5%; Score 60.5; DB 6; Length 313;
Best Local Similarity 34.3%; Pred. No. 6.6;
Matches 23; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

Qy 45 SSSLSE-----RLGRFYLRWTGASEPEPGWF-----MLATQVCSLRDMRK 86
Db 191 SESESEEEQDQQRVETVXRAGVARLGVGAARP-PRWRSRRPAAAAATLQVVVLRDQR 249

Qy 87 RQKHGLA 93
Db 250 AREGVA 256

RESULT 10
US-11-165-586-67
; Sequence 67, Application US/11165586
; Publication No. US20060121060A1
; GENERAL INFORMATION:
; APPLICANT: Seattle Biomedical Research Institute
; APPLICANT: Kappe, Stefan H.I.
; APPLICANT: Matschewski, Kai
; TITLE OF INVENTION: LIVE GENETICALLY ENGINEERED PROTOZOAN VACCINE
; FILE REFERENCE: SBHUI24889
; CURRENT APPLICATION NUMBER: US/11/165,586
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: PCT/US2004/043023
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: US 60/633,242
```

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; PRIOR FILING DATE: 2004-12-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-11-165-586-67

Query Match      12.4%; Score 60; DB 7; Length 450;
Best Local Similarity 31.5%; Pred. No. 12;
Matches 23; Conservative 7; Mismatches 19; Indels 24; Gaps 3;

QY 18 ALXLLAEAT-----LAVLPGHFLYGNVDVF--RSSLSRSLG----- 54
||| ||| : : : : : : : : : : : : : : : : : : : : : : :
Db 86 ALTLLAQSPPPGRKPTAVFLNGVVIQNSDIYWTLSHLSKARLGTENCCLPDQCAALIE 145
||| ||| : : : : : : : : : : : : : : : : : : : : : : :

QY 55 -RFYLRWTGASEP 66
||| ||| : : : : : : : : : : : : : : : : : : : : : : :
Db 146 KRFRQGWGGASTP 158
||| ||| : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 11
US-11-270-040-6
; Sequence 6, Application US/11270040
; Publication No. US20060110762A1
; GENERAL INFORMATION:
; APPLICANT: Kapil, Sanjay
; APPLICANT: Kim, Jeong-Ki
; TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY
; TITLE OF INVENTION: SYNDROME VIRUS RECEPTOR COMPONENTS AND USES THEREOF
; FILE REFERENCE: 14337/004001
; CURRENT APPLICATION NUMBER: US/11/270,040
; CURRENT FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: 60/680,297
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/626,788
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1730
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-270-040-6
```

```
Query Match      12.4%; Score 60; DB 7; Length 1730;
Best Local Similarity 29.4%; Pred. No. 59;
Matches 15; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 10 AGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFYLRLW 60
: ||| : : : : : : : : : : : : : : : : : : : : : : :
Db 693 SALGNASASATLDAQATLVLTPTSHTLQEGIEANLTCNVRSAGSPANFSW 743
: ||| : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 12
US-10-449-902-34748
; Sequence 34748, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34748
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-34748

Query Match      12.3%; Score 59.5; DB 6; Length 503;
Best Local Similarity 23.1%; Pred. No. 15;
Matches 21; Conservative 14; Mismatches 27; Indels 29; Gaps 3;

QY 8 ERAGLANPFAALYLLAE-----ATLAVLPGHFLYGNVD----- 41
||| : : : : : : : : : : : : : : : : : : : : : : :
Db 210 ERSVVNVGGANYWLTEDEESVWKHAVVTDLSEELFQWLQLPAVDPPANYVLGDPDQWL 269
: ||| : : : : : : : : : : : : : : : : : : : : : : :

QY 42 --VFRSSLSRSLGRFYLRLWTGASEPPEGW 70
||| : : : : : : : : : : : : : : : : : : : : : : :
Db 270 TEVDNSVSVYVETGKLHI-WTIDSKIEQSW 299
||| : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 13
US-10-449-902-51740
; Sequence 51740, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51740
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51740
```

```
Query Match      12.3%; Score 59.5; DB 6; Length 1207;
Best Local Similarity 33.9%; Pred. No. 44;
Matches 21; Conservative 5; Mismatches 17; Indels 19; Gaps 3;

QY 5 REGERAGLANPFAALY-----LLAEATLAVLG-----PGHFLYGNVDVFRSS 46
: ||| : : : : : : : : : : : : : : : : : : : : : : :
Db 643 QEGEAGGTTQOIGATYPTTENIRRTKELKADATLKVGLLVDTFGHESFSNLR-SRGS 701
: ||| : : : : : : : : : : : : : : : : : : : : : : :

QY 47 SL 48
|||
Db 702 SL 703
|||
```

```
RESULT 14
US-10-474-853-2
; Sequence 2, Application US/10474853
; Publication No. US20060088546A1
; GENERAL INFORMATION:
; APPLICANT: RIDING, GEORGE ALFRED
; APPLICANT: HOPE, MICHELLE ANNE
; APPLICANT: WILLADSEN, PETER
; TITLE OF INVENTION: Antigens for raising an immune response against Rickettsiae and Ehrlichiae pathogens
; FILE REFERENCE: RICE-025
; CURRENT APPLICATION NUMBER: US/10/474,853
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: AU PR4400
; PRIOR FILING DATE: 2001-04-12
```



```
; PRIOR APPLICATION NUMBER: AU PR7597
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: AU PS0861
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Anaplasma marginale
US-10-474-853-2

Query Match      12.2%; Score 59; DB 6; Length 422;
Best Local Similarity 32.3%; Pred. No. 14;
Matches 20; Conservative 6; Mismatches 20; Indels 16; Gaps 3;

Qy 22 LAEATLAVLGGHFLYGNVDVFRSSSLSSRLGRFYL-----RWTGASE-----PEPGWF 71
Db 27 LVGATLAVLLPAVELYG-----TGSSAAEAAGFPVSGYTPAWGGVRLNLYVGIPGETWY 80

Qy 72 ML 73
Db 81 VL 82

RESULT 15
US-10-449-902-48555
; Sequence 48555, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48555
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48555

Query Match      12.1%; Score 58.5; DB 6; Length 507;
Best Local Similarity 26.0%; Pred. No. 21;
Matches 26; Conservative 9; Mismatches 24; Indels 41; Gaps 5;

Qy 12 LANPFAALYLLAETLAVLGGHFLYGNVDVFRSSSLSSRLGR-----FYLR 59
Db 262 LANDGDFLFLADAAATA-----FQYGNPDALCSPIVEAKKNGTDLVETFARYVKDYIG 316

Qy 60 WTGAS-----EPEPG-----WFMLATEQVCS 80
Db 317 TFGASVASDYQEYLNKVTTPPAESAYRLWNY-----QVCS 351
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Search completed: June 16, 2006, 20:25:55  
Job time : 5.00732 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 62.2846 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-7  
Perfect score: 459  
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKRRPTIMRGLMI 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	100.0	94	5	ABB80775 A. salmon
2	179.5	38.3	107	7	ABO81311 Pseudomon
3	88.5	18.9	232	8	ADx66930 Plant ful
4	81	17.3	1289	4	AG81208 Mycobacte
5	81	17.3	1289	6	ABU36881 Protein e
6	79.5	17.0	211	3	AAB54325 Human pan
7	79.5	17.0	483	7	ADC31377 Human nov
8	76	16.2	323	3	AAB50381 Human unc
9	76	16.2	323	4	AAB94434 Human pro
10	76	16.2	323	5	ABP69215 Human pol
11	75.5	16.1	177	6	ABU36046 Protein e
12	74.5	15.9	204	8	ADx72136 Plant ful
13	74.5	15.9	1175	6	ABU29788 Protein e
14	74.5	15.9	1179	8	ADc96499 E. faeciu
15	73.5	15.7	364	8	ADJ50279 Oil-assoc
16	73.5	15.7	384	6	ABU37047 Protein e
17	73.5	15.7	678	4	AG81107 Mycobacte
18	73.5	15.7	678	6	ABU36410 Protein e
19	73.5	15.7	822	6	ABU34753 Protein e
20	73.5	15.7	957	7	ABO72358 Pseudomon
21	72.5	15.5	274	7	ABO73243 Pseudomon
22	72.5	15.5	548	7	ABO71633 Pseudomon
23	72.5	15.5	1162	8	ADS24694 Bacterial

24	71.5	15.2	402	7	ABO76543	Abo76543 Pseudomon
25	70.5	15.0	453	7	ABO76084	Abo76084 Pseudomon
26	70.5	15.0	943	4	ABB62085	Abb62085 Drosophil
27	70	14.9	310	5	ABP65928	Abp65928 Bifidobac
28	70	14.9	564	8	ADY12097	Ady12097 Plant ful
29	69.5	14.8	360	6	ABU40257	Abu40257 Protein e
30	69	14.7	395	9	AEA33981	Aea33981 Macrolide
31	69	14.7	452	7	ABO76649	Abo76649 Pseudomon
32	69	14.7	607	7	ABO77391	Abo77391 Pseudomon
33	68.5	14.6	164	2	AAV07985	Aay07985 Human sec
34	68.5	14.6	182	3	AAV87320	Aay87320 Human sig
35	68.5	14.6	220	8	ADY12346	Ady12346 Plant ful
36	68.5	14.6	440	4	ABG02713	Abg02713 Novel hum
37	68.5	14.6	613	6	ABU33831	Abu33831 Protein e
38	68.5	14.6	675	7	ABO80415	Abo80415 Pseudomon
39	68.5	14.6	859	9	ABM95021	Abm95021 M. xanthu
40	68.5	14.6	939	5	ABJ04708	Abj04708 Mycobacte
41	68	14.5	186	2	AAR41974	Aar41974 Human c-m
42	68	14.5	186	2	AAR53077	Aar53077 Helix-loo
43	68	14.5	201	3	AAB57068	Aab57068 Human pro
44	68	14.5	201	4	AAG74117	Aag74117 Human col
45	68	14.5	201	5	ABP41271	Abp41271 Human ova

ALIGNMENTS

RESULT 1

ABB80775  
ID ABB80775 standard; protein; 94 AA.

AC ABB80775;

DT 23-SEP-2002 (first entry)

DE A. salmonicida type III secretion protein acrG sequence.

XX Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
KW acrV; acrH; antibiotic; vaccine; fish.

XX Aeromonas salmonicida.

XX WO200240514-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001WO-CA001589.

XX 15-NOV-2000; 2000US-0248864P.

XX (FREY/) FREY J.

XX (STUB/) STUBER K.

XX (THOR/) THORNTON J C.

XX (KUZ/) KUZYK M A.

XX (BUR/) BURIAN J.

XX Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;

XX WPI; 2002-537338/57.

XX N-PSDB; ABN86172.

XX Novel protein from Aeromonas salmonicida and nucleic acid encoding the  
PT protein, useful for reducing susceptibility of fish to infection by a  
PT virulent strain of Aeromonas salmonicida.

XX Claim 13; Page 28; 39pp; English.

XX The invention relates to A. salmonicida type III secretion genes and  
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.  
CC A. salmonicida type III secretion apparatus is useful for producing  
CC selected products, especially AexT. AcrV in vaccine, epitope or epitopic  
CC region of AcrV or any other protein of A. salmonicida type III secretion  
CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present  
CC sequence represents the *A. salmonicida* type III secretion protein acrG  
XX  
XX  
SQ Sequence 94 AA;  
Query Match 100.0%; Score 469; DB 5; Length 94;  
Best Local Similarity 100.0%; Pred. No. 3.3e-51;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKQPRADSETISQAEHGADSDHRNALLQELMGLALSDQTCQLLFEAPTEQVAEQ 60  
DB 1 MKQPRADSETISQAEHGADSDHRNALLQELMGLALSDQTCQLLFEAPTEQVAEQ 60  
QY 61 ELLAEIQRQALLPAQPGEGKSRRTIMRGLMI 94  
DB 61 ELLAEIQRQALLPAQPGEGKSRRTIMRGLMI 94  
RESULT 2  
ID ABO81311 standard; protein; 107 AA.  
XX AC ABO81311;  
XX DT 29-JUL-2004 (first entry)  
XX DE Pseudomonas aeruginosa polypeptide #13486.  
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX OS Pseudomonas aeruginosa.  
XX US6551795-B1.  
XX PD 22-APR-2003.  
XX PF 18-FEB-1999; 99US-00252991.  
XX PR 18-FEB-1998; 98US-0074788P.  
XX PR 27-JUL-1998; 98US-0094190P.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
XX DR N-PSDB; ABD14882.  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX Disclosure; SEQ ID NO 30057; 455pp; English.  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 107 AA;  
Query Match 38.3%; Score 179.5; DB 7; Length 107;  
Best Local Similarity 47.6%; Pred. No. 2.2e-14;  
Matches 40; Conservative 15; Mismatches 28; Indels 1; Gaps 1;  
QY 12 TISQAEHGADSDHRNALLQELMGLALSDQTCQLLFEAPTEQVA-VAEQELLAEIQRQ 70  
DB 24 TVQAELAIRDSEERGLLAEMWQGLAADAAGELLFOAPERELARAABEELAEURMR 83  
QY 71 ALLPAQPGEGKSRRTIMRGLMI 94  
DB 84 SSQPTQGEQGTTPRRPTMRLI 107  
RESULT 3  
ID ADX66930 standard; protein; 232 AA.  
XX AC ADX66930;  
XX DT 21-APR-2005 (first entry)  
XX DE Plant full length insert polypeptide seqid 37773.  
XX KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content.  
XX OS Unidentified.  
XX US2004034888-A1.  
XX PN 19-FEB-2004.  
XX PD 28-APR-2003; 2003US-00425114.  
XX PF 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAO/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX Claim 1; SEQ ID NO 37773; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in

polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation.

CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1289 AA;

Query Match 17.3%; Score 81; DB 6; Length 1289;  
Best Local Similarity 20.1%; Pred. No. 1.8;  
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;  
  
QY 5 RFADHSETISQAEHGIAADSDHNRALQEMLAGL-ALS---DOTCOLL----- 47  
Db 345 RLAVASEELAHHESAVALSTRAESIQHTWFGLSALAERVDATVTRASERAHLDIEPVA 404  
QY 48 -----FRAPTEQVAVAQELLAEIQRQALLPAQGE 79  
Db 405 VSDTPDKRPKEAEAAQQAQVAVABQQLLAELDAARLDRAAE 447

RESULT 6  
AAB54325  
ID AAB54325 standard; protein; 211 AA.  
XX  
AC AAB54325;  
XX  
DT 09-MAR-2001 (first entry)  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:777.  
XX  
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;  
KW diagnosis; identification; cytostatic; neuroprotective; nontropic;  
KW immunomodulatory; relaxant; contraceptive; gynaecological;  
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;  
KW linkage analysis; tissue identification; tissue typing; forensic; neural;  
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;  
KW cardiovascular; renal; proliferative.  
XX  
OS Homo sapiens.  
XX  
FN WO200055320-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005989.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX  
XX WPI; 2000-579444/54.  
DR N-PSDB; AAC99090.  
XX  
PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
PT treating, or ameliorating a medical condition, particular pancreatic  
PT cancer, or for use in assays for diagnosing a pathological condition.  
XX  
PS Claim 11; Page 1215-1216; 1379pp; English.

XX AAC98773 to AAC99231 encode the human pancreatic cancer associated  
CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
CC neuroprotective, nontropic, immunomodulatory, relaxant, contraceptive,  
CC gynaecological, cardiant and antiinflammatory activities, and can be used  
CC in gene therapy. The polynucleotide and proteins can be used for  
CC preventing treating, or ameliorating a medical condition or in assays  
CC for diagnosing a pathological condition or a susceptibility to one in a  
CC subject. Binding partners to the proteins and the activity of the  
CC proteins can be identified. The pancreatic cancer antigens can be used to  
CC detect, treat or prevent pancreatic disorders, especially cancer.  
CC Agonists and antagonists to the antigens can be screened for. The  
CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
CC acid hybridisation probes that can be used in chromosome mapping, linkage  
CC analysis, tissue identification and/or typing and a variety of forensic  
CC and diagnostic methods. The proteins can be used to generate antibodies  
CC which are used to purify, detect and target the polypeptides, including  
CC both in vivo and in vitro diagnostic and therapeutic methods. The  
CC proteins can be used to treat or prevent neural, immune system, muscular,  
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 211 AA;  
  
Query Match 17.0%; Score 79.5; DB 3; Length 211;  
Best Local Similarity 31.0%; Pred. No. 0.26;  
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;  
  
QY 2 KQPRFADHSETISQAEHGIAADSDHNRAL---LQEML-----AGLAL 39  
Db 27 KSKQFLDLNETIDKQEEVAKSRASARVKGLOEALNHRHSIINALKAKLQWTEAALAL 86  
QY 40 SDQTCQLLFEAPTEQVAVAQELLAEIQRQALLPAQGEGRKSRRTIMRGL 92  
Db 87 SEQKAQDL---GELLATAEQQLSQRQAKELKLEQQEAAE-RESKLLRDL 134  
  
RESULT 7  
ADC31377  
ID ADC31377 standard; protein; 483 AA.  
XX  
AC ADC31377;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human novel polypeptide sequence, SEQ ID NO:1459.  
XX  
KW Human; diagnostic; drug screening; forensics; gene mapping;  
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;  
KW ulcers; osteoporosis; autoimmune disease; cancer;  
KW molecular weight marker; food supplement; antiparkinsonian; nontropic;  
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnery;  
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
KW gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO2003029271-A2.  
XX  
XX 10-APR-2003.  
XX  
XX 24-SEP-2002; 2002WO-US030474.  
XX  
XX 24-SEP-2001; 2001US-0324631P.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;  
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
PI Halley-Vicente D, Drmanac RT;

XX WPI: 2003-371981/35.  
DR N-PSDB; ADC30406.  
XX  
PT New polynucleotide and polypeptide useful for diagnosing, preventing or  
PT treating conditions such as neurodegenerative diseases, anemias, platelet  
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
PT cancer.  
XX  
PS Claim 20; SEQ ID NO 1459; 1185pp; English.  
XX  
CC The invention relates to 971 novel human cDNA sequences (ADC29919-  
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The  
CC invention also relates to nucleic acid sequences over 99% identical with  
CC the novel human cDNAs. The invention additionally encompasses expression  
CC vectors and host cells comprising a nucleic acid of the invention; the  
CC recombinant production of a polypeptide of the invention; an antibody  
CC against a polypeptide of the invention; a method of detecting  
CC polynucleotides or polypeptides of the invention; and methods of  
CC identifying a compound which binds to a polypeptide of the invention. The  
CC invention further discloses methods of preventing, treating or  
CC ameliorating a medical condition; kits comprising polynucleotide probes  
CC and/or monoclonal antibodies for carrying out the methods of the  
CC invention; methods for the identification of compounds that modulate the  
CC expression or activity of the polynucleotide and/or polypeptide; and 767  
CC contig sequences corresponding to the cDNA sequences of the invention  
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628  
CC -ADC33394). The nucleic acids and polypeptides of the invention are  
CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
CC identification of mutations responsible for genetic disorders or other  
CC traits, for assessing biodiversity, and in producing many other types of  
CC data and products dependent on DNA and amino acid sequences. They are  
CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
CC disease and other neurodegenerative diseases, anaemia, platelet  
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
CC cancer. The nucleic acids may also be used as hybridisation probes or  
CC primers, and in the recombinant production of a protein. The polypeptides  
CC are also useful in generating antibodies, as molecular weight markers,  
CC and as food supplements. The present sequence represents a specifically  
CC claimed human polypeptide sequence of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 483 AA;  
Query Match 17.0%; Score 79.5; DB 7; Length 483;  
Best Local Similarity 31.0%; Pred. No. 0.78;  
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;  
Qy 2 KQPRFADHSETISOAEHGIADSDHRNAL----LQEML-----AGIAL 39  
Db 255 KSKQFLDLMETIDKOREMAKSSRAARVQQLQEALNERHSIINALKAKLQMTFALAL 314  
Qy 40 SDQTCOLLFEAPTEQVAEQLLAETORRQALLPAQGEGRKSRRTIMRGL 92  
Db 315 SEQKAQDL----GELLATAEQEQLSLQRQAKELKLEQEEAAE-RESKLLRDL 362  
RESULT 8  
AAB50381  
ID AAB50381 standard; protein; 323 AA.  
AC AAB50381;  
XX  
DT 12-MAR-2001 (first entry)  
DE Human uncoupling protein #4.  
XX  
KW Human; uncoupling protein; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cardiant; vasotropic;  
KW cerebroprotective; neuroprotective; antibacterial; ophthalmological;  
KW gastrointestinal; nephrotropic; gynaecological; vulnery; thrombolytic;

KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;  
KW infertility.  
XX  
OS Homo sapiens.  
XX  
PN WO2000061614-A2.  
XX  
PD 19-OCT-2000.  
XX  
PF 06-APR-2000; 2000WO-US009534.  
XX  
PR 09-APR-1999; 99US-0128701P.  
PR 08-JUL-1999; 99US-0142821P.  
PR 18-AUG-1999; 99US-0149448P.  
PR 12-NOV-1999; 99US-0164751P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR;  
XX  
DR WPI; 2000-656322/63.  
DR N-PSDB; AAC90455.  
XX  
PT Uncoupling proteins and nucleic acid sequences encoding them, useful for  
PT detecting, preventing and treating proliferative, neurological, immune  
PT system, cardiovascular and gastrointestinal disorders.  
XX  
PS Claim 11; Page 320-321; 343pp; English.  
XX  
CC The present sequence is a human uncoupling protein. The nucleotide  
CC sequences encoding the uncoupling proteins may be used for the detection  
CC of various disorders such as cancer, for chromosome identification, as  
CC chromosome markers and for numerous other diagnostic or research  
CC purposes. The uncoupling protein encoded by the nucleotide sequences may  
CC be used to treat disorders such as neural, immune, muscular,  
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal and  
CC proliferative disorders, wounds, infectious diseases, thrombosis,  
CC arthritis, and infertility  
XX  
SQ Sequence 323 AA;  
Query Match 16.2%; Score 76; DB 3; Length 323;  
Best Local Similarity 30.0%; Pred. No. 1.3;  
Matches 24; Conservative 14; Mismatches 30; Indels 12; Gaps 3;  
Qy 18 HGIADSDHRNALQEMLAGLALSDQTCOLLFEAPTEQVAV-----AEQELLAEIQR 68  
Db 92 HQLSKDGQKLTLLKEMLAGGAG--TCQVITVTPEMLKTLQDAGRIRAAQRKILAAQGG 149  
Qy 69 RQALLPAQPG-EGRKSRRT 87  
Db 150 LSAQGGQAQPSVEAPAPRPT 169  
RESULT 9  
AAB94434  
ID AAB94434 standard; protein; 323 AA.  
XX  
AC AAB94434;  
XX  
DT 26-JUN-2001 (first entry)  
DE Human protein sequence SEQ ID NO:15054.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-00116126.







The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational

CC treating Enterococcus faecium infections. The present sequence represents  
CC one if the disclosed E. faecium proteins.

XX  
SQ Sequence 1179 AA;

Query Match 15.9%; Score 74.5; DB 7; Length 1179;  
Best Local Similarity 39.2%; Pred. No. 11;  
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

Qy 19 GIADSDHRNALLQEMLAGIALSDQTCQLLFEAPTEQVAVARQELIAEQRR 69  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 12 GNGKKDHQVLIDEASAWLD-QDASNQVFLVPNYSKFEQEILAEWRR 61

RESULT 15

ADJ50279  
ID ADJ50279 standard; protein; 364 AA.

XX AC ADJ50279;

XX DT 06-MAY-2004 (first entry)

XX DE Oil-associated gene related protein #1779.

XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX OS Unidentified.

XX PN US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

XX PA (LAUR/) LAURIE C C.

XX PA (RAVA/) RAVANELLO M.

XX PA (SAVA/) SAVAGE T.

XX PA (LEDE/) LEDEAUX J R.

XX PA (ROGE/) ROGERS J A.

XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX DR WPI; 2004-142683/14.

XX PT Novel recombinant DNA construct comprising a promoter functional in  
XX PT plants operably linked to an oil-associated gene for producing transgenic  
XX PT plant seed.

XX PS Example 3; SEQ ID NO 2283; 22pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a  
XX CC promoter functional in plants operably linked to an oil-associated gene.  
XX CC The construct is useful for transgenic plant seed which has in its genome  
XX CC the construct, that is functional in the plant to transcribe the oil-  
XX CC associated gene. The transgenic plant seed grows into a plant having  
XX CC enhanced seed oil as compared to wild type. The construct is useful for  
XX CC producing hybrid maize seed. The transgenic plant seed is useful for  
XX CC producing vegetable oil. The present sequence represents the amino acid  
XX CC sequence of an oil-associated gene related protein.

XX SQ Sequence 364 AA;

Query Match 15.7%; Score 73.5; DB 8; Length 364;  
Best Local Similarity 29.5%; Pred. No. 3.1;  
Matches 26; Conservative 16; Mismatches 37; Indels 9; Gaps 4;

Qy 1 MKQPRFADHSBTISOABHGIAADSDHRNALLQEMLAGL-----ALSDQTCQLLFEAPTEQV 55  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 MLEPN-ADHRAVAQAA-GVNASRTITLVMLDEWAGADARRRAVADTVCALATCCSLAA 58

Qy 56 AVARQELIAEQRRQALLPAQPGEGRKS 83  
| | | | | : | | | | | : | | | | | : | | | | | :  
Db 59 AIAEGPLAGDLAR--TLSSGEAGEGQKA 84

Search completed: June 16, 2006, 19:06:47  
Job time : 64.2846 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 9.55285 Seconds  
(without alignments)  
946.773 Million cell updates/sec

Title: US-10-813-908A-7  
Perfect score: 459  
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKRRPTIMRGLMI 94  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	41.7	95	2 A33601	low calcium respon
2	195.5	41.7	95	2 A37314	regulatory protein
3	179.5	38.3	98	2 F83432	regulator in type
4	81	17.3	1289	2 B70748	probable smc prote
5	75.5	16.1	177	2 B87146	SOS ribosomal prot
6	74	15.8	222	2 T16731	hypothetical prote
7	73.5	15.7	364	1 PAQXF	fructose-bisphosph
8	73.5	15.7	678	2 B70913	probable penicilli
9	72.5	15.5	496	2 B83160	hypothetical prote
10	71.5	15.2	1829	2 T26135	hypothetical prote
11	71	15.1	477	2 F87329	hypothetical prote
12	68.5	14.6	939	2 C70876	hypothetical prote
13	68.5	14.6	1148	2 T13347	Cnn protein - frui
14	68	14.5	439	1 TVHUM	transforming prote
15	68	14.5	440	4 TVHUT	transforming prote
16	68	14.5	2670	2 A46719	inositol 1,4,5-tri
17	67.5	14.4	492	2 S76612	ATP-dependent RNA
18	67	14.3	675	2 F85071	hypothetical prote
19	67	14.3	728	2 S59964	procollagen-lysine
20	67	14.3	1426	2 T00337	hypothetical prote
21	66.5	14.2	873	2 B87049	conserved hypothet
22	66	14.1	2434	2 S44861	DNA topoisomerase
23	66	14.1	2671	2 A49873	inositol 1,4,5-tri
24	65.5	14.0	115	2 P70027	tandem repeat prot
25	65.5	14.0	608	2 T37864	hypothetical prote
26	65	13.9	379	2 E69824	two-component sens
27	65	13.9	449	2 A35762	mannosyltransferas
28	64.5	13.8	1075	1 OYRTHX	heat-stable entero
29	64.5	13.8	1115	2 A70990	carbamoyl-phosphat

probable cell divi  
probable endonucle  
probable transcrip  
hypothetical prote  
two-component sens  
intermediate filam  
ATP-dependent heil  
homolog to yeast c  
calcium-binding pr  
conserved hypothet  
protein (imported  
ornithine cyclodea  
glycine dehydrogen  
actin-related prot  
probable chaperone  
phosphoribosyl-AMP

ALIGNMENTS

RESULT 1  
A33601  
Low calcium response protein G - Yersinia peestis plasmid pCD1  
N:Alternate names: V-antigen  
C:Species: Yersinia pestis  
C:Date: 17-Jan-1990 #sequence revision 17-Jan-1990 #text\_change 09-Jul-2004  
C:Accession: A33601; T42888  
R:Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C.  
J. Bacteriol. 171, 5646-5653, 1989  
A:Title: Molecular analysis of lcrGVH, the V antigen operon of Yersinia pestis.  
A:Reference number: A33601; MUID:9000806; PMID:2477361  
A:Accession: A33601  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-95 <PRI>  
A:Cross-references: UNIPROT:P19394; UNIPARC:UPI000012E2B4; GB:M26405; NID:gl55448; PIDN:AF053946; EMBL:AF053946; NID:g2996222; PIDN:AAC62573.1  
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998  
A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis.  
A:Reference number: 222578; MUID:98422474; PMID:9748454  
A:Accession: T43593  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-95 <HUP>  
A:Cross-references: UNIPARC:UPI000012E2B4; EMBL:AF053946; NID:g2996222; PIDN:AAC62573.1  
R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998  
A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis.  
A:Reference number: 222273; MUID:98427122; PMID:9746557  
A:Accession: T42888  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-95 <PER>  
A:Cross-references: UNIPARC:UPI000012E2B4; EMBL:AF074612; NID:g3822037; PIDN:AAC69798.1  
C:Experimental source: strain KIMS  
C:Genetics:  
A:Gene: lcrG  
A:Genome: plasmid  
A>Note: plasmid pCD1

Query Match 41.7%; Score 195.5; DB 2; Length 95;  
Best Local Similarity 43.2%; Pred. No. 2.6e-13;  
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;  
Oy 1 MKQPRFADHSETISQAEHGIADSDHRNALLOEMAGIALSDQTCLLFEA-PTQOVAVE 59  
Db 1 MKSSHFDYDKTLQAEALAIADSDHRNAKLQEMCADIGLTPEAVMKIFAGRSABEIKPAE 60  
Oy 60 QELLAEIQRQALLPAQPGEGKRRRPTIMRGLMI 94  
Db 61 RELLEIKRQERQFQHPYDGKRPKPTIMRQGII 95

```
RESULT 2
A37314
regulatory protein LcrG - Yersinia pseudotuberculosis
C:Species: Yersinia pseudotuberculosis
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: A37314
R; Bergman, T.; Hakansson, S.; Foreberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;
J. Bacteriol. 173, 1607-1616, 1991
A:Title: Analysis of the v antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis: e
A:Reference number: A37314; MUID:91154114; PMID:1705541
A:Accession: A37314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <BER>
A:Cross-references: UNIPROT:P19394; UNIPARC:UPI000012E2B4; GB:M57893; NID:g155456; PIDN:
Query Match 41.7%; Score 195.5; DB 2; Length 95;
Best Local Similarity 43.2%; Pred. No. 2.6e-13;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKQPRFADHSETTSQAEHGADSDHRNALQEMLAGLSQTCQLLFEA-PTEQVAVAE 59
Db 1 MKSSHFEYDKTLKQAEALAIADSDHRAKLQEMCADIGLTPEAVMKIFAGRSAAEIKPAE 60
QY 60 QELLAEIQRQALLPAOPGEGRSRRPTIMRGLMI 94
Db 61 RELLEIKRQRQRPQHPYDGKPRKPTMRGQII 95
RESULT 3
F83432
regulator in type III secretion PA1705 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83432
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83432
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <STO>
A:Cross-references: UNIPROT:Q9I326; UNIPARC:UPI00000C5454; GB:AE004597; GB:AE004091; NID
A:Experimental source: strain PA01
A:Genetics:
A:Gene: pcrG; PA1705
Query Match 38.3%; Score 179.5; DB 2; Length 98;
Best Local Similarity 47.6%; Pred. No. 1.2e-11;
Matches 40; Conservative 15; Mismatches 28; Indels 1; Gaps 1;
QY 12 TTSQAEHGADSDHRNALQEMLAGLSQTCQLLFEAPTEQVA-VAEQELLAEIQRQ 70
Db 15 TVQAEALARDSEERGLAEAMWQGLGADAGELLFOAPERELARAAEEELLAEIURMR 74
QY 71 ALLPAOPGEGRSRRPTIMRGLMI 94
Db 75 SSQPTQGEQGTTPRRPTMRGLLI 98
RESULT 4
B70748
probable smc protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70748
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sqaers, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70748
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1289 <COL>
A:Cross-references: UNIPARC:UPI0000165322; GB:274697; GB:AL123456; NID:g3261602; PIDN:C
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: smc
C:Superfamily: chromosome segregation protein SMC1
Query Match 17.3%; Score 81; DB 2; Length 1289;
Best Local Similarity 30.1%; Pred. No. 3.9;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;
QY 5 RFADHSETTSQAEHGADSDHRNALQEMLAGL-ALS---DQTCQLL----- 47
Db 345 RLAVASEELAAHSAVAELSTRAESIQHTWFGLSALAEVDAVTVRIASERAHHLIDIEPVA 404
QY 48 -----FPAPTEQVAVAEQELLAEIQRQALLPAQPG 79
Db 405 VSDTPRKPEELEAEAAQVAVAEQQLLAELDAARLDAARAE 447
RESULT 5
B87146
50S ribosomal protein L10 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87146
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: B87146
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <STO>
A:Cross-references: UNIPROT:Q9CBK7; UNIPARC:UPI0000133B3A; GB:AL450380; NID:g13093566;
A:Gene: rplJ
C:Genetics:
C:Superfamily: Escherichia coli ribosomal protein L10
Query Match 16.1%; Score 75.5; DB 2; Length 177;
Best Local Similarity 32.8%; Pred. No. 1.4;
Matches 22; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 9 HSETTSQAEHGADSDHRNALQEMLAGLSQTCQLLFEAPTEQVAVAEQELLAEIQR 68
Db 113 HPMTVAEVR-IADLESREVLAKLAGAMKGTFAKAIGLFNAPTSOMA----RLTAALOE 167
QY 69 ROALLPA 75
Db 168 KKAFFPA 174
RESULT 6
T16731
hypothetical protein R12C12.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16731
R; Faveillo, T.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid R12C12.
A:Reference number: Z18568
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A;Accession: T16731  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-222 <FAV>  
A;Cross-references: UNIPROT:Q21959; UNIPARC:UPI000017A00C; EMBL:U23510; NID:g746453; PID  
A;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:R12C12.5  
A;Introns: 98/3; 185/3

Query Match 15.8%; Score 74; DB 2; Length 222;  
Best Local Similarity 29.9%; Pred. No. 2.6;  
Matches 29; Conservative 12; Mismatches 28; Indels 28; Gaps 5;

Qy 9 HSETIS-----QAEHGTAADSHRNALQEMLAGLSDDTCQLLFEAPTQVAVAE 59  
Db 116 HNEIVIDVLGKTTETLKKEHAKMDIDKVHDLMDIADGLAMSEELNEAI-SAPIGDVA-DE 173  
Qy 60 QELLAETORRQ-----ALLPAQP-GE 79  
Db 174 DELMOELQELQDNVADLSTTTKLDPVPATLPEAPSGE 210

RESULT 7  
PAQXP  
fructose-bisphosphatase (EC 3.1.3.11) - Xanthobacter flavus  
N;Contains: sedoheptulose-bisphosphatase (EC 3.1.3.37)  
C;Species: Xanthobacter flavus  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: A45867; S13576  
R;Meijer, W.G.; Enequist, H.G.; Terpstra, P.; Dijkhuizen, L.  
J. Gen. Microbiol. 136, 2225-2230, 1990  
A;Title: Nucleotide sequences of the genes encoding fructosebisphosphatase and phosphori  
A;Reference number: A45867; MUID:91178501; PMID:1964170  
A;Accession: A45867  
A;Molecule type: DNA  
A;Residues: 1-364 <ME2>  
A;Cross-references: UNIPROT:P23014; UNIPARC:UPI000012A3E0; EMBL:X17252; NID:g48543; PIDN  
R;Meijer, W.G.; Arnborg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen,  
Mol. Gen. Genet. 225, 320-330, 1991  
A;Title: Identification and organization of carbon dioxide fixation genes in Xanthobacte  
A;Reference number: S13573; MUID:91172133; PMID:1900916  
A;Accession: S13576  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-364 <ME1>  
A;Cross-references: UNIPARC:UPI000012A3E0; EMBL:X17252; NID:g48543; PIDN:CAA35118.1; PID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989  
C;Genetics:  
A;Gene: cfxP  
C;Superfamily: fructose-1,6-bisphosphatase  
C;Keywords: Calvin cycle; phosphoric monoester hydrolase

Query Match 15.7%; Score 73.5; DB 1; Length 364;  
Best Local Similarity 23.5%; Pred. No. 5.3;  
Matches 26; Conservative 16; Mismatches 37; Indels 9; Gaps 4;

Qy 1 MKQPRFADHSFTISQAEHGTAADSHRNALQEMLAGL-----ALSDQTCQLLFEAPTQEV 55  
Db 1 MLEFN-ADHRAVAQA-A-GVAASRITLTVMLDEWAGARRAVADTVCALATCASIAA 58

Qy 56 AVAQELLAEIQRQALLPAQPGGRKS 83  
Db 59 AIAEGLAGDLAR--TLSSGEAGEGQKA 84

RESULT 8  
B70913  
probable penicillin-binding protein - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: B70913  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: B70913  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-678 <COL>  
A;Cross-references: UNIPROT:P71707; UNIPARC:UPI00000D4705; GB:Z80775; GB:AL123456; NID  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: ponA  
C;Superfamily: penicillin-binding protein 1B

Query Match 15.7%; Score 73.5; DB 2; Length 678;  
Best Local Similarity 40.4%; Pred. No. 11;  
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy 48 FEAPTEQVAVAEQELLAEIQRQALL-PAQPGEGKSRRTIMRGLM 93  
Db 172 FDKPVEQLTVAEGALLAALIRRPSTLDPVDPGAGAHARNWVLDGMV 218

RESULT 9  
B83160  
hypothetical protein PA3894 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: B83160  
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: B83160  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-496 <SPO>  
A;Cross-references: UNIPROT:Q9HXB9; UNIPARC:UPI00000C5B62; GB:AE004806; GB:AE004091; NI  
C;Genetics:  
A;Gene: PA3894

Query Match 15.5%; Score 72.5; DB 2; Length 496;  
Best Local Similarity 33.3%; Pred. No. 9.6;  
Matches 27; Conservative 12; Mismatches 29; Indels 13; Gaps 3;

Qy 21 ADSDHRNALQEMLAGLSDDTCQ-----LLFEAPTQVAVAEQ-----LLAEIQRQA 71  
Db 191 AEMDIKAMLQQQORDILALAQRRILGGIGTHFEVSAQAEVPLPETERIEVIDEIIQLTRN 250

Qy 72 LLPA----QPGEGRKSRRTI 88  
Db 251 LLAALAGKPGEGRTIRRPDL 271

RESULT 10  
T26135  
hypothetical protein Y6B3B.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26135; T27328  
R;Dobson, R.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z20158  
A;Accession: T26135  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1829 <WIL>  
A;Cross-references: UNIPROT:O18164; UNIPARC:UPI0000007C881; EMBL:Z82068; PIDN:CAB04901.1

A;Experimental source: clone W04A4  
R;White, S.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z20345  
A;Accession: T27328  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1829 <W12>  
A;Cross-references: UNIPARC:UPI000007C881; EMBL:AL032655; PIDN:CAA21727.1; GSPDB:GN00019  
A;Experimental source: clone Y6B3B  
C;Genetics:  
A;Gene: CBSP:Y6B3B.1  
A;Map position: 1  
A;Introns: 20/2; 53/3; 82/3; 329/3; 332/3; 355/3; 396/3; 462/3; 1799/3

Query Match 15.2%; Score 71.5; DB 2; Length 1829;  
Best Local Similarity 27.2%; Pred. No. 56;  
Matches 31; Conservative 14; Mismatches 36; Indels 33; Gaps 6;

QY 1 MKOPREAD-----HS-----ETISQAEH-----GIADSDHRNALLQEMLAGLALSD 41  
Db 1421 VKDPRMQEVLQRQNSHLEDLRPQIDQAEHLEPNQGVERRDRRGGIATLUSA---SH 1477

QY 42 QTCLLFEAPTEQVAVAEQLAEIQRQALLPAQFGE-----GRKSRP 86  
Db 1478 QDCQTGSEEP--QVSQVWPESPATERQEPSPQSDGDPVGPRAIKKGLSRQP 1529

RESULT 11  
F87329  
hypothetical protein CC0649 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: F87329  
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: F87329  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-477 <STO>  
A;Cross-references: UNIPROT:Q9AAR2; UNIPARC:UPI00000C7105; GB:AE005673; NID:g13421864; E  
C;Genetics:  
A;Gene: CC0649

Query Match 15.1%; Score 71; DB 2; Length 477;  
Best Local Similarity 33.3%; Pred. No. 13;  
Matches 26; Conservative 12; Mismatches 36; Indels 4; Gaps 2;

QY 12 TTSQAEHGADSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQVAVAEQLAEIQRROA 71  
Db 158 TVARADGG-NDGKRRAIMSVQGLDGVESPDVYPLLFGARTRHTAVVEG---ADGRRRTL 213

QY 72 LLPAQEGEGKSRRTIM 89  
Db 214 VAPAVSLEQRRAQRPRM 231

RESULT 12  
C70876  
hypothetical protein Rv1179c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: C70876  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: C70876  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-939 <COL>  
A;Cross-references: UNIPROT:O50435; UNIPARC:UPI00000C152C; GB:AL010186; GB:AL123456; N  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv1179c  
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1179c

Query Match 14.6%; Score 68.5; DB 2; Length 939;  
Best Local Similarity 34.7%; Pred. No. 52;  
Matches 25; Conservative 10; Mismatches 24; Indels 13; Gaps 4;

QY 20 IADSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQVAVAEQLAEIQRQALLPAQFGE 79  
Db 455 LAASDHR---RTPLHALLVTGQT-----FACP-----AAIEDDLIAFCARGALVTAEPD 503

QY 80 GRKSRPTIMRG 91  
Db 504 AHPSLR--VMRG 513

RESULT 13  
T13347  
Cnn protein - fruit fly (Drosophila melanogaster)  
N;Alternate names: centrosomin  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: T13347  
R;Heuer, J.G.; Li, K.; Kaufman, T.C.  
Development 121, 3861-3876, 1995  
A;Title: The Drosophila homeotic target gene centrosomin (cnn) encodes a novel centrosom  
A;Reference number: Z17655; MUID:96102828; PMID:8582295  
A;Accession: T13347  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1148 <HEU>  
A;Cross-references: UNIPROT:P54623; UNIPARC:UPI0000127C2A; EMBL:U35621; NID:g2570233; P  
A;Experimental source: strain Oregon R  
C;Genetics:  
A;Gene: Cnn  
A;Cross-references: FlyBase:FBgn0013765  
A;Map position: 2  
C;Function:  
A;Description: may participate in mitotic spindle assembly and the mechanics of morphog  
C;Keywords: leucine zipper

Query Match 14.6%; Score 68.5; DB 2; Length 1148;  
Best Local Similarity 29.6%; Pred. No. 66;  
Matches 24; Conservative 10; Mismatches 30; Indels 17; Gaps 2;

QY 9 HSETISQAEHGADSDHR-----NALLQEMLAGLALSDQTCQL-----LFEP 51  
Db 720 NSERTIALEEQAQKDERMLNVQCMVELDNRKYKQELRCLDITQOLELRALNEALTAD 779

QY 52 TEQVAVAEQLAEIQRROAL 72  
Db 780 LQAIGSHSEERWVLEQLQLEL 800

RESULT 14  
TVHUM  
transforming protein C-myc - human  
N;Alternate names: p64 myc oncogene  
C;Species: Homo sapiens (man)  
C;Date: 14-Nov-1983 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: A01349; A26245; A26246; A21061; I67315; I53224; I61947; I38052; I57605; I3  
R;Watson, D.K.; Psallidopoulos, M.C.; Samuel, K.P.; Dalla-Favera, R.; Papas, T.S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 3642-3645, 1983  
A;Title: Nucleotide sequence analysis of human c-myc locus, chicken homologue, and myelc  
A;Reference number: A01349; MUID:83221652; PMID:6304729





Qy 4 PRFADHSETISOAEHGIADSDHRNALQEMLAGLALSDQ-----TC 44  
Db 346 PRSSDTEENVKRRTHNVLERQRNELKRSP---FALRDOIPELENNEKAPKVILKKATA 402  
Qy 45 QLLFEAPTEQVAVAEQELLAEIORRQAL 72  
Db 403 YILSVQAEQKLISEEDLR--KRREQ 428

Search completed: June 16, 2006, 19:25:07  
Job time : 11.5528 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 73.8244 Seconds  
(without alignments)  
1177.815 Million cell updates/sec

Title: US-10-813-908A-7  
Perfect score: 459  
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKRRPTIMRGLMI 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	100.0	94	2 Q8GA89	AERSONAS s
2	422	90.0	94	2 Q5CC98	AERSONAS s
3	421	89.8	94	2 Q699R1	AERSONAS h
4	400	85.3	94	2 Q5XL05	AERSONAS h
5	198.5	42.3	95	2 Q93K03	YERSINIA en
6	196.5	41.9	95	2 Q52157	YERSINIA en
7	195.5	41.7	95	1 LCRG_YERPE	
8	179.5	38.3	98	2 Q91326	PSEUDOMONAS
9	179.5	37.4	98	2 Q30526	PSEUDOMONAS
10	175.5	37.4	98	2 Q6TLM3	AERSONAS h
11	168	35.8	99	2 Q6TLM3	AERSONAS h
12	140	29.9	94	2 Q87P58	VIBRIO para
13	137.5	29.3	92	2 Q4G16	PHOTORHABDU
14	137.5	29.3	92	2 Q7N0X0	PHOTORHABDU
15	128	27.3	96	2 Q6QV51	VIBRIO harv
16	126	26.9	96	2 Q66PT5	PASTEURILLA
17	81	17.3	842	2 Q54MH2	DICTYOSTELI
18	81	17.3	1205	1 SMC	MYCOBACTERI
19	81	17.3	1205	2 Q7TXM2	MYCOBACTERI
20	79.5	17.0	670	1 LRC45	HOMO sapien
21	79	16.8	325	2 Q4J2M9	AZOTOBACTER
22	77	16.4	236	2 Q21959	CAENORHABDI
23	77	16.4	323	2 Q5RDB1	PONGO pygma
24	76.5	16.3	1104	2 Q9W6R6	FUGU rubrip
25	76	16.2	323	1 GHCL1	HUMAN
26	75.5	16.1	177	1 RL10	MYCLE
27	74.5	15.9	699	2 Q4UUA6	XANCP
28	74.5	15.9	699	2 Q8P918	XANCP
29	74.5	15.9	829	2 Q40PN4	DESAC
30	74.5	15.9	1175	2 Q3XZV8	ENTFC
31	74	15.8	692	2 Q2UEG2	ASPERGILLUS

32	74	15.8	1168	2	Q873C1	NEUCR
33	73.5	15.7	326	2	Q35Q10	BRADYRHIZOB
34	73.5	15.7	364	1	F16P	XANFL
35	73.5	15.7	678	2	P71707	MYCTU
36	73.5	15.7	680	2	Q7U2Y6	MYCBO
37	73.5	15.7	820	2	Q8VK55	MYCCTU
38	73	15.6	233	2	Q621B2	CAENORHABDI
39	73	15.6	456	2	Q44D99	CHRSU
40	72.5	15.5	496	2	Q9HXB9	PSEAE
41	72.5	15.5	697	2	Q7UHM1	RHOBA
42	72.5	15.5	1162	2	Q3KFB4	PSEPF
43	72	15.4	100	2	Q5KVL9	GEOKA
44	72	15.4	603	2	Q89N77	BRADYRHIZOB
45	72	15.4	681	2	Q356X6	9BRAD

ALIGNMENTS

RESULT 1  
Q8GA89 AERSONAS PRELIMINARY; PRT; 94 AA.  
AC Q8GA89;  
DT 01-MAR-2003, integrated into UniProtKB/TREMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Acrg protein.  
GN Name:acrg;  
OS Aeromonas salmonicida subsp. salmonicida.  
OG Plasmid pASvira.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267; PubMed=12374830;  
RX MEDLINE=2262111; PubMed=12374830;  
RX DOI=10.1128/JB.184.21.5966-5970.2002;  
RA Burr S.E., Stuber K., Wahli T., Frey J.;  
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida";  
RL J. Bacteriol. 184:5966-5970(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267; PLASMID=pASvira;  
RX MEDLINE=22957181; PubMed=14594831;  
RX DOI=10.1128/JB.185.22.6583-6591.2003;  
RA Burr S.E., Stuber K., Frey J.;  
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";  
RL J. Bacteriol. 185:6583-6591(2003).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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EMBL: AJ458292; CAD30220.1; -; Genomic DNA.  
EMBL: AJ516009; CAD56768.1; -; Genomic DNA.  
EMBL: AJ516218; CAB83107.1; -; Genomic DNA.  
DR InterPro: IPR009863; LcrG.  
DR Pfam: PF07216; LcrG; 1.  
KW Plasmid.  
SQ SEQUENCE 94 AA; 10461 MW; F17EFD8A18205EC CRC64;

Query Match 100.0%; Score 469; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 3e-38;  
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
Db 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94

RESULT 2
Q5CC98_AERSO
ID Q5CC98_AERSO PRELIMINARY; PRT; 94 AA.
AC Q5CC98;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Acrg protein.
GN Name=acrg;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150 (2005).
CC -----
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CC -----
DR EMBL; AJ749609; CAG44557.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10482 MW; 1B962F431578F69B CRC64;

Query Match 90.0%; Score 422; DB 2; Length 94;
Best Local Similarity 89.4%; Pred. No. 1.2e-33;
Matches 84; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
Db 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94

RESULT 3
Q699R1_AERHY
ID Q699R1_AERHY PRELIMINARY; PRT; 94 AA.
AC Q699R1;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acrg.
GN Name=acrg;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/ARM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpull G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
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RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919 (2004).
CC -----
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CC -----
DR EMBL; AY528667; AAS91818.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10622 MW; 99BA1C5E7B3815F5 CRC64;

Query Match 89.8%; Score 421; DB 2; Length 94;
Best Local Similarity 90.4%; Pred. No. 1.6e-33;
Matches 85; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
Db 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 4
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ID Q5XL05_AERHY PRELIMINARY; PRT; 94 AA.
AC Q5XL05;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acrg.
GN Name=acrg;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457 (2005).
CC -----
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CC -----
DR EMBL; AV763611; AAV30232.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10624 MW; B7C944CD55ED6C7B CRC64;

Query Match 85.3%; Score 400; DB 2; Length 94;
Best Local Similarity 83.0%; Pred. No. 1.8e-31;
Matches 78; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
Db 1 MKQPRFADHSETISQAEHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94

RESULT 5
Q93KU3_YEREN
ID Q93KU3_YEREN PRELIMINARY; PRT; 95 AA.
AC Q93KU3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
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07-FEB-2006, entry version 12.  
LcrG.  
Name=lcrG;  
Yersinia enterocolitica.  
Plasmid pYve8081, and Plasmid pYval27/90.  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Yersinia.  
NCBI\_TaxID=630;  
[1]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=8081; PLASMID=pYve8081;  
RX MEDLINE=21295118; PubMed=11402007;  
DOI=10.1128/JAI.69.7.4627-4638.2001;  
RA Snellings N.J., Popok M., Lindler L.E.;  
RT "Complete DNA sequence of Yersinia enterocolitica serotype 0:8 low-  
calcium response plasmid reveals a new virulence plasmid-associated  
replicon.";  
RL Infect. Immun. 69:4627-4638(2001).  
[2]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=A127/90; PLASMID=pYval27/90;  
RA Foulter B.G.F., Bernard A., Purnelle B., Cornelis G.R.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AF336309; AAK69214.1; -; Genomic DNA.  
DR EMBL; AY150843; AAN37512.1; -; Genomic DNA.  
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AC O52157;  
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-1998, sequence version 1.  
DT 07-FEB-2006, entry version 19.  
DE LcrG.  
GN Name=lcrG;  
OS Yersinia enterocolitica.  
OG Plasmid pYve227.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=630;  
[1]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=W22703;  
RX MEDLINE=98143428; PubMed=9484897;  
RA Boyd A.P., Sory M.P., Iriarte M., Cornelis G.R.;  
RT "Heparin interferes with translocation of Yop proteins into Hela cells  
and binds to LcrG, a regulatory component of the Yersinia Yop  
apparatus.";  
RL Mol. Microbiol. 27:425-436(1998).  
[2]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=W22703;

RA Iriarte M., Lambermont I., Kerbouch C., Cornelis G.R.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; AF102990; AAD16816.1; -; Genomic DNA.  
DR InterPro; IPR009863; LcrG.  
DR Pfam; PF07216; LcrG; 1.  
KW Plasmid.  
SQ SEQUENCE 95 AA; 10961 MW; 474CB07840EABD6E CRC64;  
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Best Local Similarity 42.1%; Pred. No. 1.8e-11;  
Matches 40; Conservative 21; Mismatches 33; Indels 1; Gaps 1;  
Yy 1 MKQPRFADHSTISQAEHGIAADSHRNALLQEMLAGIALSDQTCLLFEA-PTQVAVAE 59  
Db 1 MKSSHDFEYDKTLQAEALADSDHRAKLQEMCADIGLTPEAVMKIFAGRSABEIKPAE 60  
Yy 60 QELLAETQRQALLPAQPGEGKRSRRPTIMRGLMI 94  
Db 61 RELLEIKRQRERQPHNDGKRPKPTMMRGQII 95  
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LCRG YERPE STANDARD; PRT; 95 AA.  
ID LCRG YERPE STANDARD; PRT; 95 AA.  
AC P69957; P19394; Q663K8;  
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.  
DT 04-JAN-2005, sequence version 1.  
DT 07-MAR-2006, entry version 8.  
DE Low calcium response locus protein G.  
GN Name=lcrG; OrderedLocusNames=YPCD1.32c, Y5046, Y0049, pCD51;  
OS Yersinia pestis.  
OG Plasmid pCD1.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=KIMS / Biovar Mediaevalis;  
RX MEDLINE=90008906; PubMed=2477361;  
RA Price S.B., Leung K.Y., Barve S.S., Straley S.C.;  
RT "Molecular analysis of lcrGVH, the V antigen operon of Yersinia  
pestis.";  
RL J. Bacteriol. 171:5646-5653(1989).  
[2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=KIMS / Biovar Mediaevalis;  
RX MEDLINE=98427122; PubMed=9746557;  
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,  
RA Blattner F.R.;  
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of  
Yersinia pestis KIMS.";  
RL Infect. Immun. 66:4611-4623(1998).  
[3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=KIMS / Biovar Mediaevalis;  
RX MEDLINE=98422474; PubMed=9748454;  
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,  
RA Kobayashi A., Brubaker R.R., Garcia E.;  
RT "Structural organization of virulence-associated plasmids of Yersinia  
pestis.";  
RL J. Bacteriol. 180:5192-5202(1998).  
[4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

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RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin H., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang L., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans."
RL DNA Res. 11:179-197(2004).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-6.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX PubMed=90330579; PubMed=1695896;
RA Barve S.S., Straley S.C.;
RT "lcrR, a low-Ca2(+)-response locus with dual Ca2(+)-dependent
RT functions in Yersinia pestis."
RL J. Bacteriol. 172:4661-4671(1990).
CC -!- FUNCTION: Not known.
CC -----
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DR EMBL; M26405; AAA27640.1; -; Genomic DNA.
DR EMBL; AF074612; AAC69798.1; -; Genomic DNA.
DR EMBL; AF053946; AAC62573.1; -; Genomic DNA.
DR EMBL; AL117189; CAB54309.1; -; Genomic DNA.
DR EMBL; AE017043; NAA58570.1; -; Genomic DNA.
DR EMBL; M35740; AAA98220.1; -; Genomic DNA.
DR PIR; A33601; A33601.
DR GenomeReviews; AE017043 GR; pCDS1.
DR GenomeReviews; AL117189 GR; YPCD1.32c.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Complete proteome; Plasmid.
FT CHAIN 1 95
FT Low calcium response locus protein G.
FT /FTID=PRO_0000084371.
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Query Match 41.7%; Score 195.5; DB 1; Length 95;
Best Local Similarity 43.2%; Pred. No. 2.3e-11;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKQPRFADHSETISQAEHGIAADSHRNALLQEMLAGLSDDTCQLLFEA-PTEQVAVAE 59
Db 1 MKSSHDFEYDKTLQKAEALADSHRAKLLQEMCADIGLTPEAVMKIFAGRSAAEIKPAE 60
QY 60 QELLAIQRRQALLPAQGEGRKSRPTIMRGIMI 94
Db 61 RELLEIKRQRQRPQHPYDGKRPKPTMWRGII 95
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AC P69958; P19394; Q663K8;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 7.
DE Low calcium response locus protein G.
GN Names=LCrG; OrderedLocusNames=pYV0058;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMIID=pIB1;
RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakansson S., Forsberg A., Norlander L., Macellaro A.,
RA Baeckman A., Boelin I., Wolf-Watz H.;
RT "Analysis of the V antigen lcrGVH-yopBD operon of Yersinia
RT pseudotuberculosis: evidence for a regulatory role of LcrH and LcrV."
RL J. Bacteriol. 173:1607-1616(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP3953 / Serotype I; PLASMIID=pYV;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenail-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Not known.
CC -----
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DR EMBL; M57893; AAA27644.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25401.1; -; Genomic DNA.
DR PIR; A37314; A37314.
DR GenomeReviews; BX936399 GR; pYV0058.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Complete proteome; Plasmid.
FT CHAIN 1 95
FT Low calcium response locus protein G.
FT /FTID=PRO_0000084372.
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Best Local Similarity 43.2%; Pred. No. 2.3e-11;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKQPRFADHSETISQAEHGIAADSHRNALLQEMLAGLSDDTCQLLFEA-PTEQVAVAE 59
Db 1 MKSSHDFEYDKTLQKAEALADSHRAKLLQEMCADIGLTPEAVMKIFAGRSAAEIKPAE 60
QY 60 QELLAIQRRQALLPAQGEGRKSRPTIMRGIMI 94
Db 61 RELLEIKRQRQRPQHPYDGKRPKPTMWRGII 95
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AC Q9I326;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Regulator in type III secretion.
GN Name=prgG; OrderedLocusNames=PA1705;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
```

RT opportunistic pathogen.";

RL Nature 406:959-964(2000).

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CC -----

DR EMBL; AE004597; AAC05094.1; -; Genomic\_DNA.

DR PIN; F83432; F83432.

DR BioCyc; PAER287:PAI705-MONOMER; -.

DR InterPro; IPR009863; LcRG.

DR Pfam; PF07216; LcRG; 1.

KW Complete proteome.

SQ SEQUENCE 98 AA; 10995 MW; 6B972DAE22C710FC CRC64;

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Best Local Similarity 47.6%; Pred. No. 8.8e-10;  
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OY 71 ALLPAPGPEGKSRPTIMEGLMI 94  
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RESULT 10

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ID OJ0526\_PSEAE PRELIMINARY; PRT; 98 AA.

AC O30526;

DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.

DT 01-JAN-1998, sequence version 1.

DT 07-FEB-2006, entry version 1.

DE PcrG.

GN Name=pcrG;

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxId=287;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=388;

RX MEDLINE=98037517; PubMed=9371466;

RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;

RT "Identification of type III secreted products of the Pseudomonas

RT aeruginosa exoenzyme S regulon.;"

RT J. Bacteriol. 179:7165-7168(1997).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=PAK;

RC MEDLINE=22830436; PubMed=12949185; DOI=10.1099/mic.0.26322-0;

RX Broms J.E., Forslund A.L., Forsberg A., Francis M.S.;

RT "Dissection of homologous translocan operons reveals a distinct role

RT for YopD in type III secretion by *Yersinia pseudotuberculosis*.;"

RL Microbiology 149:2615-2626(2003).

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DR EMBL; AF010149; AAC45934.1; -; Genomic DNA.

DR ENBL; AY232997; AAO91770.1; -; Genomic\_DNA.

DR InterPro; IPR009863; LcRG.

DR Pfam; PF07216; LcRG; 1.

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Best Local Similarity 46.4%; Pred. No. 2.2e-09;  
Matches 39; Conservative 15; Mismatches 29; Indels 1; Gaps

OY 12 TISQAEGHIDSHRNALLOEMAGIALSDQTCLLFEPAPTEQVA-VAEQELLAETORRQ 70  
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Db 1 MKQP---FTETIENSELAIRNAEDRTDVFNELLEGLGVGPVAGNILLDGLNASPQLMKQ 56  
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3	74.5	15.9	1179	2	US-09-107-532A-6126	Sequence 6126, App		
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7	72.5	15.5	548	2	US-09-252-991A-20379	Sequence 20379, A		
8	71.5	15.2	402	2	US-09-252-991A-25289	Sequence 25289, A		
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11	69	14.7	607	2	US-09-252-991A-26137	Sequence 26137, A		
12	68.5	14.6	675	2	US-09-252-991A-29161	Sequence 29161, A		
13	68.5	14.6	859	2	US-09-902-540-14220	Sequence 14220, A		
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17	68	14.5	455	2	US-09-949-016-11307	Sequence 11307, A		
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21	66.5	14.2	330	2	US-09-252-991A-18311	Sequence 18311, A		
22	66.5	14.2	355	2	US-09-902-540-15046	Sequence 15046, A		
23	66	14.1	845	2	US-09-252-991A-17856	Sequence 17856, A		
24	65.5	14.0	183	2	US-09-248-796A-18172	Sequence 18172, A		
25	65.5	14.0	214	2	US-09-248-796A-18171	Sequence 18171, A		
26	65.5	14.0	258	2	US-09-252-991A-25067	Sequence 25067, A		

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; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 1289
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-259

Query Match      17.3%; Score 81; DB 2; Length 1289;
Best Local Similarity 30.1%; Pred. No. 0.27; Indels 28; Gaps 3;
Matches 31; Conservative 12; Mismatches 32;

QY 5 RFADHSETTSQAEHGADSDHRNALQEMLAGL-ALS---DQTCQLL-----47
Db 345 RLAVASEELAAHESAVAEELSTRAESIOHTWFGLSALAEVDATVRIASERAHLDIEPVA 404
QY 48 -----FPATEQVAVAEQELLAEIQRQALLPQPG 79
Db 405 VSDTPRKPPELEAEQAQVAVAEQELLAEIDARARLDAARAE 447

RESULT 3
US-09-107-532A-6126
; Sequence 6126, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
```

```
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1179
; SEQUENCE DESCRIPTION: SEQ ID NO: 6126:
US-09-107-532A-6126

Query Match      15.9%; Score 74.5; DB 2; Length 1179;
Best Local Similarity 39.2%; Pred. No. 1.7;
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

QY 19 GIADSDHRNALQEMLAGLSDDTCQLLFEAPTEQVAVAEQELLAEIQR 69
Db 12 GNGKKDHRQVLIDEASAWLD-QDASNQVFLVPNYSKFQEQEILAE 61

RESULT 4
US-09-712-363-158
; Sequence 158, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-158

Query Match      15.7%; Score 73.5; DB 2; Length 678;
Best Local Similarity 40.4%; Pred. No. 1.1;
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 48 FPATEQVAVAEQELLAEIQRQALL-PAQPGEGRKSRRPTIMRGLM 93
Db 172 FDKPVEQLTVAECALLAIRRPSTLDPADVDEGAHARWNWVLDGMV 218
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RESULT 7
US-09-252-991A-20379
; Sequence 20379, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20379
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20379

Query Match 15.5%; Score 72.5; DB 2; Length 548;
Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 29; Indels 13; Gaps 3;

Qy 21 ADSHRNALLQELMAGLALSDQTCQ----LLFEAPTEQVAVAEQE-----LLAEIQRRQA 71
Db 243 AEMDIAKAMLQQRDILALAQRLRGIGTHFEVSAQEVPLPETERRIEVIDEIIQLTRN 302
Qy 72 LLPA----QPGEGRKSRPTI 88
Db 303 LLAAAGKGGEGRTIRPSSL 323

RESULT 8
US-09-252-991A-25289
; Sequence 25289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25289
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25289

Query Match 15.2%; Score 71.5; DB 2; Length 402;
Best Local Similarity 33.7%; Pred. No. 0.95;
Matches 29; Conservative 8; Mismatches 34; Indels 15; Gaps 6;

Qy 9 HSETISQAEHGI-----ADSDHRNALLQELMAGLALSDQTCQLLFEAPTE---QVAVAEQ 61
Db 40 HREALDAAEHQVLIHQQAD-QHHGQAGEYLVGV----QLVAVLENNVPABPALAAAEHQ 94
Qy 62 LLAEIQRRQALLPA--QPGEGRKSR 85
Db 95 FRGD-ORAPGEGPADIQGENRRQR 119

RESULT 9
US-09-252-991A-24830

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; Sequence 24830, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24830
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24830

Query Match 15.0%; Score 70.5; DB 2; Length 453;
Best Local Similarity 30.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 32; Indels 21; Gaps 3;

QY 5 RFAD--HSETISOAEHGIA-----DSDHRNALLQEMLAGLALSDOTCQLLFEAPTEQV 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 211 RVADVVAAEQVEAAEHRIAGRGQQPEQGRGAILVEGVADF-----LPVEIL 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 56 AVAQELLAEIQRQALLPAQPGEGRKSRR 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 259 HQEQQRHQDQHEERQCGQPAQAPAPVRAARR 288
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 10
US-09-252-991A-25395
; Sequence 25395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25395
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25395

Query Match 14.7%; Score 69; DB 2; Length 452;
Best Local Similarity 29.0%; Pred. No. 2.4;
Matches 29; Conservative 10; Mismatches 31; Indels 30; Gaps 4;

QY 1 MKQPRFADHSETISOAEHGIA-----SDH--RNALLQEMLAGLALSDOTCQLL---- 47
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 98 LRDSRVAQHGETQAEAEETGTGRFQAGYLVAHLLRQARRQRRRAALAKDFQKACHVAGA 157
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 48 -----FEAPTEQVAEQELLAEIQRQALLP 74
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 158 ADHPRPAGRIGRRFEGPTRLEANAD-----AVLERRHGLPP 193
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 11
US-09-252-991A-26137
; Sequence 26137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```

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; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26137
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26137

Query Match 14.7%; Score 69; DB 2; Length 607;
Best Local Similarity 23.5%; Pred. No. 3.5;
Matches 23; Conservative 18; Mismatches 39; Indels 18; Gaps 3;

QY 7 ADHSETISOAEHGIAADSDHRNALLQEMLAGLALSDOTCQLLFEAPTEQVAEQL----- 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 355 AEYLRLLVDQFEQGLGVAERNRHQAQARMGLQGQFQRRGMLPG---QLQVADQHLHRRFG 411
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 63 -----LAEIQRQALLPAQPGEGRKSRRPTIMRGLMI 94
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 412 VQPHRLQGVARAQQMPAGMAEG-----PDAVQGRV 444
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 12
US-09-252-991A-29161
; Sequence 29161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29161
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29161

Query Match 14.6%; Score 68.5; DB 2; Length 675;
Best Local Similarity 29.5%; Pred. No. 4.7;
Matches 26; Conservative 12; Mismatches 29; Indels 21; Gaps 4;

QY 2 KOPR--FADHSETISOAEHGIAADSDHRNALLQEMLAGLALSDOTCQLLFEAPTEQVAE 59
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 415 RHPRHRHFAPHASAAGADQGD-----TVVHQRFAGLAVADQ-----QLAQVR 457
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 60 QELLAEIQR--RQALLPAQPGEGRKSRR 85
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 458 RRIAAEGPRGTLEQCLAGQCGEGGLRR 485
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13
US-09-902-540-14220
; Sequence 14220, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```

APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 14220  
LENGTH: 859  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-14220

Query Match 14.6%; Score 68.5; DB 2; Length 859;  
Best Local Similarity 31.0%; Pred. No. 6.5;  
Matches 27; Conservative 13; Mismatches 34; Indels 13; Gaps 5;

QY 9 HSETISQAEHGIADSDHNRNALLQEMLAGLALSDQTCOLLFEAPTEQVA--VAEQELLAE 65  
DB 2 HSTLFGPRIGAAKAVGRRAL----RAGLPLSLMCLVLSLAVPSSAAQAQAEAEAPAK 57

QY 66 IQRQALL----PAQPG--EGRKSRP 86  
DB 58 VKRRKRVKPAAPARPAKTAKP 84

RESULT 14  
US-07-960-981-5  
Sequence 5, Application US/07960981  
Patent No. 5322801  
GENERAL INFORMATION:  
APPLICANT: Kingston, Robert E.  
APPLICANT: Bunker, Christopher  
TITLE OF INVENTION: Protein Partner Screening Assays and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
STREET: 1225 Connecticut Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/960,981  
FILING DATE: 19921014  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michelle A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0609.3630004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 833-7533  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-07-960-981-5

Query Match 14.5%; Score 68; DB 1; Length 186;  
Best Local Similarity 25.0%; Pred. No. 0.96;  
Matches 22; Conservative 13; Mismatches 29; Indels 24; Gaps 3;

QY 4 PRFADHSETISQAEHGIADSDHNRNALLQEMLAGLALSDQ-----TC 44

DB 92 PRSDTEENVKRRTHNVLERQRRNELKRSF---FALRDQIPELENNEKAPKVILKKATA 148

QY 45 QLLFEAPTEQVAQAEQELLAEIQRRQAL 72

DB 149 YILSVQAEQKLISEEDLLR--KRREQ 174

RESULT 15  
PCT-US93-09634-5  
Sequence 5, Application PC/TUS9309634  
GENERAL INFORMATION:  
APPLICANT: Kingston, Robert E.  
APPLICANT: Bunker, Christopher Alden  
TITLE OF INVENTION: Protein Partner Screening Assays and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
STREET: 1100 New York Avenue, N.W.; Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09634  
FILING DATE: (herewith)  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0609.274PC03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 186 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: protein  
PCT-US93-09634-5

Query Match 14.5%; Score 68; DB 5; Length 186;  
Best Local Similarity 25.0%; Pred. No. 0.96;  
Matches 22; Conservative 13; Mismatches 29; Indels 24; Gaps 3;

QY 4 PRFADHSETISQAEHGIADSDHNRNALLQEMLAGLALSDQ-----TC 44

DB 92 PRSDTEENVKRRTHNVLERQRRNELKRSF---FALRDQIPELENNEKAPKVILKKATA 148

QY 45 QLLFEAPTEQVAQAEQELLAEIQRRQAL 72

DB 149 YILSVQAEQKLISEEDLLR--KRREQ 174

Search completed: June 16, 2006, 19:28:57  
Job time : 18.348 secs

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Result No.	Score	Match	Length	DB	ID	Description	7, Appli
1	469	100.0	94	5	US-10-813-908-7	Sequence 7, Appli	
2	88.5	18.9	232	4	US-10-425-114-37773	Sequence 37773, A	
3	81	17.3	1889	3	US-09-712-363-259	Sequence 259, App	
4	81	17.3	1889	4	US-10-282-122A-64805	Sequence 64805, A	
5	79.5	17.0	211	3	US-09-925-297-777	Sequence 777, App	
6	76.5	16.3	1104	5	US-10-732-923-1294	Sequence 1294, Ap	
7	76	16.2	323	4	US-10-116-255-23	Sequence 23, Appl	
8	75.5	16.1	177	4	US-10-282-122A-63970	Sequence 63970, A	
9	74.5	15.9	204	4	US-10-425-114-41502	Sequence 41502, A	
10	74.5	15.9	175	4	US-10-282-122A-57712	Sequence 57712, A	
11	73.5	15.7	364	4	US-10-389-566-2283	Sequence 2283, Ap	
12	73.5	15.7	364	5	US-10-732-923-17917	Sequence 17917, A	
13	73.5	15.7	364	6	US-11-188-298-3185	Sequence 3185, Ap	
14	73.5	15.7	384	4	US-10-282-122A-64971	Sequence 64971, A	
15	73.5	15.7	678	3	US-09-712-363-158	Sequence 158, App	
16	73.5	15.7	678	4	US-10-282-122A-64334	Sequence 64334, A	
17	73.5	15.7	822	4	US-10-282-122A-62677	Sequence 62677, A	
18	72.5	15.5	102	4	US-10-425-115-228565	Sequence 228565, A	
19	72.5	15.5	1162	4	US-10-369-493-13727	Sequence 13727, A	
20	72	15.4	754	4	US-10-437-963-103758	Sequence 103758, A	
21	72	15.4	897	4	US-10-425-115-236512	Sequence 236512, A	
22	72	15.4	1220	5	US-10-732-923-12924	Sequence 12924, A	
23	71	15.1	149	4	US-10-424-599-176461	Sequence 176461, A	
24	71	15.1	344	4	US-10-767-701-41882	Sequence 41882, A	
25	71	15.1	369	4	US-10-425-115-340472	Sequence 340472, A	
26	70.5	15.0	91	4	US-10-424-599-158966	Sequence 158966, A	
27	70.5	15.0	943	6	US-11-097-143-13047	Sequence 13047, A	



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; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 777
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-777
```

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Query Match 17.0%; Score 79.5; DB 3; Length 211;
Best Local Similarity 31.0%; Pred. No. 0.75;
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;

QY 2 KQRFADHSETISQAEHGIADSDHRNAL-----LQEML-----AGLAL 39
Db 27 KSKQFLDMETIDQREEMAKSSASAAVVGKLOEALNERHSIINALKAKIQMTEAALAL 86

QY 40 SDQTCOLLFEAPTOVAEOLLAETORQALLPAQPGEGKRSRRPTIMRGL 92
Db 87 SEKAQADL-----GELLATAEQEQLSLSORAKELKLEQEEAAE-RESKLLRDL 134
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RESULT 6
US-10-732-923-1294
; Sequence 1294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1294
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-732-923-1294
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Query Match 16.3%; Score 76.5; DB 5; Length 1104;
Best Local Similarity 29.4%; Pred. No. 14;
Matches 30; Conservative 11; Mismatches 32; Indels 29; Gaps 5;

QY 4 PRF-----ADHSETISQAEHGIADSDHRNALQEMLAGLALSDQTCOLLFEAPTEQVA 56
Db 228 PRFHGIRFPSTVHTQTLRRYQGI-----LSGLML-DLMKNLLLNPTERY- 272

QY 57 VAEOL-----LAEITORQALLPAQPGEGKRSRRPTIMRG 91
Db 273 LTEQSLNHPAQPLQRVERERPAPPSPNPPRSSKRTKTHHG 314
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RESULT 7
US-10-116-255-23
; Sequence 23, Application US/10116255
; Publication No. US20030036646A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and
```

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; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT009P1
; CURRENT APPLICATION NUMBER: US/10/116,255
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/685,897
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09534
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,701
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/142,821
; PRIOR APPLICATION NUMBER: 60/149,448
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/164,751
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-255-23

Query Match 16.2%; Score 76; DB 4; Length 323;
Best Local Similarity 30.0%; Pred. No. 3.3;
Matches 24; Conservative 14; Mismatches 30; Indels 12; Gaps 3;

QY 18 HGTADSDHRNALQEMLAGLALSDQTCOLLFEAPTEQVAV-----AEQELLAEIQR 68
Db 92 HQSKQGGKUTLUKLEMLAGGAG--TCQVITTPMEMLKITQLQDAGRIAAQRKILAAQGG 149

QY 69 RQALLPAQPG-EGKRSRRPT 87
Db 150 LSAQGGAGPSVEAPAPRPT 169

RESULT 8
US-10-282-122A-63970
; Sequence 63970, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63970
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63970

Query Match      16.1%; Score 75.5; DB 4; Length 177;
Best Local Similarity 32.8%; Pred. No. 1.8;
Matches 22; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

QY 9 HSETISQAEHGADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQELLAEIOR 68
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 113 HPMTVAEVER-IADLESREVLLAKLAGAMKGTAKAIGLEFNAPTISQWA-----RLTAALQE 167
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|

QY 69 RQALLPA 75
    :|| |||
Db 168 KKAFEPA 174

RESULT 9
US-10-425-114-41502
; Sequence 41502, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41502
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3078-002-H8_FLI.pep
US-10-425-114-41502

Query Match      15.9%; Score 74.5; DB 4; Length 204;
Best Local Similarity 30.8%; Pred. No. 2.8;
Matches 16; Conservative 12; Mismatches 15; Indels 9; Gaps 1;

QY 37 LALSDQTCOLLFEAPTEQVAVAEQELLAEIORQALLPQPGEGKSRPPTI 88
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 14 MAIAGOCSSCYTSPTLQL-----QLQRHSHLPLQQAARARRPRL 56

RESULT 10
US-10-282-122A-57712
; Sequence 57712, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
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; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57712
; LENGTH: 1175
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57712

Query Match      15.9%; Score 74.5; DB 4; Length 1175;
Best Local Similarity 39.2%; Pred. No. 26;
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

QY 19 GIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQELLAEIORR 69
    |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 8 GNGKDHROVLIDEASAWLD-QDASNQVFFLVNYSKFEQOEILAEIMRRR 57

RESULT 11
US-10-389-566-2283
; Sequence 2283, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2283
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Xanthobacter flavus
US-10-389-566-2283

Query Match      15.7%; Score 73.5; DB 4; Length 364;
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; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-158

Query Match      15.7%   Score 73.5; DB 3; Length 678;
Best Local Similarity 40.4%   Pred. No. 17;
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy      48 FEAPTEQVAVAEQELLAEIQRRQALL-PAQPGEGKSRREPTIMRGILM 93
Db      172 FDKPEVQLTVAEGLAALIRREPSTLDPAVDPEGAHARNWNWLDGMV 218
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: June 16, 2006, 20:24:56
Job time : 54.5789 secs

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; SEQ ID NO 784
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-784

Query Match      14.1%; Score 66; DB 6; Length 2671;
Best Local Similarity 27.5%; Pred. No. 76;
Matches 22; Conservative 16; Mismatches 40; Indels 2; Gaps 1;

Qy 10 SETISOAEHGIADSDHNRNALLQEMLAGLSDQTCQLLFEAPTEQVAVAEQELLAEIQ 67
Db 1746 NEKIFQESIGLAHLLDGGNTEIQSFHNLMSDKSERFFKVLHDKRMKRAQQETKTVA 1805

Qy 68 RQALLPAQPGEGKRRRPT 87
Db 1806 VNMNDLGSQPHEDRPVDP 1825

RESULT 7
US-10-449-902-52171
; Sequence 52171, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52171
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52171

Query Match      14.0%; Score 65.5; DB 6; Length 618;
Best Local Similarity 27.8%; Pred. No. 16;
Matches 25; Conservative 14; Mismatches 36; Indels 15; Gaps 5;

Qy 10 SETISOAEHGIADSDHNRNALLQEMLAGLSDQTCQLLFEAPTEQVAVAEQEL----- 62
Db 253 SRNVSPHLHGGDGNSEH-----QETVGGDVADNPFIHTL-ETPPEDTPNQSEIHRGSIK 306

Qy 63 LAETQRQALLPAQPGEGR-KSRPTTMRG 91
Db 307 LA-VDKSNALSPSQGKHGKGNKQPSKRG 335

RESULT 8
US-10-449-902-35865
; Sequence 35865, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 5458
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; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35865
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35865

Query Match      13.8%; Score 64.5; DB 6; Length 234;
Best Local Similarity 27.5%; Pred. No. 6.5;
Matches 19; Conservative 16; Mismatches 29; Indels 5; Gaps 2;

Qy 9 HSTISOAEHGIADSDHNRNALLQ-----EMLAGLSDQTCQLLFEAPTEQVAVAEQELLA 64
Db 5 HSAEILDG-HNVADFLDPDILQRCLEEREGLRLEEAQAQAFQIDGHTELTEEQREILG 63

Qy 65 EIQRRQALL 73
Db 64 QIRKKALL 72

RESULT 9
US-10-449-902-35269
; Sequence 35269, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35269
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35269

Query Match      13.5%; Score 63.5; DB 6; Length 394;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 31; Conservative 7; Mismatches 44; Indels 11; Gaps 4;

Qy 3 QPRFADHSETISOAEHGIADSDH--RNALLQEMLAGLSDQTCQLLFEAPTEQ-----VA 56
Db 185 QPRPHDQLSYNGNETKILSLERPLRFADFAARLAGLAGSPGDFCVKYQLPGEDLALVS 244

Qy 57 VAEQE-----LLAFIQRQALLPAQPGEGKRRR 85
Db 245 VTNDEDLHLVLEVDRLHLRPA-PGSGGSSR 276

RESULT 10
US-11-293-697-4145
; Sequence 4145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
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Db	105	SRTIPACNAVVDSTNSRDLIERLSAFQGSNDNSLCRL-----PATPQALLLEALGSNGA	160
Qy	60	--QELLAEIQRROALLPAQPGEGRKSRPTIMR	90
Db	161	TGSEAVAAAEKHAALLTARAGARDPSAVPSICR	193

RESULT 15  
US-10-449-902-40851  
; Sequence 40851, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40851  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-40851

Query Match	13.4%	Score 63;	DB 6;	Length 431;
Best Local Similarity	27.5%	Pred. No. 19;		
Matches	19;	Conservative 15;	Mismatches 27;	Indels 8; Gaps 2;
Qy	18	HGIADSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQVAV-AEQELLAEIQRROALLPAQ	76	
Db	271	HPSSDSYDRDSILSRVHPGISMVD-----EAVDRVGYRRELDLRDEERRDLLERE	323	
Qy	77	PGEGRKSR	85	
Db	324	KERDRER	332	

Search completed: June 16, 2006, 20:25:53  
Job time : 4.05041 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 239.199 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-8  
Perfect score: 1816  
Sequence: 1 MSTIPDYNTPGAFVGLDV.....ALNRPIQKYSIMRDLGAI 361

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	5	ABB80776
2	625	34.4	307	6	ABM69448
3	560	30.8	349	9	ADY73654
4	557	30.7	326	9	ADY73655
5	557	30.7	326	9	ADZ97834
6	557	30.7	326	9	AEb09748
7	557	30.7	326	10	AEF93450
8	557	30.7	329	2	AAR79961
9	557	30.7	329	2	AAW01041
10	557	30.7	329	2	AAW01040
11	557	30.7	478	9	AEb09750
12	557	30.7	501	2	AAW01044
13	554	30.5	329	2	AAR79962
14	554	30.5	480	2	AAW01045
15	474	26.1	297	7	ABO81312
16	253	13.9	142	2	AAZ29686
17	253	13.9	142	5	AAU93812
18	253	13.9	142	7	ADE10800
19	253	13.9	142	7	ADM33705
20	253	13.9	142	8	ADG63900
21	253	13.9	142	8	ADP73435
22	253	13.9	142	8	ADR12727
23	129	7.1	459	8	ADO15316

ALIGNMENTS

RESULT 1

ABB80776	24	129	7.1	2013	4	ABB62322	Abb62322	Drosophil
ID	ABB80776	standard; protein; 361 AA.					Aab05956	Protein d
AC	ABB80776;						Adf06555	Bacterial
XX							Adu25430	L. acidop
DT	23-SEP-2002	(first entry)					Abu40893	Protein e
XX							Aar07503	Merzoite
DE	A. salmonicida	type III secretion protein acrV sequence.					Aaw24575	Merzoite
XX	Type III	secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG; acrV; acrH; antibiotic; vaccine; fish.					Abu24813	Protein e
KW							Adj67914	T. mariti
XX							Adj68126	T. mariti
OS	Aeromonas salmonicida.						Adk01204	DNA polym
XX							Adj79423	T. mariti
PN	WO200240514-A2.						Adm77651	DNA polym
XX	23-MAY-2002.						Adm66318	T. mariti
XX							Ado04371	T. mariti
PF	15-NOV-2001; 2001WO-CA001589.						Adp82448	Thermotog
XX							Adsi15655	T. mariti
PR	15-NOV-2000; 2000US-0248864P.						Ady55146	T. mariti
XX							Adz76722	T. mariti
XX							Aea24730	Thermotog
XX	(FREY/) FREY J.							
PA	(STUB/) STUBER K.							
PA	(THOR/) THORNTON J C.							
PA	(KUZU/) KUZUK M A.							
PA	(BUR/) BURIAN J.							
PI	Frey J, Stuber K, Thornton JC, Kuzyk WA, Burian J;							
XX	WPI; 2002-537338/57.							
DR	N-PSDB; ABN86172.							
XX								
PT	Novel protein from Aeromonas salmonicida and nucleic acid encoding the							
PT	protein, useful for reducing susceptibility of fish to infection by a							
PT	virulent strain of Aeromonas salmonicida.							
XX	Claim 13; Page 28-29; 39pp; English.							
PS								
XX	The invention relates to A. salmonicida type III secretion genes and							
CC	encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.							
CC	A. salmonicida type III secretion apparatus is useful for producing							
CC	selected products, especially Aext. AcrV in vaccine, epitope or epitopic							
CC	region of AcrV or any other protein of A. salmonicida type III secretion							
CC	apparatus is useful for reducing the susceptibility of fish to infection							

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are  
CC useful for manufacturing a diagnostic agent. Detecting the presence of  
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type  
CC III secretion apparatus is useful for the production or quality control  
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present  
CC sequence represents the *A. salmonicida* type III secretion protein acrv  
XX  
XX

SQ Sequence 361 AA;

Query Match 100.0%; Score 1816; DB 5; Length 361;

Best Local Similarity 100.0%; Pred. No. 1.1e-135;

Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTIPDYNTPGAFVGVLDVQALNTPLGNKNPKLTVELLKGKTIISADSTALSKEQL 60

DB 1 MSTIPDYNTPGAFVGVLDVQALNTPLGNKNPKLTVELLKGKTIISADSTALSKEQL 60

QY 61 EKLLAAYLTDPAISINGWANGQFKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFMLS 120

DB 61 EKLLAAYLTDPAISINGWANGQFKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFMLS 120

QY 121 LSAWTERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

DB 121 LSAWTERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NQTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240

DB 181 NQTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240

QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300

DB 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300

QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360

DB 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360

QY 361 I 361

DB 361 I 361

#### RESULT 2

ABM69448

ID ABM69448 standard; protein; 307 AA.

XX

AC ABM69448;

XX

DT 20-NOV-2003 (first entry)

XX

DE Photorhabdus luminescens protein sequence #2545.

XX

KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

KW whooping cough.

XX

OS Photorhabdus luminescens.

XX

PN WO200294867-A2.

XX

PD 28-NOV-2002.

XX

PF 07-FEB-2002; 2002WO-IB003040.

XX

PR 07-FEB-2001; 2001FR-00001659.

XX

XX (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

XX

DR WPI; 2003-148459/14.

XX

PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX

PS Claim 2; SEQ ID NO 2545; 1205pp; French.

XX

CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of *P. luminescens*  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than *P. luminescens* and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by *P.*  
CC *luminescens*. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically to treat microbial infection by bacteria or fungi that  
CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which *P.*  
CC *luminescens* is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated *P. luminescens* proteins  
XX

SQ Sequence 307 AA;

Query Match 34.4%; Score 625; DB 6; Length 307;

Best Local Similarity 41.8%; Pred. No. 3.7e-41;

Matches 151; Conservative 47; Mismatches 101; Indels 62; Gaps 6;

QY 4 IPDYNTPGAFVGVLDVQALNTPLGNKNPKLTVELLKGK-ITISADSTAL-SKEQLE 61

DB 5 IRPYQNDPOLFLADLEKVSQAQGGSGSELDRLNLPDKGKIKITSDSVVTENKELLK 64

QY 62 KLLAAYLTDPAISINGWANGQFKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFMLS 121

DB 65 KLIAYFLPADAVVEGGHLDQIKNG-----INNESFLNSSTLTKT-----WTKDFLAAVH 115

QY 122 SALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASN 181

DB 116 FNLTPDRLDDDDVIDIFVSVWSGHDKKRLRLRDELATLTAELKIYSVIOSEINAKLAANGE 175

QY 182 QTFKTN-FNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240

DB 176 LKIDNNSFNLDDHKYGFSDQPTFEKSAEYKLLRKISSGSE----- 216

QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300

DB 217 -----LSITFLLESSNKQSGAMGLSENSYEDKE 245

QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360

DB 246 NNRLANFSTVSDRVSPLNNTVQKTRLNNEASSRYNAIAEALNRFIOKYDSIIRNILGA 305

QY 361 I 361

DB 306 I 306

#### RESULT 3

ADY73654

ID ADY73654 standard; protein; 349 AA.

XX

AC ADY73654;

XX

DT 02-JUN-2005 (first entry)

XX

DE Yersinia pestis tPA/V antigen construct.

XX V antigen; immune stimulation; tissue plasminogen activator; tPA;  
KW Yersinia pestis infection; antibacterial; vaccine; gene therapy.  
XX Synthetic.  
OS Yersinia pestis.  
XX WO2005023205-A2.  
PN 17-MAR-2005.  
XX 08-MAR-2004; 2004WO-US007190.  
XX 07-MAR-2003; 2003US-0452657P.  
XX (UYMA-) UNIV MASSACHUSETTS.  
XX Lu S, Goguen JD, Wang S;  
XX WPI; 2005-223254/23.  
DR N-PSDB; ADY73643.  
XX New polynucleotide comprising a nucleic acid encoding a signal sequence  
PT and a second nucleic acid encoding a Yersinia pestis antigen polypeptide,  
PT useful in preparing a composition for treating Yersinia pestis infection.  
XX Disclosure; SEQ ID NO 12; 79pp; English.  
XX This invention describes a novel fusion construct comprising a tissue  
CC plasminogen activator (tPA) fused to a nucleic acid that encodes a  
CC Yersinia pestis antigen polypeptide, selected from V, Fl, Pla, YopB,  
CC YopD, YopO or YscF antigen polypeptide. The invention also describes 1)  
CC an expression vector containing the construct; 2) a cell comprising the  
CC construct; 3) a process for producing a Yersinia pestis antigen  
CC polypeptide; 4) a composition comprising the construct, preferably a  
CC multimeric V antigen; 5) a kit comprising the construct; 6) a modified  
CC Yersinia pestis antigen polypeptide sequence linked to a signal sequence  
CC sufficient for secretion from a cell; 7) a method of inducing a  
CC protective immune response in a mammal and 8) an isolated immunoglobulin  
CC that specifically binds to a modified Yersinia pestis antigen polypeptide  
CC or its fragment. The signal sequence is sufficient for secretion, however  
CC when expressed in a cell, the polynucleotide produces a Yersinia pestis  
CC antigen polypeptide that is free of the signal sequence. The isolated  
CC polynucleotide is useful in preparing a composition for treating Yersinia  
CC pestis infection. This sequence represents the tPA/V antigen construct.  
XX Sequence 349 AA;  
Query Match 30.8%; Score 560; DB 9; Length 349;  
Best Local Similarity 37.5%; Pred. No. 6.5e-36;  
Matches 139; Conservative 61; Mismatches 107; Indels 64; Gaps 9;  
QY 2 STIPDYNTPGAFVGLDVOALNTLPGNKPKLTVELLKGK-ITIS-----ADSTTA 54  
DB 23 SMIRAYQNFQHFIEDLEKVRVEQLTGHSVLEELVQLVKDKNIDISIKYDPRKSEVF 82  
QY 55 LSK-----EQLEKLLAAYLTDPASINGWAMQFGQGDAAIAAIGVIERGAKQTPPV 108  
DB 83 ANRVITDDIELKKILAYFLPEDAILKGHYDNLQNG----IKRVKEFLE-----SSPN 133  
QY 109 THWTIPFLLLSALTNWERTDDDLITFTGVMFQDNQRKGLRDELAEWTAELKIYGV 168  
DB 134 TOWELRAFMAVMHFSLTADRIDDDILKVIYDVMNHHGDARSKLRELAELTAEIKIYSVI 193  
QY 169 QSEINOVLSAASN-QTFKTFNFMIDYKLYGVESLAKFMEGGEFKLLSKMFSDEQVTKAQ 227  
DB 194 QAEINKHLSSGGINIHDKNINLMKWLTYGTDEEIFKAAEYKILEM---POTT----- 246  
QY 228 DFTNAKNELENVTSTSLNPKIQABAKTDYERKKAIFEEIVETOITILKTFLESDLKSGA 287  
DB 247 -----IQVDGS-----EKKIVSIKDFLGSNKRETA 272  
QY 288 MSGIEABYKDKONNKLGNFSTSVSDRSRPRNDLVSEKTLARLNDVSSRYNAEALNRFI 347

DB 273 LGNLKNSYSYNKONNELSHFATTCSDKSRPLNDLVSKQTTQLSDITSRFSNAEALNRFI 332  
QY 348 QKYDSIMRDIL 358  
DB 333 QKYDSVMQRL 343  
RESULT 4  
ADY73655  
ID ADY73655 standard; protein; 326 AA.  
XX AC ADY73655;  
XX 02-JUN-2005 (first entry)  
XX Yersinia pestis V antigen.  
XX V antigen; immune stimulation; Yersinia pestis infection; antibacterial;  
KW vaccine; gene therapy.  
XX Yersinia pestis KIM.  
XX WO2005023205-A2.  
PN 17-MAR-2005.  
XX 08-MAR-2004; 2004WO-US007190.  
XX 07-MAR-2003; 2003US-0452657P.  
XX (UYMA-) UNIV MASSACHUSETTS.  
XX Lu S, Goguen JD, Wang S;  
XX WPI; 2005-223254/23.  
DR N-PSDB; ADY73644.  
XX New polynucleotide comprising a nucleic acid encoding a signal sequence  
PT and a second nucleic acid encoding a Yersinia pestis antigen polypeptide,  
PT useful in preparing a composition for treating Yersinia pestis infection.  
XX Claim 3; SEQ ID NO 13; 79pp; English.  
XX This invention describes a novel fusion construct comprising a tissue  
CC plasminogen activator (tPA) fused to a nucleic acid that encodes a  
CC Yersinia pestis antigen polypeptide, selected from V, Fl, Pla, YopB,  
CC YopD, YopO or YscF antigen polypeptide. The invention also describes 1)  
CC an expression vector containing the construct; 2) a cell comprising the  
CC construct; 3) a process for producing a Yersinia pestis antigen  
CC polypeptide; 4) a composition comprising the construct, preferably a  
CC multimeric V antigen; 5) a kit comprising the construct; 6) a modified  
CC Yersinia pestis antigen polypeptide sequence linked to a signal sequence  
CC sufficient for secretion from a cell; 7) a method of inducing a  
CC protective immune response in a mammal and 8) an isolated immunoglobulin  
CC that specifically binds to a modified Yersinia pestis antigen polypeptide  
CC or its fragment. The signal sequence is sufficient for secretion, however  
CC when expressed in a cell, the polynucleotide produces a Yersinia pestis  
CC antigen polypeptide that is free of the signal sequence. The isolated  
CC polynucleotide is useful in preparing a composition for treating Yersinia  
CC pestis infection. This sequence represents the Yersinia pestis V antigen.  
XX Sequence 326 AA;  
Query Match 30.7%; Score 557; DB 9; Length 326;  
Best Local Similarity 37.4%; Pred. No. 1e-35;  
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;  
QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTVELLKGK-ITIS-----ADSTLSK-- 57  
DB 5 YEONPOHFIEDLEKVRVEQLTGHSVLEELVQLVKDKNIDISIKYDPRKSEVFANRVI 64  
QY 58 -----EQLEKLLAAYLTDPASINGWAMQFGQGDAAIAAIGVIERGAKQTPPVTHWTI 113

Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSPNTQWEL 115  
 QY 114 PEFMLLSLALTWERTDDDLITFTTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEIN 173  
 Db 116 RAFMAVMHFLSTADRIDDDILKIVVDSMNHGHDARGSKRELAELTAELKIYSVIOAEIN 175  
 QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKRWEGGEFKLLSKWFSDEQVTKAQDPTNA 232  
 Db 176 KHLSSSGTINIHKSNLMDKNLYGYTDEIFKASAEYKILEKM---PQTT----- 223  
 QY 233 KNELENVTSLSNPKIQAEAKTDYERKKAIFEBIVETQIITLTFLESDLKSGMSGIE 292  
 Db 224 -----IQVDGS-----EKKIVSIKDFLGSSEKRTGALGNLK 254  
 QY 293 AEYKYDKNNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFIQKYS 352  
 Db 255 NSYSYNKNNELSHFATTCDSKRPLNDLVSKTQLSDITSRFSNAEALNRFIQKYS 314  
 QY 353 IMRDIL 358  
 Db 315 VMQRL 320

## RESULT 5

ADZ97834  
 ID ADZ97834 standard; protein; 326 AA.

AC ADZ97834;

DT 28-JUL-2005 (first entry)

XX Amino acid sequence for Yersinia pestis V-antigen.

XX monoclonal antibody; antibody production; antibody therapy;

KW virulence antigen; V-antigen; yersinia pestis infection; infection;

KW antibacterial; vaccine; epitope mapping.

XX Yersinia pestis.

XX Key Location/Qualifiers

FT Region 2..135

FT /note= "Wildly protective sequence identified by prior art"

FT Peptide 4..18

FT /note= "tryptic peptide binding tightly to mAb 84-1.

FT Given as SEQ ID No:3 in the specification and

FT specifically claimed in Claim 26"

FT Region 135..245

FT /note= "Wildly protective sequence identified by prior art"

FT Peptide 166..176

FT /note= "tryptic peptide binding tightly to mAb 141-1.

FT Given as SEQ ID No:2 in the specification and

FT specifically claimed in Claim 25"

XX WO2005047309-A2.

XX 26-MAY-2005.

XX 12-NOV-2004; 2004WO-US038480.

XX 12-NOV-2003; 2003US-0519384P.

XX (USSA ) US ARMY MEDICAL RES INST INFECTIOUS DISE.

XX Chanh TC, Andrews GP, Adamovicz JJ, Powell BS;

XX WPI; 2005-372342/38.

XX New monoclonal antibody, useful for preventing and treating Yersinia

PT pestis infection, specifically pneumonic plague infection.

XX

PS Example 6; SEQ ID NO 1; 43pp; English.

XX The invention relates to monoclonal antibodies (mAb) against the  
 CC virulence antigen (V-antigen) of Yersinia pestis, where the antibody  
 CC protects against an aerosol challenge with Y. pestis. Also described are:  
 CC (1) an antibody which competes with the antibody above for binding to Y.  
 CC pestis V-antigen; (2) a composition comprising one or more antibodies  
 CC selected from an antibody produced by hybridomas 74-1, 84-1, 125-1, or  
 CC 141-1, or comprising one or more antigenic peptide epitopes recognized by  
 CC any monoclonal antibody, e.g. mAb 74-1, mAb 84-1, mAb141-1, or mAb 124-1;  
 CC (3) a therapeutic composition, for ameliorating symptoms of Y. pestis  
 CC infection, comprising the composition of (2); a passive vaccine against  
 CC pneumonic plague infection comprising the composition of (2); (4) a  
 CC prophylactic composition, for reducing severity of Y. pestis infection,  
 CC comprising the composition of (2); (5) a hybridoma selected from 74-1, 84  
 CC -1, 125-1, or 141-1; (6) a method for detecting, in a sample, Y. pestis;  
 CC and (7) a method of treating Y. pestis infection. The antibody,  
 CC composition, and methods are useful for preventing and treating Y. pestis  
 CC infection, specifically pneumonic plague infection. This sequence  
 CC represents Y. pestis V-antigen to which monoclonal antibodies are  
 CC generated.

XX Sequence 326 AA;

Query Match 30.7%; Score 557; DB 9; Length 326;

Best Local Similarity 37.4%; Pred. No. 1e-35;

Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFVGLDVQALNTLPGNKNPKLTVELVLLKGK-ITIS-----ADSTALSK-- 57

Db 5 YEQNPOHFTEDLEKVRVEQLTGHGSSVLEELVOLVKDKNIDISIKYDPRKDEVFANRVI 64

QY 58 ----EOLEKLLAAYLTDPASINGHWGQFGQDAAIAAIKGVIERGAKQTPPVTHWTI 113

Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSPNTQWEL 115

QY 114 PEFMLLSLALTWERTDDDLITFTTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEIN 173

Db 116 RAFMAVMHFLSTADRIDDDILKIVVDSMNHGHDARGSKRELAELTAELKIYSVIOAEIN 175

QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKRWEGGEFKLLSKWFSDEQVTKAQDPTNA 232

Db 176 KHLSSSGTINIHKSNLMDKNLYGYTDEIFKASAEYKILEKM---PQTT----- 223

QY 233 KNELENVTSLSNPKIQAEAKTDYERKKAIFEBIVETQIITLTFLESDLKSGMSGIE 292

Db 224 -----IQVDGS-----EKKIVSIKDFLGSSEKRTGALGNLK 254

QY 293 AEYKYDKNNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFIQKYS 352

Db 255 NSYSYNKNNELSHFATTCDSKRPLNDLVSKTQLSDITSRFSNAEALNRFIQKYS 314

QY 353 IMRDIL 358

Db 315 VMQRL 320

## RESULT 6

AEB09748

ID AEB09748 standard; protein; 326 AA.

AC AEB09748;

DT 25-AUG-2005 (first entry)

XX Yersinia pestis V antigen.

XX vaccine; yersinia pestis infection; V antigen; growth; antibacterial.

XX Yersinia pestis.

XX WO2005056769-A2.

XX



PD		23-JUN-2005.
XX		
XX		09-DEC-2004; 2004WO-USO41282.
PR		
XX		09-DEC-2003; 2003US-0528140P.
PR		02-APR-2004; 2004US-055259P.
PR		22-MAY-2004; 2004US-0573517P.
PR		16-SEP-2004; 2004US-0610474P.
XX		(AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
XX		
XX		Size more D, Tinge SA, Killeen KP;
PI		
XX		WPI; 2005-435585/44.
DR		N-PSDB; AEB09747.
XX		
PT		New live vaccine composition comprising live attenuated serovar of
PT		Salmonella enterica, useful for protecting against plague.
XX		
PS		Example 4; SEQ ID NO 4; 50pp; English.
XX		
CC		The invention relates to a live vaccine composition, for protecting
CC		against plaque, comprising a live attenuated bacterium that is a
CC		Typhimurium serovar of salmonella enterica. The vaccine composition
CC		comprises an attenuating mutation in a genetic locus of the chromosome of
CC		the bacterium that attenuates virulence of the bacterium and where the
CC		attenuating mutation is not a single mutation in a gene that encodes a
CC		protein that is essential for the synthesis of an aromatic compound and
CC		is not a single mutation in a gene for galactose utilization, a lethal
CC		mutation in a genetic locus in the chromosome of the bacterium where the
CC		lethal mutation prevents expression from the genetic locus of a protein
CC		that has an activity that is essential for cell wall synthesis of the
CC		bacterium, and an antigen-expressing, multi-copy plasmid comprising: (1)
CC		a nucleotide sequence coding for an immunogenic polypeptide comprising a
CC		Yersinia pestis V antigen, an immunogenic portion of the V antigen, a Y.
CC		pestis FI antigen, an immunogenic portion of the FI antigen, or their
CC		combination, where the nucleotide sequence is operably linked to a
CC		promoter that permits intracellular expression of the immunogenic
CC		polypeptide from the plasmid, (2) a gene encoding a protein that has an
CC		activity that is essential for cell wall synthesis, where expression of
CC		the protein essential for cell wall synthesis complements the lethal
CC		mutation in the chromosome of the bacterium and thus permits growth of
CC		the bacterium, and (3) an origin of replication that permits multiple
CC		copies of the plasmid to be maintained in the bacterium, where the live
CC		vaccine composition elicits an immune response to one or more Y. pestis
CC		antigen when administered orally to an individual. The live vaccine
CC		composition is administered to an individual by swallowing from the
CC		mouth, by a nasogastric tube, by a gastrostomy tube, or by a suppository.
CC		The live vaccine composition is useful for protecting an individual
CC		against plague. The strains of S. enterica serovar Typhimurium stated
CC		above are useful for manufacturing a live vaccine composition to protect
CC		against plague. This sequence represents Yersinia pestis V antigen.
XX		
SQ		Sequence 326 AA;
		Query Match 30.7%; Score 557; DB 9; Length 326;
		Best Local Similarity 37.4%; Pred. No. 1e-35;
		Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps
QY	7	YNTNPGAFVGLWDVALNTLPONKNPKUTELVELLKKK-KTIS-----ADSTALSK-- 57
Db	5	YEQNPQHFTEDLEKRVVEQLTHGSSVLEEVLQVKDKNDIDISTIKYDPRKDSVFANRVI 64
QY	58	---EOLEKLAAYLTDPASJNGWMGQFKGGODAAIAAKGVIERGAQTTPVTHWTI 113
Db	65	TTDIELLKKILAYFLPEDAILKGHHYNQLONG----IKRVKGFLE-----SSPNTQEWL 115
QY	114	PEFMLLSLSAWTERTDDDLITFTFGVMFQDNORKGLRDLEAEMTAELKIYVIOSEIN 173
Db	116	RAFMAVMHFSLATRIDDDILKVIVDSNNVHGCDARSKRLRELAETALIELKIYVIOAEIN 175
QY	174	QVLSAASN-OPTKTWNMDYKLVESLAKFMEGGBFKLLSKMFSDEQVTQAQODFTNA 232

Db	176	KHLSSSGTINIHDKSINIMDKNLNLYGYTDDEEIKFAAEYKILEKM---	PQTT-----	222
Qy	233	KNELENTVSTSLNPKIQAEAKTDYERKKAIFEEIVETOIITLKTPLESLDKKSGAMSGIE	292	
Db	224	-----IQVGS-----	EKKIVSIKDFLGSNKKITGALGNJK	254
Qy	293	AEYKYDKONNKLGNFSTSVSDRSPDLNDLVSEKTLARLNDVSRYNAAIEALNRFIOKYDS	352	
Db	255	NSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTLQSLDITSRFRNSAIEALNRFIOKYDS	314	
Qy	353	IMRDIL 358		
Db	315	VMQRL 320		
RESULT 7				
ID	AEF93450	standard; protein; 326 AA.		
AC	AEF93450;			
DT	20-APR-2006	(first entry)		
XX	Y. pestis F1 capsule antigen (Caf1).			
DE	gram-neg. bacterium; outer surface protein; pharmaceutical; vaccine;			
KW	F1 capsule antigen; Caf1.			
XX	Yersinia pestis.			
OS	WO2006014292-A2.			
FN	09-FEB-2006.			
PD	30-JUN-2005; 2005WO-US23106.			
PF	02-JUL-2004; 2004US-0585057P.			
PR	(DATT/) DATTWYLER R J.			
PA	(GOME/) GOMES-SOLECKI M.			
XX	Dattwyler RJ, Gomes-Solecki M;			
PI	WPI; 2006-145890/15.			
DR	New composition comprising a bacterium engineered to express at least one			
XX	outer surface protein of <i>Borrelia burgdorferi</i> , useful for immunizing a			
PT	subject against <i>Borrelia burgdorferi</i> infections.			
PT	Disclosure; SEQ ID NO 18; 95pp; English.			
PS	The invention relates to a composition comprising a bacterium engineered			
XX	to express at least one outer surface protein of <i>Borrelia burgdorferi</i> ,			
CC	selected from OspA or OspC antigens. It is especially useful as an oral			
CC	vaccine composition also containing a food carrier or an excipient. The			
CC	oral vaccine composition comprises a bacterium selected from <i>Escherichia</i>			
CC	<i>coli</i> , and <i>Lactobacillus plantarum</i> . The bacterium is lyophilized. The food			
CC	carrier comprises a dairy product selected from milk, yogurt, and cheese,			
CC	or a grain product selected from grain, seed, bread, and cereal. The			
CC	excipient is selected from a sugar, a starch, a gum, and a protein. The			
CC	food carrier comprises animal chow. The composition is useful for			
CC	immunizing a subject against <i>Borrelia burgdorferi</i> infections. The present			
CC	sequence represents a <i>Y. pestis</i> F1 capsule antigen (Caf1).			
XX	Sequence 326 AA;			
SQ	Query Match			
	Best Local Similarity 30.7%; Score 557; DB 10; Length 326;			
	Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9			
Qy	7	YNTNPGAFVGMLDVQALNTLPGNKNPKLTETVELLKGK-ITIS-----	ADGSTALSK--	57
Db	5	YEQNPQHFIEDLEKVRVEQTLTGHGSSVLEELVQLVKDKNIDISIKYDPRKQSEVFANRVI	64	



XX Yersinia pestis V antigen (AAW01041) is capable of evoking protective  
CC immune responses in animals. A combined vaccine of V and F1 antigens (see  
CC also AAW01042) can at least match the protection afforded by live  
CC attenuated EV76 vaccine without any of the hazards that have kept the EV  
CC vaccine from general use. The V antigen is produced using the lcrV gene  
CC (see also AAT38243) obtd. from Y. pestis by PCR amplification. It can  
CC also be prepd. as a fusion with F1 antigen (see also AAW01044-45) and  
CC expressed by attenuated AroA or C Salmonella typhi and gut-colonising  
CC bacteria for protection against plague. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX SQ Sequence 329 AA;

Query Match 30.7%; Score 557; DB 2; Length 329;  
Best Local Similarity 37.4%; Pred. No. 1e-35;  
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;  
QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTTELVELLKGK-ITIS-----ADSSALSK-- 57  
Db 8 YEQNPOHFIEDLEKVRVEQLTGHGSSVLELVQLVKDKNIDISIKYDPRKDSVFANRVI 67  
QY 58 ----EOLKLLAAYLTPASINGWAMGQPKGQDAALAAIKGVIERGAKOTPPVTHWTI 113  
Db 68 TDDIELLKKILAYFLPEDAILKGHDYDNLQNG-----IKRVKEFLE-----SSNTQWEL 118  
QY 114 PEFMLLSALTMERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173  
Db 119 RAFMAVMHFSLTADRIDDDILKIVVDSNMHHGDARSKLRELAELTAELKIYSVIOAEIN 178  
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMGEGFKLLSKMFSDEQVTKAQODFTNA 232  
Db 179 KHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKM---PQT----- 226  
QY 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFFLESDLKSGAMSGIE 292  
Db 227 -----IQVDGS-----EKKIVSIKDFLGSNKRTGALGNLK 257  
QY 293 AEKYDKDNKKNLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDS 352  
Db 258 NSYSYNKDNNELSHFATTCDSKSRPLNDLVSQKTTQLSDITSRNSAIEALNRFIOKYDS 317  
QY 353 IMRDIL 358  
Db 318 VMORLL 323

RESULT 10  
AAW01040  
ID AAW01040 standard; protein; 329 AA.  
XX AAW01040;  
AC AAW01040;  
XX  
XX 16-OCT-2003 (revised)  
DT 28-DEC-1996 (first entry)  
XX Y. pestis V antigen.  
DE  
XX Plague; vaccine; genetic immunisation; V antigen; lcrV; F1 antigen.  
KW Yersinia pestis; strain GB.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..4  
FT /note= "vector-encoded peptide"  
XX  
XX W09628551-A1.  
XX  
XX 19-SEP-1996.  
PD  
XX  
XX 13-MAR-1996; 96WO-GB000571.  
XX  
XX 13-MAR-1995; 95GB-00005059.

PR 15-SEP-1995; 95GB-00018946.  
PR 05-DEC-1995; 95GB-00024825.  
XX  
XX (MINA ) UK SEC FOR DEFENCE.  
XX  
XX Titball RW, Williamson ED, Leary SEC, Oyston PCF, Bennett AM;  
XX WPI; 1996-433824/43.  
XX DR N-PSDB; AAT38242.  
XX  
XX Yersinia pestis V antigen and F1 antigen or their protective epitopic  
PT parts - useful in vaccine for protection against plague.  
XX  
XX Disclosure; Page 25-28; 98pp; English.  
XX  
XX Yersinia pestis V antigen (AAW01040) is capable of evoking protective  
CC immune responses in animals. A combined vaccine of V and F1 antigens (see  
CC also AAW01042) can at least match the protection afforded by live  
CC attenuated EV76 vaccine without any of the hazards that have kept the EV  
CC vaccine from general use. The V antigen is produced using the lcrV gene  
CC (see also AAT38242) obtd. from Y. pestis by PCR amplification. It can  
CC also be prepd. as a fusion with F1 antigen (see also AAW01044-45) and  
CC expressed by attenuated AroA or C Salmonella typhi as a live vaccine for  
CC long-term protection against plague. Expression by gut-colonising  
CC bacterial transformants produces a protective response against Y. pestis.  
CC (Updated on 16-OCT-2003 to standardise OS field)  
XX SQ Sequence 329 AA;

Query Match 30.7%; Score 557; DB 2; Length 329;  
Best Local Similarity 37.4%; Pred. No. 1e-35;  
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;  
QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTTELVELLKGK-ITIS-----ADSSALSK-- 57  
Db 8 YEQNPOHFIEDLEKVRVEQLTGHGSSVLELVQLVKDKNIDISIKYDPRKDSVFANRVI 67  
QY 58 ----EOLKLLAAYLTPASINGWAMGQPKGQDAALAAIKGVIERGAKOTPPVTHWTI 113  
Db 68 TDDIELLKKILAYFLPEDAILKGHDYDNLQNG-----IKRVKEFLE-----SSNTQWEL 118  
QY 114 PEFMLLSALTMERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173  
Db 119 RAFMAVMHFSLTADRIDDDILKIVVDSNMHHGDARSKLRELAELTAELKIYSVIOAEIN 178  
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMGEGFKLLSKMFSDEQVTKAQODFTNA 232  
Db 179 KHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKM---PQT----- 226  
QY 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFFLESDLKSGAMSGIE 292  
Db 227 -----IQVDGS-----EKKIVSIKDFLGSNKRTGALGNLK 257  
QY 293 AEKYDKDNKKNLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDS 352  
Db 258 NSYSYNKDNNELSHFATTCDSKSRPLNDLVSQKTTQLSDITSRNSAIEALNRFIOKYDS 317  
QY 353 IMRDIL 358  
Db 318 VMORLL 323

RESULT 11  
AEB09750  
ID AEB09750 standard; protein; 478 AA.  
XX AEB09750;  
AC AEB09750;  
XX  
XX 25-AUG-2005 (first entry)  
DT  
XX Yersinia pestis F1-V antigen fusion protein.  
DE  
XX vaccine; yersinia pestis infection; F1 antigen; V antigen; growth;



PS Example 3; Page 65-69; 98pp; English.

XX A fusion protein (AAW01044) comprises the F1 antigen (see also AAW01043) and V antigen (see also AAW01041) of Yersinia pestis joined by a linker that allows each protein to attain its conformational state. It is the product of a gene fusion (AAT38249) obtd. by PCR amplification of Y. pestis DNA. F1/V fusion protein can be expressed by gut-colonising CC organism transformants, to induce an immune response against Y. pestis, CC the causative organism of plague

XX Sequence 501 AA;

Query Match 30.7%; Score 557; DB 2; Length 501;  
Best Local Similarity 37.4%; Pred. No. 1.8e-35;  
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFVGLVDVQALNTLPGNKNPKLTBLVELLKGK-ITIS-----ADSSALSK-- 57  
DB 180 YEQNPHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 239  
QY 58 ----EOLKLAAYLTDPASINGGWAMGQPKGGQDAIAAIAKGVIERGAKQTPPVTHWTI 113  
DB 240 TDDIELLKILAYFLPEDAILKGCHYDNLQNG---IKRVKEFLE-----SSPTQWEL 290  
QY 114 PEFMLLSALTMTERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173  
DB 291 RAFMAVNHFSLTADRIDDDILKVTDSMNHHGDARSKLREELAEELTAELKIYSVIOAEIN 350  
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNA 232  
DB 351 KHLSSSTGTTNIHDSINLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 398  
QY 233 KNELENTVSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLFTFLESDLKKGAMSGIE 292  
DB 399 -----IQVDS-----EKKIVSIKDFLGSNKRTGALGNLK 429  
QY 293 AEYKYDKNNKLNKFNSTVSRSRPLNDLVSEKTLARLNDVSSRYNAEIALNRFIQKYDS 352  
DB 430 NSYSYNKDNNELSHFATCDSKSRPLNDLVSQKTTQLSDITSRFSNAIEALNRFIQKYDS 489  
QY 353 IMRDIL 358  
DB 490 VMQRL 495

RESULT 13  
AAR79962  
ID AAR79962 standard; protein; 329 AA.  
XX AAR79962;  
AC AAR79962;  
XX 18-APR-1996 (first entry)  
DT Partial LcrV (V antigen) of Y. pestis.  
DE LcrV; V antigen; virulence; plague; vaccine; epitope.  
XX Yersinia pestis.  
OS Yersinia pestis.  
XX WO9524475-A1.  
PN 14-SEP-1995.  
XX 06-MAR-1995; 95WO-GB000481.  
XX 08-MAR-1994; 94GB-00004577.  
XX (MINA ) UK SEC FOR DEFENCE.  
PA Titball RW, Williamson ED, Leary SE;  
PI WPI; 1995-328268/42.  
XX N-PSDB; AAT04223.

XX Recombinant DNA expressing Yersinia pestis V antigen - useful in oral or  
PT parenteral vaccines for protection against plague.

XX Claim 6; Page 15-16; 25pp; English.

XX AAR79961-62 are encoded by AAT04222-23 (resp.), DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione-S-transferase in 3 different CC plasmid vectors. Y. pestis is the highly virulent causative organism of CC plague in a wide range of animals, including man. The V antigen (lcrV) is CC an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb lcr CC plasmid. The V antigen is postulated to act as a virulence antigen, and CC transformed microorganisms contg. recombinant DNA encoding a V antigen CC protein/peptide are useful in vaccines to protect against plague

XX Sequence 329 AA;

Query Match 30.5%; Score 554; DB 2; Length 329;  
Best Local Similarity 37.2%; Pred. No. 1.8e-35;  
Matches 136; Conservative 62; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFVGLVDVQALNTLPGNKNPKLTBLVELLKGK-ITIS-----ADSSALSK-- 57  
DB 8 YEQNPHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 67  
QY 58 ----EOLKLAAYLTDPASINGGWAMGQPKGGQDAIAAIAKGVIERGAKQTPPVTHWTI 113  
DB 68 TDDIELLKILAYFLPEDAILKGCHYDNLQNG---IKRVKEFLE-----SSPTQWEL 118  
QY 114 PEFMLLSALTMTERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173  
DB 119 RAFMAVNHFSLTADRIDDDILKVTDSMNHHGDARSKLREELAEELTAELKIYSVIOAEIN 178  
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNA 232  
DB 179 KHLSSSTGTTNIHDSINLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 226  
QY 233 KNELENTVSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLFTFLESDLKKGAMSGIE 292  
DB 227 -----IQVDS-----EKKIVSIKDFLGSNKRTGALGNLK 257  
QY 293 AEYKYDKNNKLNKFNSTVSRSRPLNDLVSEKTLARLNDVSSRYNAEIALNRFIQKYDS 352  
DB 258 NSYSYNKDNNELSHFATCDSKSRPLNDLVSQKTTQLSDITSRFSNAIEALNRFIQKYDS 317  
QY 353 IMRDIL 358  
DB 318 VMQRL 323

RESULT 14  
AAW01045  
ID AAW01045 standard; protein; 480 AA.  
XX AAW01045;  
AC AAW01045;  
XX 28-DEC-1996 (first entry)  
DT Y. pestis F1/V antigen fusion.  
DE Plague; vaccine; genetic immunisation; V antigen; lcrV; F1 antigen; cafl.  
XX Yersinia pestis; strain GB.  
OS Synthetic.  
OS Chimeric.  
XX Key Location/Qualifiers  
FH 1. .149  
FT Protein /label= F1 antigen  
FT notes= "mature F1 antigen"  
FT Peptide 150. .155

```
FT FT /label= Linker
FT FT /note= "6-amino acid peptide linker"
FT 156 480
FT /label= V_antigen
FT /note= "mature V antigen"
XX
XX WO9628551-A1.
PN
XX
XX 19-SEP-1996.
XX
XX 13-MAR-1996; 96WO-GB000571.
XX
XX 13-MAR-1995; 95GB-00005059.
PR
XX 15-SEP-1995; 95GB-00018946.
PR
XX 05-DEC-1995; 95GB-00024825.
XX
XX (MINA ) UK SEC FOR DEFENCE.
PA
XX
XX Titball RW, Williamson ED, Leary SEC, Oyston PCF, Bennett AM;
XX
XX WPI; 1996-433824/43.
DR
XX N-PSDB; AAT38256.
XX
XX Yersinia pestis V antigen and F1 antigen or their protective epitopic
FT parts - useful in vaccine for protection against plague.
XX
XX Disclosure; Page 51-55; 98pp; English.
XX
XX A fusion protein (AAW01045) comprises the F1 antigen (see also AAW01042)
CC and V antigen (see also AAW01041) of Yersinia pestis joined by a linker
CC that allows each protein to attain its conformational state. It is the
CC product of a gene fusion (AAT38256) obtd. by PCR amplification of Y.
CC pestis DNA. F1/V fusion protein can be expressed by gut-colonising
CC organism transformants, to induce an immune response against Y. pestis,
CC the causative organism of plague
XX
XX Sequence 480 AA;
XX
XX Query Match 30.5%; Score 554; DB 2; Length 480;
XX Best Local Similarity 37.2%; Pred. No. 3e-35;
XX Matches 136; Conservative 62; Mismatches 104; Indels 64; Gaps 9;
XX
XX 7 YNTNPGAFVGLVDQALNTLPNGNPKLTVELVLLKGGK-ITIS-----ADSGTSLSK-- 57
DB 159 YEONPQHFIEDLEKVRVEQLTGHGSSVLELVQLVKDKNIDISIKYDPRKDSVFANRVI 218
XX
XX 58 -----EQLKLLAAYLTDPASINGCWANGQFKGGQDAIAAIAKGVIERGAKQTPPVTHWTI 113
DB 219 TDDIELLKILAYFLPELPAALKGGHYDNLQNG-----IKRVKEFL-----SSPNTQWEL 269
XX
XX 114 PEFMLLSLSALTMTERTDDDLITTTGVMFMQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
DB 270 RAFPMAVHFSLTADRIDDDLKLVIVDSNMHHGARSKLREELAEALTAELKIYSVIOAEIN 329
XX
XX 174 QVLSAASN-QTEKTNFNLMDYKLYGYESLAKFMWEGEFKLLSKMFSDEQVTKAQOQFTNA 232
DB 330 KHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKM-----PQT----- 377
XX
XX 233 KNELENTVSTSLNPKIQAEAKTDYERKKAIFEIVETQITUTKTFLESCLKSGAMSGIE 292
DB 378 -----IQVDGS-----EKKIVSKINDFLGSENKRTGALGNLK 408
XX
XX 293 AEYKDKNNKLGNFSTVSDRSRPLNDLVSEKTAFLRNDVSSRYNAALAEALNRFIOKYDS 352
DB 409 NSYSYKNNKNNELSHFATTCSDKSRPLNDLVSQKTTQVSDITSRFSNAIEALNRFIOKYDS 468
XX
XX 353 IMRDIL 358
DB 469 VMQRLL 474
XX
XX RESULT 15
XX ABO81312
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Search completed: June 16, 2006, 19:06:40  
Job time : 243.199 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 36.687 Seconds  
(without alignments)  
946.773 Million cell updates/sec

Title: US-10-813-908A-8  
Perfect score: 1916  
Sequence: 1 MSTIPDYNTPGAFVGLDV.....ALNRFIQKYSIMRDILGAI 361

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	564	31.1	326	2 B37314	regulatory protein
2	556	30.6	326	2 B33601	lcrv protein - yer
3	474	26.1	294	2 G83432	type III secretion
4	133.5	7.4	624	2 PG6003	surface membrane p
5	129	7.1	841	2 A86188	hypothetical prote
6	128.5	7.1	1939	2 T18372	repeat organellar
7	124	6.8	1252	2 B42771	reticulocyte-bind
8	123.5	6.8	2269	2 T28677	rhoptery protein -
9	121.5	6.7	2166	2 G70163	hypothetical prote
10	121	6.7	366	2 E72400	DNA polymerase III
11	121	6.7	616	2 G82885	hypothetical prote
12	121	6.7	629	2 A29666	keratin, 65k type
13	121	6.7	1302	1 JC6009	surface-located me
14	120.5	6.6	995	2 T27327	hypothetical prote
15	120	6.6	628	2 A82889	hypothetical prote
16	120	6.6	1736	2 F86178	hypothetical prote
17	119.5	6.6	1312	1 EWBVDL	RAD50 protein - ye
18	119	6.6	1025	2 E86355	hypothetical prote
19	119	6.6	2116	2 A26655	myosin heavy chain
20	119	6.6	4919	2 T31105	hypothetical prote
21	118.5	6.5	1098	2 B70232	hypothetical prote
22	118	6.5	2052	2 C97038	phage-related prot
23	117.5	6.5	478	2 E43599	toxin apid secret
24	117.5	6.5	880	2 F75103	conserved hypothet
25	117.5	6.5	982	2 I64232	protein p115 homol
26	117.5	6.5	1268	2 S33411	botulinum neurotox
27	117	6.4	935	2 T51930	kinesin [imported]
28	116	6.4	390	2 H64603	probable aspartate
29	116	6.4	581	2 S63183	CNM1 protein - yea

30 116 6.4 1170 2 A56157 chromosome segrega  
31 115.5 6.4 1751 2 A45604 major blood-stage  
32 115 6.3 1271 2 D64237 hypothetical prote  
33 114.5 6.3 864 2 B90395 purine NTPase [imp  
34 114.5 6.3 1127 2 T28317 ORF MSV156 hypothe  
35 114.5 6.3 2017 1 A36014 myosin heavy chain  
36 114.5 6.3 2057 2 S61477 myosin II heavy ch  
37 114 6.3 1005 2 A64465 hypothetical prote  
38 114 6.3 1279 2 G86684 probable pil prote  
39 113.5 6.2 461 2 S23420 unknown protein, 7  
40 113.5 6.2 555 2 C96667 hypothetical prote  
41 113 6.2 781 2 F90547 pil5 protein homol  
42 113 6.2 982 2 S73741 hypothetical prote  
43 113 6.2 1718 2 T31638 giantin - human  
44 113 6.2 3225 2 I52300 B. subtilis negati  
45 112.5 6.2 571 2 AC1637

ALIGNMENTS

RESULT 1

B37314  
regulatory protein lcrv - Yersinia pseudotuberculosis  
C;Species: Yersinia pseudotuberculosis  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 09-Jul-2004  
C;Accession: B37314  
R;Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;  
J. Bacteriol. 173, 1607-1616, 1991  
A;Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis:  
A;Reference number: A37314; MUID:91154114; PMID:1705541  
A;Accession: B37314  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-326 <BER>  
A;Cross-references: UNIPROT:P23994; UNIPARC:UPI000012E2BC; GB:M57893; NID:g155456; PIDN

Query Match 31.1%; Score 564; DB 2; Length 326;  
Best Local Similarity 37.7%; Pred. No. 9.7e-28;  
Matches 138; Conservative 59; Mismatches 105; Indels 64; Gaps 8;

QY 7 YNTNPGAFVGLDVOALNTLPGNKNPKLTVELLKGK-ITIS-----ADSTALSK-- 57  
Db 5 YEQNPQHFTEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 64  
QY 58 ----EOLEKLAAYLTDPASINGGWAMGQFKGQDAAIAAIGKVIERGAKQTPPVTHWTI 113  
Db 65 TDDIELLKILAYFLPEDAILKGGHYDNLQNG----IKRVKEFLR-----SSPNTQWEL 115  
QY 114 PEFMLSLSALTMTERTDDDLITFTTGMFMFQDNQRKGLRDELAEMTAELKIYGVIOSEIN 173  
Db 116 RAPMAVTHFSLTADRIDDDILKVIYVDSNMHHGDARSKREELAEALTAELKIYSVIOAEIN 175  
QY 174 QVLSAASN-QTFKTNFMNDYKLYGYESLAKPMWEGEFKLLSKMFSDEQVTKAQQFTNA 232  
Db 176 KHLSSGGTINIHKSNLMDKNLYGYTDEEIFKASAEYKILEKM---POTT----- 223  
QY 233 KNELENVTSLNPKIQAEAKTDYERKKAIFEIVETQIITLTFLESLDKKSGAMSGIE 292  
Db 224 -----IQGETEKKIVSVINKNFLESEKRTGALGNLK 254  
QY 293 AEYKYDKNNKLGNFSTSVSDSRPLNDLVSEKTRNLNDVSSRYNAIAIALNRFIOKYS 352  
Db 255 DSYSYKNNKNNELSHFATTCDSKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIOKYS 314  
QY 353 IMRDIL 358  
Db 315 VMQRL 320

RESULT 2

B33601  
lcrv protein - Yersinia pestis plasmid pCD1



Db 49 TNPYSTLISELTSKSDSKNSITSSNKSNDIETANTTELKQALAKANTDKAQADNLARSTK 108  
QY 58 BOLEK-----LLAAYLTD-----PASINGGWAMQFGGQDAA 90  
Db 109 BQLNKSISANTLLAKLTDKNTIQQAQTELEKEVQKQAVASNTTASMQSAKSSLDAAK 168  
QY 91 IAAIKGVLE-----RGAK-QTPPVTHWTIPFEMLLS-----LSALTWERTDDDLIT 135  
Db 169 VTEITKKLETNFKDAKFKELQOQTRKNIDFINTNPNYSBELISQLTSKRDSKNSVT 228  
QY 136 TFTGVMPQ-----DNQRKGLRDE-----LAEMT----- 159  
Db 229 NSSNKSNDIETANTTELKQALAKANTDKQADNLAKSAKQOLNNSVSSANTLLAKLTDKNT 288  
QY 160 ---AELKIYGVIOSEINQVLSAASNTQFTKNFNLMDYKL-----YGVESIAKPMF- 206  
Db 289 IQQAQTELEKEVQ-KANQAVASNTTASMQSAKSSLDAAKVTETKKLETFNFKDKAKFKEL 347  
QY 207 -----GGEFKLLSKMFSQVTKAQODFTNAKNELENTVTSI-- 244  
Db 348 EOTRKDIDEFIQIENDPQTKKNYQNVINKLKKAEKNSITFSNNKKEIQDANKSLQDE 407  
QY 245 --NPKIOAEAKTDYERKAIFEEIVEQTIIITLKTFLSDDLKKGAMSGIAEYKYDKDN 302  
Db 408 LNNAKIYKGTDFNSKKQLEDIKT-----DDAKVGT-----TEADTILDHYKN 454  
QY 303 KLGNFSTSVSRPLNDLVSEKTLARLNDVS-----SRYNAAIBALNRFI 347  
Db 455 -----ISDASK-NEEIKQATOKINDIKKIIETKIQEKRNFEQFEQIKNELQSF 504  
QY 348 -----QKYDSIMEDI 357  
Db 505 NKDLKQKYNISRTKI 520

RESULT 5  
A86188  
hypothetical protein [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: A86188  
R/Theologus, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Hughes, B.; Huizart, L.  
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: A86188  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-841 <STO>  
A/Cross-references: UNIPROT:023037; UNIPARC:UPI00000AAABE8; GB:AE005172; NID:G2388564; PI  
C/Genetics:  
A/Map position: 1

Query Match 7.1%; Score 129; DB 2; Length 841;  
Best Local Similarity 19.7%; Pred. No. 2.5;  
Matches 70; Conservative 75; Mismatches 138; Indels 72; Gaps 13;  
QY 33 KTELVELLKGKITISADSSFALSKEQLEKLAAYLTPASINGGWAMQFGGQDAAIA 92  
Db 272 KKLQLEAIQVNSLEATLSVAMEKER-----DUSENLNVAWEKLSSEER--- 317  
QY 93 AIKGVIERGAKQTPPVTHWTIPFEMLLSLSALTWERTDDDLITFTGVMMFQDNQKRLR 152  
Db 318 -----LEKQAREIDEATRSIELEALHSHSELVKQKTWEDFS-----RDTEAKSLT 364  
QY 153 DELAEMTAELKIY-----VIQSEINQVLSAASNTQFTKNFNLMDYKLYGYESL 201

Db 365 EKSKDLEEKIRVVEGKLAEACGOSLSLQEELDQ--SSAENELLADTNNQIKIKI--QEL 419  
QY 202 AKFMEGEEFKLLSKMFSDEQVTKAQODFTNAKNELENTVTSIINPKIOAEAKTDYERKKA 261  
Db 420 EGYLDSEKETAIEKL--NQKDTAKOLITKLKSH-ENVIEHKRQVLEASGVAD-TRKVE 475  
QY 262 IFBEIVETQIITLKTFLSDDLKKGAMSGIAEYKYDKDNKNGFNSTSVSRPLNDL 321  
Db 476 VEEALL--KLNTLESTIEELEKENGDLAEVNI-----KLQKLANQSGSTDDDFQAKLSVL 528  
QY 322 VSEK-----TARLNDVSSRYNAAIEAL-----NRFIOKYDYSIMRDL 358  
Db 529 EAEKYQQAQKELQITIEDLTQKLTSERLSRSSLSSEEEKNQVNEIYQSTKNELV 583

RESULT 6  
T18372  
repeat organellar protein - Plasmodium chabaudi  
C/Species: Plasmodium chabaudi  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T18372  
R/Werner, E.B.; Taylor, W.R.; Holder, A.A.  
Mol. Biochem. Parasitol. 94, 185-196, 1998  
A/Title: A Plasmodium chabaudi protein contains a repetitive region with a predicted sp  
A/Reference number: Z18922; MUID:98418765; PMID:9747969  
A/Accession: T18372  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1939 <WER>  
A/Cross-references: UNIPROT:Q25662; UNIPARC:UPI00000823AE; EMBL:U43145; NID:g1151157; P

Query Match 7.1%; Score 128.5; DB 2; Length 1939;  
Best Local Similarity 21.8%; Pred. No. 8.2;  
Matches 59; Conservative 46; Mismatches 103; Indels 63; Gaps 11;  
QY 119 LLSALTMTERTDDDLITFTGVMMFQDNQKRLDELAEMTAELKIYGVITQSEINQVLSA 178  
Db 193 MSLDKLTCE-----VQEKDNLEK-INKKVIEKENNLRELKEPMKNEKIEIS 239  
QY 179 ASNQTKTNFNLMDYKLYGVESIAKMEGFEKLLSKMFSDEQVTKAQODFTN--AKNEL 236  
Db 240 LDG-TINDKKNAYEKLSEFEKKRMIEMLDLSKLEK-----EENFANKQAKLEK 288  
QY 237 ENVTSTSLNPKIOAEAKTDYERKAIFEEIVEQTIIITLKTFLSDDLKKGAMSGI----- 291  
Db 289 ENIIIEKLDIESREK-DFKSKEKFPAS-MENELNTLK-----SDLSKNACQMEVYKLEI 342  
QY 292 -----EAEYKYDKDNKNGFNSTSVSDR-----SRPLNDLVSEKT 326  
Db 343 KQLSQSLVEKEREIFEIKNEYDDKINNKEKLSSINDKIGDINTVLHSEEEKINKLLEKE 402  
QY 327 ARLNDVSSRYNAAIEAL-NRFIOKYDYSIMRD 356  
Db 403 TELNEIHKYNEIETIKNELNEKEBELEKN 433

RESULT 7  
B42771  
reticulocyte-binding protein 2 - Plasmodium vivax (fragment)  
C/Species: Plasmodium vivax  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Sep-1997  
C/Accession: B42771  
R/Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.  
Cell 69, 1213-1226, 1992  
A/Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.  
A/Reference number: A42771; MUID:92315338; PMID:1617731  
A/Accession: B42771  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-1252 <GAL>  
A/Cross-references: UNIPARC:UPI0000178645; GB:M88098; NID:g160627; PID:g160628  
A/Experimental source: strain Belem, merozoites

C;Genetics:  
A;Gene: RBP2

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Query Match          6.8%; Score 124; DB 2; Length 1252;
Best Local Similarity 20.2%; Pred. No. 8.;
Matches 76; Conservative 74; Mismatches 138; Indels 88; Gaps 17;

QY 21 QALNTLPNGKNPKLTVELLKGKTTI---SADSTALSKE-OLEKLLAAVLTDPASING 76
Db 841 EAVSVKIGNVKHSEL-----SKITCSKSYDNITALEKQTELQNLRSFTQKTNNTS 895

QY 77 GWAGQPKGGODA---AIAAIKGV-----ERGAQKQTPPVTHWTIPEFMLSLSA 123
Db 896 DSKLEKIKTDFSLKNAKLTLEGEVNAKASSDNHEHVQSKSEPVNP-----ALSE 946

QY 124 LTWERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASQNT 183
Db 947 IEKEETDIDSLNALDELL-----KKG-----RTCEVSRYLKIDTVTKEISDDTELI 994

QY 184 FKTNFMNDYKLY---GYESLAKFMEGGEFKLSKMFSDQVTKAQ-QDFTNAKNELENV 239
Db 995 NTIEKNVKAVALIKKNYEDTVQ-----DVLTLNEHFNKYQVSNHPTNFDKSNKSEEL 1049

QY 240 TSTSLNPKIOAEAKTYERKAIFIEIVETQIITLKTFLSCLKSGAMSGIEAEYKYDK 299
Db 1050 T-----KAVTDSKTIISKLGVIIEVNE--TEMNTIESSAKE-----IEALY---- 1090

QY 300 DNNKLGNFSTVSDRSRPLNDL---VSEKTARLNDVSSRYNAIE-----ALN 344
Db 1091 --NELKNKKTSLNEIYQTSNEVKLQEMKNADKYIDVSKIFNVLTDTQKSNIVTNQHSIN 1148

QY 345 RFIQKYDSIMRDLGA 360
Db 1149 NVKDKLKGKQLQELIDA 1164

RESULT 8
rhoptry protein - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28677; C45521
R;Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A;Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii.
A;Reference number: Z20508; MUID:95021522; PMID:7935623
A;Accession: T28677
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2269 <KEE>
A;Cross-references: UNIPROT:Q26223; UNIPARC:UPI0000080871; EMBL:L27838; NID:g457145; PID
R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple co
A;Reference number: A45521; MUID:91101660; PMID:2270106
A;Accession: C45521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 2131-2269 <KE2>
A;Cross-references: UNIPARC:UPI0000178646; GB:M34283
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Query Match          6.8%; Score 123.5; DB 2; Length 2269;
Best Local Similarity 21.6%; Pred. No. 21;
Matches 80; Conservative 55; Mismatches 103; Indels 133; Gaps 17;

QY 35 TELVELLKGKTTISA---DSSTALSKE-----QLEKLLA 65
Db 1656 TTLAETLKIKTDYSKFIESATKFSKEFLKYIGDTSNLSLNDIATLQKLYDLHQINKYVT 1715

QY 66 AVLTDPASINGGWAMQPKGGODAAATKGV-----IERGAQKQTPPV----- 108
Db 1716 SKLSDATDNNNLIEKEATQ-----AIKNLTKLFTDSSNIDANALHNNKIOMVYFNS 1770
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QY 109 -THWTIPE-----FMLLSLSALTWERTDDDLITFTGVMMFQDNQKGLRDELA 157
Db 1771 ELHKSIESIKQLYKQKHVFKLLNIGQINGKYP--DISKOFDNLILQOE-----SE 1818

QY 158 MTAEL-----KIYGVIOSEINQVLSAASQNTFKTNFNLMDYKLYGYESLAKFMEGGBFKLL 213
Db 1819 LTANLNDLKEIGKISDKKKNFHAL-NETPIPNFN-----TL 1855

QY 214 SKMFSDQVTKAQDFTNAKNELENVTS-----TSLNPKIOA--EAKTDYER 258
Db 1856 KIIHDIIVYKRRQID-----EENITSEENENITLYIDITLKLKEKVQSILNFVTYEN 1909

QY 259 KKAIFEEIV---ETQII---TLKTFLESCLKSGAMSGIEAEYKYDKDNNKLGNFST 310
Db 1910 DSNIIKQHIQDNTENDVSKIESLTKTQSFQILNKINGIKAQF---YDNNNNINNT 1966

QY 311 VSDRSRPLNDL 321
Db 1967 ISTISQDVNDV 1977

RESULT 9
G70163
hypothetical protein BB0512 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70163
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70163
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2166 <KLE>
A;Cross-references: UNIPROT:O51465; UNIPARC:UPI00000574E8; GB:AE001153; GB:AE000783; NIT
A;Experimental source: strain B31
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Query Match          6.7%; Score 121.5; DB 2; Length 2166;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 77; Conservative 79; Mismatches 113; Indels 131; Gaps 21;

QY 29 NK-NPKLTVELLKGK-ITISADSTALSKEQLEKLLAAVLTDPASINGWAMQPKGG 86
Db 644 NKTNEEFLSLIQIKDKGIELSESVFNDLSDIHQKAI-----DMHGSW----- 687

QY 87 ODAATAAIKGVIERCAKQTPPVTHWTIP-----EFMLL-----S 120
Db 688 KDELIALNKSLLDIKVSSEELSSATLKIESLKVDNRMVLLKTGDIESLVIEKYKE 747

QY 121 LSALTWERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 748 LKDMYSQSDEAIL---GIKEFINRQTEIIKDKSVFMLEDL----- 785

QY 181 NQTF--KTNPNL-----MDYKLYGYE-----SLAKFMEGGEFKLSKMFSDQ 221
Db 786 NKKFDQKNFVISKTEECYDKLKPFIESEDILNKNFKSLDNEFIE-SKLQIVSNITKSDNQ 844

QY 222 -----VTQAQDFTNAKNELENVTS--TSLNP-----KIQ---AEAKTDYERKKA 262
Db 845 KQIDDFLRISKDILNRKDSINNEVDSKLSDWQSKLNITVTKIENLSSGKVDLD----L 900

QY 263 FEEIVETQIITLKTFLSCLKSGAMSGIEAEY--KYDKDNNKLGNFSTVSDRSRPLND 320
Db 901 IDSEVTTIKELKFSIES-----LESYLEKIDEFNRQGAISDEL-----LQD 944

QY 321 LV---SEKTARLND-VSSRYNAATEALNRFQKYDSIMRD 356
Db 945 IMNHFNKETRELENLSKFAAVLNNNSEFVKVEVDSLQD 984
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C:Genetics:
A:Gene: CESP:Y6B3B.3
A:Map position: 1
A:Introns: 365/2; 800/2; 936/3

Query Match      6.6%; Score 120.5; DB 2; Length 995;
Best Local Similarity 20.8%; Pred. No. 11;
Matches 75; Conservative 51; Mismatches 127; Indels 107; Gaps 13

Qy 17 WLDVQALNTLPGNNK-N-PKLTVELVLLKGI-TISADSSSTALSKEQLEKLLAAYLTDPASI 74
Db 5 WSRVGDLSKLPDKATFKKLGDKLSLNGTITIDVDS-----IISKLDD---- 48

Qy 75 NGWAMQFGKGGQDAAIAAKGVIERGAKQTTPVTHWTIPFMLLSLSALTWERTDDDL- 133
Db 49 -----GSDKSAVAANTTILEFAKSIATVT-----SALDKTSMETLE 85

Qy 134 ---ITFTGYMMFQDNOR-----KGLRDELAEMTAELKIYGVIOSEINOVLS 177
Db 86 TLKEITNVAKLFQYDINSQAIYKAAATDDDIKGLDNLSTKITPNSNSTIFSDFIKMLTT 145

Qy 178 AASNQTFKTNFLNDYKLYGYESIAKFMGEGFKLLSKM-----FSDEQVTKAQ 226
Db 146 ETSSLIRQHTSGLWN-----GYHDFSLLKDKIKNKFLLRIILRVFFHFTCFESHAGMSLDE 201

Qy 227 QDFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIA---PFEIVETQIITLKTFLSCLK 283
Db 202 EDFADAGEFUL-----CDLKRNGIPISFPERI---FVSFSKFLKSEEF 242

Qy 284 KSGAMSGIEAEYKYDKONNKLGNFSTVSORSRPLNDLVSEKTLARLNDVSSRYNAAI 343
Db 243 KSSMRSIIET-----SIDATLNRMKKLEDKIAELTEDLTKQKKRLDLALVEL 290

RESULT 15
A82889
hypothetical protein UU443 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82889
R:Glass, J.I.; Lerkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell,
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views
A:Reference number: A82870
A:Accession: A82889
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-528 <GLA>
A:Cross-references: UNIPARC:UPT00000C1C6D; GB:AB002141; GB:AF222894; NID:G68999
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU443
A:Genetic code: SGC3

Query Match      6.6%; Score 120; DB 2; Length 628;
Best Local Similarity 23.3%; Pred. No. 6.2;
Matches 60; Conservative 48; Mismatches 114; Indels 36; Gaps 10

Qy 118 LLSLSALTMTERTDDDLITFTGYMMFQDNORKGLRDELAEMTAELKIYGVIOSEINOVLS 177
Db 13 LSMISAIPLIAT---IITACAKV---DTQKAKEELQSSLNKAVLKEIVDQSSYEDFK 65

Qy 178 AASNQTFKTNF-----NLMDYKLYGYESIAKFM-----EGGFKLLSKMFSB---EQV 222
Db 66 KIYNQTLKSNLENINKLSEQLKQEQTKNLIQTQSVLNELDISKMSDLIDVVELENT 125

Qy 223 TKAQDFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSCLK 282
Db 126 KKQLQDFNFQYKELN---QASVDTTITDKLSDAHQRLLHTKAIQKTIIDLANKIKNLI 183

Qy 283 KKSAMSG---IEAEYKYDKDNKNGLNFTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAA 339
Db 184 KTSGNKNIVEISDIOKLVNNTKANFKKLYEDFK---LYTK---LNDINDLNKE 235

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Qy 340 IEALNRFIQYDSIMRDI 357  
: : | | : | : |  
Db 236 LKAL-PFIKLLDDIVNVI 252

Search completed: June 16, 2006, 19:25:02  
Job time : 39.687 secs

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GenCore version 5.1.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 18:53:15 ; Search time 283.517 Seconds  
(without alignments)  
1177.815 Million cell updates/sec  
Title: US-10-813-908A-8  
Perfect score: 1816  
Sequence: 1 MSTIPDNTNPGAFVGHLDV.....ALNRFQKDYDSIMRDIILGAI 361

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	2	Q70WN7_AERSA
2	1804	99.3	361	2	Q5ISV9_AERSA
3	1799	99.1	361	2	Q5ISW0_AERSA
4	1790	98.6	361	2	Q5ISV8_AERSA
5	1615	88.9	361	2	Q5ISV7_9GAMM
6	1512.5	83.3	374	2	Q5ISV5_9GAMM
7	1481.5	81.6	362	2	Q5ISV6_9GAMM
8	1386	76.3	361	2	Q699K0_AERHY
9	1384.5	76.2	362	2	Q5CC97_AERSO
10	1196.5	65.9	312	2	Q5XL04_AERHY
11	625	34.4	304	2	Q7N0X1_PHOLL
12	605.5	33.3	325	2	Q84GV5_PHOLJ
13	570.5	31.4	334	2	Q56896_YEREN
14	569.5	31.4	333	2	Q84GT5_YEREN
15	569.5	31.4	334	2	Q56853_YEREN
16	567	31.2	325	2	Q56880_YEREN
17	564	31.1	324	2	Q93K04_YEREN
18	564	31.1	326	1	LCRV_YERPS
19	561	30.9	324	2	Q56846_YEREN
20	561	30.9	324	2	Q56879_YEREN
21	560	30.8	324	2	Q87495_YEREN
22	558	30.7	324	2	Q56882_YEREN
23	557	30.7	326	1	LCRV_YERPE
24	491.5	27.1	367	2	Q5ISV4_AERHY
25	488.5	26.9	367	2	Q6TLM2_AERHY
26	474	26.1	294	2	O30527_PSEAE
27	281	15.5	607	2	Q87P59_VIBPA
28	253	13.9	605	2	Q6QV52_VIBPA
29	159	8.8	1813	2	Q513P3_ENTHI
30	138.5	7.6	1612	2	Q5ESB7_VIBF1
31	133.5	7.4	624	2	Q49548_MYCHO

32	133	7.3	965	2	Q7QJ14_ANOGA	Q7qji4 anopheles g
33	131.5	7.2	820	2	Q50Q54_ENTHI	Q50q54 entamoeba h
34	131.5	7.2	1398	2	Q6FKE6_CANGA	Q6fke6 candida gla
35	130.5	7.2	775	2	Q4A7M2_MYCH7	Q4a7m2 mycoplasma
36	130	7.2	1128	2	Q3D3M0_STRAG	Q3d3m0 streptococc
37	130	7.2	1913	2	Q4AA31_MYCHJ	Q4aa31 mycoplasma
38	130	7.2	1975	2	Q600Y2_MYCH2	Q600y2 mycoplasma
39	129.5	7.1	775	2	Q4A917_MYCHJ	Q4a917 mycoplasma
40	129.5	7.1	2162	2	Q661A9_BORGA	Q661a9 borrelia ga
41	129	7.1	699	2	Q56WB1_ARATH	Q56wb1 arabidopsis
42	129	7.1	841	2	Q23037_ARATH	Q23037 arabidopsis
43	129	7.1	1404	2	Q8RJN9_MYCHO	Q8rjn9 mycoplasma
44	129	7.1	2013	2	Q9VK10_DROME	Q9vki0 drosophila
45	129	7.1	2244	2	Q9NCG0_DROME	Q9ncg0 drosophila

ALIGNMENTS

RESULT 1  
Q70WN7\_AERSA  
ID Q70WN7\_AERSA PRELIMINARY; PRT; 361 AA.  
AC Q70WN7;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Acrv protein.  
GN Name=acrv;  
OS Aeromonas salmonicida subsp. salmonicida.  
OG Plasmid pASvira.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=JF2267; PLASMID=pASvira;  
RX MEDLINE=22957181; PubMed=14594831;  
RA DOI=10.1128/JUB.185.22.6583-6591.2003;  
RA Burr S.E., Stuber K., Frey J.;  
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";  
RL J. Bacteriol. 185:6583-6591(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
CC  
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CC  
CC EMBL; AJ516009; CAD56769.1; -; Genomic DNA.  
DR EMBL; AY649419; AAV67428.1; -; Genomic DNA.  
DR EMBL; AY649420; AAV67429.1; -; Genomic DNA.  
DR EMBL; AJ616218; CAE83108.1; -; Genomic DNA.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR005413; LCRV\_antigen.  
DR Pfam; PF04792; Lcrv; 1.  
DR PRINTS; PR01592; LCRVANTIGEN.  
SQ SEQUENCE 361 AA; 40165 MW; 66FBEE940891510 CRC64;  
Query Match 100.0%; Score 1816; DB 2; Length 361;  
Best Local Similarity 100.0%; Pred. No. 6.3e-100;

	Matches	361;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MSTIPDYNTPGAFVGLWDVQALNTLPGNKPKLTETVELLKGKITISADSSSTALSKEQL	60							
Dd	1	MSTIPDYNTPGAFVGLWDVQALNTLPGNKPKLTETVELLKGKITISADSSSTALSKEQL	60							
Qy	61	EKLAAAYLTDPASINGHGAMQPGGGQDAATAAIAKGVIERGAKKQTPTPPTHWTIPPEFMLLS	120							
Dd	61	EKLAAAYLTDPASINGHGAMQPGGGQDAATAAIAKGVIERGAKKQTPTPPTHWTIPPEFMLLS	120							
Qy	121	LSALTMBERTDDDLITTFGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS	180							
Dd	121	LSALTMBERTDDDLITTFGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS	180							
Qy	181	NQTEKTNFLNMDYKLYGYESLAKFMEGGEFKLLSKMPSDEQVTAKAQODFTNAKNELENV	240							
Dd	181	NQTEKTNFLNMDYKLYGYESLAKFMEGGEFKLLSKMPSDEQVTAKAQODFTNAKNELENV	240							
Qy	241	STSINPKIQAEAKTIDYERKKAIPBEIVETOIITLKTFLFESDLKSGSAMSGIEAEYKYDKD	300							
Dd	241	STSINPKIQAEAKTIDYERKKAIPBEIVETOIITLKTFLFESDLKSGSAMSGIEAEYKYDKD	300							
Qy	301	NNKLGNFSTSVDRSRPLNDLVSEKSTARLNDVSSRYNAAIEALNRFIQKYDSIMRDILGA	360							
Dd	301	NNKLGNFSTSVDRSRPLNDLVSEKSTARLNDVSSRYNAAIEALNRFIQKYDSIMRDILGA	360							
Qy	361	I 361								
Dd	361	I 361								

## RESULT 2

```

Q5ISV9_AERSA
ID Q5ISV9_AERSA PRELIMINARY; PRT; 361 AA.
AC Q5ISV9;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acrv.
GN Name=acrv;
OS Aeromonas salmonicida subsp. masoucida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OC NCBI_TaxID=197700;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RJ;
RA Fan W., Macintyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; AY649422; AAV67431.1; -; Genomic DNA.
CC GO; GO:0005576; C:extracellular region; IEA.
CC GO; GO:0009405; P:pathogenesis; IEA.
CC InterPro; IPR005413; LCRV_antigen.
CC Pfam; PF04792; Lcrv; 1.
CC PRINTS; PR01592; LCRVANTIGEN.
CC SEQUENCE 361 AA; 40194 MW; 7D76B652308C1510 CRC64;
SQ

```

[illegible]

Qy	121	LSALTMTERTDDDLTTTGTVMVFQDNQKGLRDELAEMTAELKIYGVIOQSEINQVLSAAS	180
Db	121	LSALTMTERTDDDLTTTGTVMVFQDNQKGLRDELAEMTAELKIYGVIOQSEINQVLSAAS	180
Qy	181	NQPTKTNFNLMYKLYGYESLAKMEGGEFKLLSKMFSDEQVTTKAQDFTNAKNELENT	240
Db	181	NQPTKTNFNLMYKLYGYESLAKMEGGEFKLLSKMFSDEQVTTKAQDFTNAKNELEKVT	240
Qy	241	STSLNPKIQAEEKTDYERKKAIFEEIVETQIIITLKTFLKESDLKXSGAMSGIEAEYKYDKD	300
Db	241	STSLNPKIQAEEKTDYERKKAIFEEIVETQIIITLKTFLKESDLKXSGAMSGIEAEYKYDKD	300
Qy	301	NNKLGNEFSTVSQSRPRLNDLVSEKTLARLNDVSSRYNAAIEALNRFIOKYDSIMRDIILGA	360
Db	301	NNKLGNEFSTVSQSRPRLNDVSEKTLARLNDVSSRYNAAIEALNRFIOKYDSIMRDIILGA	360
Qy	361	I 361	
Db	361	I 361	

RESULT 3

QSI5W0_AERSA		
ID	QSI5W0_AERSA	PRELIMINARY; PRT; 361 AA.
AC	QSI5W0;	
DT	15-FEB-2005,	integrated into UniProtKB/TrEMBL.
DT	15-FEB-2005,	sequence version 1.
DE	07-FEB-2006,	entry version 4.
DE	Acrv.	
GN	Name=acrv;	
OS	Aeromonas salmonicida subsp. achromogenes.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;	
OC	Aeromonadaceae; Aeromonas.	
OX	NCBI_TaxID=113288;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=R2.	
RA	Fan W., MacIntyre S.;	
RT	"Cross reactivity of V-antigen from different Aeromonas species.";	
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
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CC	Distributed under the Creative Commons Attribution-NoDerivs License	
CC	-----	
DR	EMBL; AY649421; AAV67430.1; -; Genomic DNA.	
DR	GO; GO:0005576; C:extracellular region; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR005413; LCRV_antigen.	
DR	Pfam; PF04792; Lcrv; 1.	
DR	PRINTS; PR01592; LCRVANTIGEN.	
SQ	SEQUENCE 361 AA; 40164 MW; 7D76B64F86510 CRC64;	

### RESULT 3

```

Q51SW0_AERSA
ID Q51SW0_AERSA PRELIMINARY; PRT; 361 AA.
AC Q51SW0;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acrv.
GN Name=acrv;
OS Aeromonas salmonicida subsp. achromogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
NCBI_TaxID=113288;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R2;
RC Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species." ;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY649421; AAV67430.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; Lcrv; 1.
DR PRINTS; PR01592; LCRVANANTIGEN.
SQ SEQUENCE 361 AA; 40164 MW; 7D76B64F86576510 CRC64;

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	Query Match	99.1%;	Score 1799;	DB 2;	Length 361;
	Best Local Similarity	99.2%;	Pred. No. 6.5e-99;		
	Matches 358;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0
Qy	1	MSIIPDYNTPGAFVGVGLDVOALNTLPGNNKPKLTETLVELLKGKITTISADSSSTALSKEQL	60		
Db	1	MSIIPDYNTPGAFVGVGLDVOALNTLPGNNKPKLTETLVELLKGKITTISADSSSTALSKEQL	60		
Qy	61	EKLLAAAYLTDPASINGGWANGQFKGGDDAAIAATKGVIERGAKOTPPVTHWTITBEFMLLS	120		
Db	61	EKLLAAAYLTDPASINGGWANGQFKGGDDAAIAATKGVIERGAKOTPPVTHWTITBEFMLLS	120		
Qy	121	LSALTWERTDDDLITFTGVWVMFDQNRKGLRDELAEMTAEKLYIGVITQSEINQVLSAAS	180		
Db	121	LSALTWERTDDDLITFTGVWVMFDQNRKGLRDELAEMTAEKLYIGVITQSEINQVLSAAS	180		
Qy	181	NOTFKTNFNLMVDYKLYGYESLAKFMWEGEGFKLLSKMFSDEQVTTAKQODFTNAKKELENVTT	240		
Db	181	NOTFKTNFNLMVDYKLYGYESLAKFMWEGEGFKLLSKMFSDEQVTTAKQODFTNAKKELEKVT	240		

```
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
Db 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
QY 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
Db 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
QY 361 I 361
Db 361 I 361

RESULT 4
Q5ISV8_AERSA
ID Q5ISV8_AERSA PRELIMINARY; PRT; 361 AA.
AC Q5ISV8;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AcrV.
GN Name=acrV;
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R722;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AY649423; AAV67432.1; -; Genomic DNA.
DR GO:0005576; C:extracellular region; IEA.
DR GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SEQUENCE 361 AA; 40210 MW; 7D6AA68109E469E2 CRC64;

Query Match 98.6%; Score 1790; DB 2; Length 361;
Best Local Similarity 98.9%; Pred. No. 2.2e-98;
Matches 357; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTIPDYNTPGAFVGLDQVALNTLPGKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
Db 1 MSTIPDYNTPGAFVGLDQVALNTLPGKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
QY 61 EKLLAAYLTDPASINGGWAMGQFKGGQDAAIAAIGKVIERGAKOTPPVTHWTIPEFMLLS 120
Db 61 EKLLAAYLTDPASINGGWAMGQFKGGQDAAIAAIGKVIERGAKOTPPVTHWTIPEFMLLS 120
QY 121 LSALTMBERTDDLLTTFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMBERTDDLLTTFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240
Db 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
Db 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
QY 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
Db 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
QY 361 I 361
Db 361 I 361

RESULT 6
Q5ISV5_9GAMM
ID Q5ISV5_9GAMM PRELIMINARY; PRT; 374 AA.
AC Q5ISV5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
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Db 361 I 361

RESULT 5
Q5ISV7_9GAMM
ID Q5ISV7_9GAMM PRELIMINARY; PRT; 361 AA.
AC Q5ISV7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE AcrV.
GN Name=acrV;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R735;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AY649424; AAV67433.1; -; Genomic DNA.
DR GO:0005576; C:extracellular region; IEA.
DR GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SEQUENCE 361 AA; 39860 MW; F71CC3A15E644648 CRC64;

Query Match 88.9%; Score 1615; DB 2; Length 361;
Best Local Similarity 88.1%; Pred. No. 5.7e-88;
Matches 318; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSTIPDYNTPGAFVGLDQVALNTLPGKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
Db 1 MSTIPDYNTPGAFVGLDQVALNTLPGKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
QY 61 EKLLAAYLTDPASINGGWAMGQFKGGQDAAIAAIGKVIERGAKOTPPVTHWTIPEFMLLS 120
Db 61 EKLLAAYLTDPASINGGWAMGQFKGGQDAAIAAIGKVIERGAKOTPPVTHWTIPEFMLLS 120
QY 121 LSALTMBERTDDLLTTFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMBERTDDLLTTFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240
Db 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVT 240
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
Db 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGSGMGEIABYKYDKD 300
QY 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
Db 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDLILGA 360
QY 361 I 361
Db 361 I 361

RESULT 6
Q5ISV5_9GAMM
ID Q5ISV5_9GAMM PRELIMINARY; PRT; 374 AA.
AC Q5ISV5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
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DT 15-FEB-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Acrv.
GN Name=acrv;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN [1]_TaxID=114517;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R739;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY649426; AAV67435.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PRO1592; LCRVANTIGEN.
DR SQ SEQUENCE 374 AA; 41603 MW; F284B0914D81BEA8 CRC64;

Query Match 83.3%; Score 1512.5; DB 2; Length 374;
Best Local Similarity 80.7%; Pred. No. 7.4e-82;
Matches 302; Conservative 25; Mismatches 34; Indels 13; Gaps 2;

QY 1 MSTIPDYNTPGAFVGLDQALNTLPGNKPKLTVELLKGKITISADSTALSKEQL 60
DB 1 MSTIPDYNTPGAFVGLDQALDLPGHKPKLTVELLKGKITISADSTALSKEQL 60

QY 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKMIERGAKQTPPVTHWTIPFMLS 120
DB 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKMIERGAKQTPPVTHWTIPFMLS 120

QY 121 LSALTWERTDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
DB 121 LSALTMDRIDDDLIITFTGVMAFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NO-TKTFNFMNDYKLYGYESLAKFMGEGFLLSKMFSDEQVTKAQDFTNAKNELENV- 239
DB 181 SQTFTNFMNDYKLYGYESLAKFMGEGFLLSKMFTNEQVYKKAQDFSEASNLNEII 240

QY 240 -----TSTSLN-PKIQAEAKTDYERKKAIFEEIVETQIITLKTFLFSDLKKSQA 287
DB 241 KNQQRNAGISTGIDINFESYSELQAVYDYSKKAILEQVAKQKITVKEFLESQKKSQA 300

QY 288 MSGIEAEYKYDKNNKGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRPI 347
DB 301 MTNIEASYDKNNKGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRPI 360

QY 348 QKYDSIMRDILGAI 361
DB 361 QKYDSIMRDILGAI 374

RESULT 7
QSISV6_9GAMM PRELIMINARY; PRT; 362 AA.
AC QSISV6;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DE Acrv.
GN Name=acrv;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN [1]
```

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R737;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY649425; AAV67434.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PRO1592; LCRVANTIGEN.
DR SQ SEQUENCE 362 AA; 39991 MW; 0F1A2FFBE93BFF4B CRC64;

Query Match 81.6%; Score 1481.5; DB 2; Length 362;
Best Local Similarity 82.3%; Pred. No. 5e-80;
Matches 298; Conservative 19; Mismatches 44; Indels 1; Gaps 1;

QY 1 MSTIPDYNTPGAFVGLDQALNTLPGNKPKLTVELLKGKITISADSTALSKEQL 60
DB 1 MSTIPDYNTPGAFVGLDQALGALPGHKNPKLTVELLKGKITISADLPTLTKAQL 60

QY 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKMIERGAKQTPPVTHWTIPFMLS 120
DB 61 EKLLAAYLTPDSINGWAAQGFQGGDAAIAAIGKMIERGAKQTPPVTHWTIPFMLS 120

QY 121 LSALTWERTDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
DB 121 LSALTWERIDDDLIITFTGVMAFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NO-TKTFNFMNDYKLYGYESLAKFMGEGFLLSKMFSDEQVTKAQDFTNAKNELENV 239
DB 181 DKPTFTNFMNDYKLYGYESLAKFLDCAEFLLSKMFTDDLQVNAQLEQFTNAKNALEKV 240

QY 240 TSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLFSDLKKSAMSGTEAEYKYDK 299
DB 241 KSASJDSKTLGASAAERKKAANLQIVATQIVTKTFLESQKKSAMENEAESYKK 300

QY 300 DNNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIQKYSIMRDILG 359
DB 301 DDNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIQKYSIMRDILG 360

QY 360 AI 361
DB 361 AI 362

RESULT 8
Q699R0_AERHY PRELIMINARY; PRT; 361 AA.
AC Q699R0;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acrv.
GN Name=acrv;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]_TaxID=644;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpull G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
CC -----
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CC -----
DR EMBL; AY528667; AAS91819.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005413; P:pathogenesis; IEA.
DR Pfam; PF04792; LcrV.1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 361 AA; 40149 MW; FAD8542D4A1C0103 CRC64;

Query Match          76.3%; Score 1386; DB 2; Length 361;
Best Local Similarity 76.2%; Pred. No. 2.4e-74;
Matches 275; Conservative 27; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MSTIPDYNTNPGAFVGMWDVQALNLPKGNPKLTVELLKGKITTISADSSTALSKEQL 60
Db 1 MSVIPDYNSNPAGFVGMGGQAVDTLPCHNNPKLAELLALLEGKITISTDQPTVLSKAQL 60

Qy 61 EKLLAAYLTDPASINGWAMQFGGQDAAIAIKGVIERGAKOTPPVTHWTIPDEFMLLS 120
Db 61 EKLLAKYLTDPATVGTGWSPTDQFLRGQEAATAIKGLIEQEKREPKVTSWTSEFMLLS 120

Qy 121 LSALTMTERTDDLLTFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 FSALTMDRIODDIINVTGVMAFQDNORKKALGNELKDMTAEKLIYGVIOSEINKVLSAAS 180

Qy 181 NOTFTKTNFNLMDYKLYGYESLAKFMEGGFEKLLSKMFSDEQVTKAQODFTNAKNELENVT 240
Db 181 SQFTNTDFNLMDYKLYGYESLAKFMDGAEFKLLSKMFTDVQVKAQQDFTNAKNELEKVK 240

Qy 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKGSGAMSGIEAEYKYDK 300
Db 241 SASLDPKTLEENADYEEKKAIKESVEKQSIIVKSFLESQKSGAMKIEASYSYDKD 300

Qy 301 NNKLGNFSTVSQRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDILGA 360
Db 301 NNKLGNFSTVSQRSRPLNDQVSEKTLRLNDVSSRYNAAEALNRFTQKYDSIMRDILGA 360

Qy 361 I 361
Db 361 I 361

RESULT 9
Q5CC97 AERSO
ID Q5CC97 AERSO PRELIMINARY; PRT; 362 AA.
AC Q5CC97;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acv protein.
GN Name=acv;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150 (2005).
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CC -----
DR EMBL; AJ749609; CAG44558.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR SQ SEQUENCE 361 AA; 40149 MW; FAD8542D4A1C0103 CRC64;

Query Match          65.9%; Score 1196.5; DB 2; Length 312;
Best Local Similarity 67.9%; Pred. No. 3.7e-63;
Matches 245; Conservative 26; Mismatches 41; Indels 49; Gaps 2;
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DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 362 AA; 40549 MW; 54F4C6F476D952F7 CRC64;

Query Match          76.2%; Score 1384.5; DB 2; Length 362;
Best Local Similarity 76.5%; Pred. No. 2.9e-74;
Matches 277; Conservative 29; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MSTIPDYNTNPGAFVGMWDVQALNLPKGNPKLTVELLKGKITTISADSSTALSKEQL 60
Db 1 MSTIPDYNSNAAGFVGMWDGQADALPCHNKLKLNELLTLDDGKITISADKPIPLTREQL 60

Qy 61 EKLLAAYLTDPASINGWAMQFGGQDAAIAIKGVIERGAKOTPPVTHWTIPDEFMLLS 120
Db 61 EKLLAQYLTDPFTVNGSWPTDQFLRGQEAATAIKGLIEQEKREPKVTSWTSEFMLLS 120

Qy 121 LSALTMTERTDDLLTFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMDRIODDIINVTGVMAFQDNORKKALGNELKDMTAEKLIYGVIOSEINKKLSAS 180

Qy 181 NQ-TFTKTNFNLMDYKLYGYESLAKFMEGGFEKLLSKMFSDEQVTKAQODFTNAKNELENV 239
Db 181 DKPTNFNLLDYKLYGYESLAKFMEGGFEKLLSKMFTNVVYNKAQQDFTNAKNELEKV 240

Qy 240 TSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKGSGAMSGIEAEYKYDK 299
Db 241 KSNALDPKILEAAKADYEEKKAIKESVEKQSIIVKAFLESQKSGAMSGIEAEYKYDK 300

Qy 300 DNKLGNFSTVSQRSRPLNDLVSEKTLARLNDVSSRYNAAEALNRFTQKYDSIMRDILG 359
Db 301 DNKLGNFSTVSQRSRPLNDQVSEKTLRLNDVSSRYNAAEALNRFTQKYDSIMRDILG 360

Qy 360 AI 361
Db 361 AI 362

RESULT 10
Q5XL04 AERHY
ID Q5XL04 AERHY PRELIMINARY; PRT; 312 AA.
AC Q5XL04;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acv.
GN Name=acv;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457 (2005).
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CC -----
DR EMBL; AV736311; AAV30233.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 312 AA; 34342 MW; A759ED1E0A7BA07E CRC64;

Query Match          65.9%; Score 1196.5; DB 2; Length 312;
Best Local Similarity 67.9%; Pred. No. 3.7e-63;
Matches 245; Conservative 26; Mismatches 41; Indels 49; Gaps 2;
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QY 1 MSTIPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVELLKGKTTISADSTALSKEOL 60  
 DB 1 MSTIPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVELLKGKTTISADSTALSKEOL 60  
 QY 61 EKLLAAYLTDPASINGWAMQFGKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120  
 DB 61 EKLLAAYLTDPASINGWAMQFGKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120  
 QY 121 LSAWERTDDDLITFTGVMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 180  
 DB 121 LSAWERTDDDLITFTGVMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 180  
 QY 181 NOTFKFNLMYKLYGYESLAKMEGGEFKLLSKMFSDEQVTKAQQDTFNKNELENT 240  
 DB 181 NOTFKFNLMYKLYGYESLAKMEGGEFKLLSKMFSDEQVTKAQQDTFNKNELENT 240  
 QY 241 STSLNPKIOAEAKTDYERKKAIFEIETVQIITLKTFLFESDLKKSGAMSGIEAEYKYDKD 300  
 DB 241 STSLNPKIOAEAKTDYERKKAIFEIETVQIITLKTFLFESDLKKSGAMSGIEAEYKYDKD 300  
 QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTRALNDVSSRYNAIAEALNRFIQKYDSIMRDLGA 360  
 DB 301 NNKLGNFSTVSDRSRPLNDLVSEKTRALNDVSSRYNAIAEALNRFIQKYDSIMRDLGA 360  
 QY 361 I 361  
 DB 312 I 312

RESULT 11  
 Q7NOX1\_PHOLL  
 ID Q7NOX1\_PHOLL PRELIMINARY; PRT; 304 AA.  
 AC Q7NOX1;  
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 11.  
 DE Similar to the virulence-associated V antigen.  
 GN OrderedLocName:plu3758;  
 OS Photorhabdus luminescens subsp. laumondii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Photorhabdus.  
 OX NCBI\_TaxID=141679;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=TT01;  
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;  
 RA Duchaud E., Ruenick C., Frangeul L., Buchrieser C., Givaudan A.,  
 RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,  
 RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,  
 RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,  
 RA Zouine M., Glaeser P., Boemare N., Danchin A., Kunst F.,  
 RT "The genome sequence of the entomopathogenic bacterium Photorhabdus  
 luminescens.";  
 RL Nat. Biotechnol. 21:1307-1313(2003).  
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 CC -----  
 DR EMBL; BX571871; CAE16130.1; -; Genomic DNA.  
 DR Photolias; plu3758;  
 DR BioCyc; PLUM243265:PLU3758-MONOMER; -;  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR005413; LCRV\_antigen.  
 DR Pfam; PF04792; LcrV; 1.  
 DR PRINTS; PR01592; LCRVANTIGEN.  
 KW Complete proteome.  
 SQ SEQUENCE 304 AA; 34067 MW; EC9144A374B02FF1 CRC64;

Query Match 34.4%; Score 625; DB 2; Length 304;  
 Best Local Similarity 41.8%; Pred. No. 3.5e-29;  
 Matches 151; Conservative 47; Mismatches 101; Indels 62; Gaps 6;

QY 4 IPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVELLKGKTTISADSTALSKEOL 61  
 DB 3 IRPYQNDPQLFLADLEKVSQAQGGSSSELDRLNLIIFDKGKITSDSSVVTENKELLK 62  
 QY 62 KLLAAYLTDPASINGWAMQFGKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 121  
 DB 63 KLLAAYLTDPADAVEGGHLDLSQIKNG-----INNESPLNSTLKT-----WTKDFLAHV 113  
 QY 122 SALTWERTDDDLITFTGVMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 181  
 DB 114 FNLTDFRLDDDDIITFTGVMFQDNQKRLRDLAEMTAELKIYGVIOSEINAKLAANGE 173  
 QY 182 QTFKFNLMYKLYGYESLAKMEGGEFKLLSKMFSDEQVTKAQQDTFNKNELENT 240  
 DB 174 LKIDNSFNLLDHHKKYGFSDQPTFEKSAEYKULRKISGSE----- 214  
 QY 241 STSLNPKIOAEAKTDYERKKAIFEIETVQIITLKTFLFESDLKKSGAMSGIEAEYKYDKD 300  
 DB 215 -----ISIKTFLESSNKQSGAMAGLENSYEYDKE 243  
 QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTRALNDVSSRYNAIAEALNRFIQKYDSIMRDLGA 360  
 DB 244 NNRLANFSTVSDRSRPLNNTVQEKTRLNLEASSRYNAIAEALNRFIQKYDSIMRDLGA 303  
 QY 361 I 361  
 DB 304 I 304

RESULT 12  
 Q84GY5\_PHOLU  
 ID Q84GY5\_PHOLU PRELIMINARY; PRT; 325 AA.  
 AC Q84GY5;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
 DE LcrV.  
 GN Name=lcrv;  
 OS Photorhabdus luminescens (Xenorhabdus luminescens).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Photorhabdus.  
 OX NCBI\_TaxID=29488;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=H14;  
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;  
 RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;  
 RT "Genomic islands in Photorhabdus";  
 RL Trends Microbiol. 10:541-545(2002).  
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 CC -----  
 DR EMBL; AY144116; AAO18053.1; -; Genomic DNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR005413; LCRV\_antigen.  
 DR Pfam; PF04792; LcrV; 1.  
 DR PRINTS; PR01592; LCRVANTIGEN.  
 SQ SEQUENCE 325 AA; 36997 MW; E413A4C51615E22C CRC64;

Query Match 33.3%; Score 605.5; DB 2; Length 325;  
 Best Local Similarity 40.8%; Pred. No. 5.4e-28;  
 Matches 155; Conservative 44; Mismatches 102; Indels 79; Gaps 9;

QY 4 IPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVELLKGKTTISADSTALSKEOL 58  
 DB 3 IRPYQNDPQLFLADLEKVSQAQGGSSSELDRLNLIIFDKGKITSDSSVVTENKELLK 62  
 QY 59 -----OLEKLLAAYLTDPASINGWAMQFGKGGQDAIAAIAKGVIERGAKQTP 106  
 DB 63 QVITQDGRDDKGLLKKLIAYFLPANAIVENGHFDQIKNG-----IKNLKSLF-----NSP 113

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Qy 107 PV-THTWIPERMLLSALTMTERTDDDLITTTGVMFQDNQKGLRDELAEMTAELKIY 165
Db 114 TLKTDWLRDPLAAVHFNLTDPRLDDDDVIDFVSMGSHDKKRDRLKELGALTAEIKY 173
Qy 166 GVIOSEINOVLSAASNQ-----TFKTNFNLMYKLYGYESLAKFMEGGFEKLLSKWFSDEQ 221
Db 174 SVIOSEINAKUSAGDKQKLDISISFDLRHKKYGFSDETAFAKDSAEYALLKKMF----- 229
Qy 222 VTQAQODFTNAKNELENVTSLSNPKIOAEAKTDYERKKAIFEIVETQIITTLTKTFLES 281
Db 230 -----PKLE-----ER-----VSIIKFLFESP 245
Qy 282 LKSGAMSGTAEYKYKDNKNLGNFSTVSDDRPLNDLVSEKTLARLNDVSSRYNAAE 341
Db 246 NKQSGAMTGLENSEYEDKNNKLANFSTVNDRVNPLNNTVQEKTTTRLNEASSRYNAAE 305
Qy 342 ALNRFIOKYSIMRDIILGAI 361
Db 306 ALNRFIOKYSIMRNILGAI 325

RESULT 13
Q56896.YEREN
ID Q56896.YEREN PRELIMINARY; PRT; 334 AA.
AC Q56896;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE V antigen (Fragment).
OS Yersinia enterocolitica (type 0:8).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=34054;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTCC;
RA MEDLINE=97162308; PubMed=9009295;
RA Roggenkamp A., Geiger A.M., Leitritz L., Kessler A., Heesemann J.;
RT "Passive immunity to infection with Yersinia spp. mediated by anti-
RT recombinant V antigen is dependent on polymorphism of V antigen.";
RL Infect. Immun. 65:446-451(1997).
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CC -----
CC EMBL; X96797; CAA65589.1; -; Genomic_DNA.
DR SMR; Q56896; 40-331.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
FT NON TER 334.
FT SEQUENCE 334 AA; 38227 MW; 43AC0567D7CCE2FA CRC64;

Query Match 31.4%; Score 570.5; DB 2; Length 334;
Best Local Similarity 38.5%; Pred. No. 6.8e-26;
Matches 141; Conservative 62; Mismatches 108; Indels 55; Gaps 9;

Qy 7 YNTNPGAFVGLDQVQALNTLPGNKNPKLTVELLKG-KITIS-----ADSSALSK-- 57
Db 5 YEONPOHFIEDLEKRVYDQGTGHGSSVLEELVQLVKDKIDISIKYDPKXKDSVFAERVI 64
Qy 58 -----EOLKLLAAYLTDPASINGWAMGQPKGQDAIAIKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSNTQWEL 115
Qy 114 PEFMLLSLSALTMTERTDDDLITTTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVMHFSLTADRIDDDILKIVDSMNHGDAKSLRELAELTAELKIYSVIOAEIN 175
Qy 174 QVLSAASN-QTFKTNFNLMYKLYGYESLAKFMEGGFEKLLSKWFSDEQVTKAQQDTNA 232
Db 176 KHLSSSGTINHEKSNLMDKNLYGYTDEIFKASAEYKILKKM-----POTTIK 225
Qy 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEIVETQIITTLTKTFLESCLKSGAMSGIE 292
Db 226 DDELHEV-----GVITAGA-----EKQIVSIKNFLESENKRTGALGNLK 263
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Db 176 KHLSSSGTINHEKSNLMDKNLYGYTDEIFKASAEYKILKKM-----POTTIK 225
Qy 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEIVETQIITTLTKTFLESCLKSGAMSGIE 292
Db 226 DDELHEV-----GVITAGA-----EKQIVSIKNFLESENKRTGALGNLK 263
Qy 293 AEYKYKDNKNLGNFSTVSDDRPLNDLVSEKTLARLNDVSSRYNAAEALNRFIOKYDS 352
Db 264 DSYNKNKNELSHFATACSKSRPLNDLVSQKTLQSLDITSRENSAIEALNRFIOKYDS 323
Qy 353 IMRDIL 358
Db 324 VMORLL 329

RESULT 14
Q84GT5.YEREN
ID Q84GT5.YEREN PRELIMINARY; PRT; 333 AA.
AC Q84GT5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LcrV.
GN Name=lcrV;
OS Yersinia enterocolitica.
OG Plasmid pYVal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90;
RA Foulter B.G.F., Bernard A., Putnelle B., Cornelis G.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AY150843; AAN37531.1; -; Genomic_DNA.
DR SMR; Q84GT5; 40-331.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
KW Plasmid.
SQ SEQUENCE 333 AA; 38128 MW; CC4067923952FA8F CRC64;

Query Match 31.4%; Score 569.5; DB 2; Length 333;
Best Local Similarity 38.5%; Pred. No. 7.8e-26;
Matches 141; Conservative 61; Mismatches 109; Indels 55; Gaps 9;

Qy 7 YNTNPGAFVGLDQVQALNTLPGNKNPKLTVELLKG-KITIS-----ADSSALSK-- 57
Db 5 YEONPOHFIEDLEKRVYDQGTGHGSSVLEELVQLVKDKIDISIKYDPKXKDSVFAERVI 64
Qy 58 -----EOLKLLAAYLTDPASINGWAMGQPKGQDAIAIAIKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSNTQWEL 115
Qy 114 PEFMLLSLSALTMTERTDDDLITTTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVMHFSLTADRIDDDILKIVDSMNHGDAKSLRELAELTAELKIYSVIOAEIN 175
Qy 174 QVLSAASN-QTFKTNFNLMYKLYGYESLAKFMEGGFEKLLSKWFSDEQVTKAQQDTNA 232
Db 176 KHLSSSGTINHEKSNLMDKNLYGYTDEIFKASAEYKILKKM-----POTTIK 225
Qy 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEIVETQIITTLTKTFLESCLKSGAMSGIE 292
Db 226 DDELHEV-----GVITAGA-----EKQIVSIKNFLESENKRTGALGNLK 263
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 66.6236 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-8  
Perfect score: 1816  
Sequence: 1 MSIPDYNTPGAFVGLDV.....ALNRFTQYDSIMRDLGAI 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /EMC Celerra\_SID33/ptodata/2/iaa/5 COMB.pep.\*
  - 2: /EMC Celerra\_SID33/ptodata/2/iaa/6 COMB.pep.\*
  - 3: /EMC Celerra\_SID33/ptodata/2/iaa/7 COMB.pep.\*
  - 4: /EMC Celerra\_SID33/ptodata/2/iaa/H COMB.pep.\*
  - 5: /EMC Celerra\_SID33/ptodata/2/iaa/PTUS COMB.pep.\*
  - 6: /EMC Celerra\_SID33/ptodata/2/iaa/RE COMB.pep.\*
  - 7: /EMC Celerra\_SID33/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	30.7	329	1	US-08-913-477-2
2	557	30.7	329	1	US-08-913-477-4
3	557	30.7	480	1	US-08-913-477-17
4	557	30.7	501	1	US-08-913-477-23
5	474	26.1	297	2	US-09-252-991A-30058
6	253	13.9	142	2	US-09-248-588-36
7	127	7.0	367	2	US-09-861-451A-46
8	127	7.0	646	2	US-09-543-681A-6840
9	121	6.7	366	2	US-09-716-964B-144
10	120	6.6	630	2	US-09-248-796A-20275
11	119.5	6.6	885	2	US-09-710-279-1660
12	119	6.6	10182	2	US-09-134-001C-3159
13	117.5	6.5	478	2	US-08-772-270A-5
14	117.5	6.5	478	2	US-09-062-126-5
15	117.5	6.5	899	2	US-09-248-796A-19542
16	117	6.4	935	2	US-09-914-259-25
17	115.5	6.4	1211	2	US-09-134-001C-4820
18	114.5	6.3	456	2	US-09-808-701A-24
19	114.5	6.3	810	2	US-09-248-796A-20281
20	113.5	6.2	436	2	US-09-543-681A-4941
21	113.5	6.2	461	1	US-08-392-625-24
22	113.5	6.2	461	1	US-08-466-961A-24
23	113.5	6.2	461	1	US-08-645-193B-26
24	113	6.2	2733	2	US-09-949-016-11433
25	112	6.2	450	2	US-09-248-796A-15183
26	112	6.2	839	2	US-09-758-282B-130

27	112	6.2	839	2	US-09-758-282B-136
28	112	6.2	839	2	US-09-577-304A-130
29	112	6.2	839	2	US-09-577-304A-136
30	112	6.2	1561	2	US-08-894-017-23
31	112	6.2	1561	2	US-09-456-474-23
32	111.5	6.1	2125	2	US-09-919-172-29
33	111	6.1	471	2	US-09-248-796A-18841
34	111	6.1	839	2	US-09-758-282B-118
35	111	6.1	839	2	US-09-758-282B-127
36	111	6.1	839	2	US-09-758-282B-142
37	111	6.1	839	2	US-09-577-304A-118
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40	111	6.1	2662	2	US-09-595-684B-31
41	111	6.1	2663	2	US-09-538-092-1252
42	110.5	6.1	506	2	US-09-328-352-7166
43	110.5	6.1	1111	2	US-09-914-259-28
44	110.5	6.1	1281	2	US-09-902-540-9864
45	110.5	6.1	2704	2	US-09-538-092-1260

#### ALIGNMENTS

#### RESULT 1

US-08-913-477-2  
; Sequence 2, Application US/08913477  
; Patent No. 5985285  
; GENERAL INFORMATION:  
; APPLICANT: Titball, Richard W.  
; APPLICANT: Williamson, Ethel D.  
; APPLICANT: Leary, Sophie E.C.  
; APPLICANT: Oyston, Petra C.F.  
; APPLICANT: Bennett, Alice M.  
; TITLE OF INVENTION: VACCINES FOR PLAGUE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 No. 5985285th Giebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,477  
; FILING DATE: 15-SEP-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/00571  
; FILING DATE: 13-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9505059.7  
; FILING DATE: 13-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9518946.0  
; FILING DATE: 15-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9524825.8  
; FILING DATE: 05-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 124-599  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

Sequence 136, App  
Sequence 130, App  
Sequence 136, App  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 29, Appl  
Sequence 18841, A  
Sequence 118, App  
Sequence 127, App  
Sequence 142, App  
Sequence 118, App  
Sequence 127, App  
Sequence 31, Appl  
Sequence 1252, Ap  
Sequence 7166, Ap  
Sequence 9864, Ap  
Sequence 1260, Ap



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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,477
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00571
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505059.7
; FILING DATE: 13-MAR-1995
; APPLICATION DATA:
; FILING DATE: 15-SEP-1995
; APPLICATION NUMBER: GB 9524825.8
; FILING DATE: 05-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-477-17

Query Match 30.7%; Score 557; DB 1; Length 480;
Best Local Similarity 37.4%; Pred. No. 5.9e-41;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

Qy 7 YNTNPGAFVGLDVQALNTLPGNKNPKLTVELLKGK-ITIS-----ADSSALSK-- 57
Db 159 YEQNPHFIEDLEKVRVEQLTGHSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 218
Qy 58 -----EQLEKLLAAYLTDPASINGCWAMGQFKGGODAAIAIKGVIERGAKOTPPVTHWTI 113
Db 219 TDDIELLKKILAYFLPEDAILKGHYDNLQNG-----IKRVKEPFE-----SSPNTQWEL 269
Qy 114 PEFMLLSLSALTMTERTDDDLITFTTGMVFNQDNRKGLRDLAEMTAELKIYGVIOSEIN 173
Db 270 RAFMAVMHFSLTADRIDDDILKVIDSMNHHGDARSKRLRELAELTAELKIYSVIOAEIN 329
Qy 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQODFTNA 232
Db 330 KHLSSSGTINIHDKSINLMDKNLYGYTDEIFKASAEYKILEKM---PQTT----- 377
Qy 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEIVETOITLTFTLESDLKSGAMSGIE 292
Db 378 -----IQVDSG-----EKKIVSIKDFLGSNKRTGALGNLK 408
Qy 293 AEKYDKDNKNLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAIEALNRFIOKYDS 352
Db 409 NSVSYNKDNHLSHFATTCDSKSRPLNDVSOQTLQSDITSRFSNAIEALNRFIOKYDS 468
Qy 353 IMRDIL 358
Db 469 VMQELL 474
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## RESULT 4

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US-08-913-477-23
; Sequence 23, Application US/08913477
; Patent No. 5985285
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; GENERAL INFORMATION:
; APPLICANT: Titball, Richard W.
; APPLICANT: Williamson, Ethel D.
; APPLICANT: Leary, Sophie E.C.
; APPLICANT: Oyston, Petra C.F.
; APPLICANT: Bennett, Alice M.
; TITLE OF INVENTION: VACCINES FOR PLAGUE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 5985285th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,477
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00571
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505059.7
; FILING DATE: 13-MAR-1995
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9518946.0
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9524825.8
; FILING DATE: 05-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-477-23

Query Match 30.7%; Score 557; DB 1; Length 501;
Best Local Similarity 37.4%; Pred. No. 6.3e-41;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

Qy 7 YNTNPGAFVGLDVQALNTLPGNKNPKLTVELLKGK-ITIS-----ADSSALSK-- 57
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Qy 58 -----EQLEKLLAAYLTDPASINGCWAMGQFKGGODAAIAIKGVIERGAKOTPPVTHWTI 113
Db 240 TDDIELLKKILAYFLPEDAILKGHYDNLQNG-----IKRVKEPFE-----SSPNTQWEL 290
Qy 114 PEFMLLSLSALTMTERTDDDLITFTTGMVFNQDNRKGLRDLAEMTAELKIYGVIOSEIN 173
Db 291 RAFMAVMHFSLTADRIDDDILKVIDSMNHHGDARSKRLRELAELTAELKIYSVIOAEIN 350
Qy 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQODFTNA 232
Db 351 KHLSSSGTINIHDKSINLMDKNLYGYTDEIFKASAEYKILEKM---PQTT----- 398
Qy 233 KNELENTVSTSLNPKIOAEAKTDYERKKAIFEIVETOITLTFTLESDLKSGAMSGIE 292
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Db 399 -----IQVDS-----EKKIVSIKDFLGSNKRKTGALGNLK 429
QY 293 AEKYDKNNKLGNFSTVSDDRPLNDLVSEKTLARLNDVSRYNAAIEALNRFIOKYDS 352
Db 430 NTSYKNNKNNELSHFATTCDSKRPLNDLVSKTQLTSDITSRFSNIAEALNRFIOKYDS 489
QY 353 IMRDIL 358
Db 490 VMQRLL 495

RESULT 5
US-09-252-991A-30058
; Sequence 30058, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30058
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30058

Query Match 26.1%; Score 474; DB 2; Length 297;
Best Local Similarity 36.0%; Pred. No. 6.8e-34;
Matches 118; Conservative 50; Mismatches 94; Indels 66; Gaps 7;

QY 36 ELVELLKGITTSADSGSTALSKEQLEKLLAAVLTDPASINGGWMQFKGGQDAATAATK 95
Db 34 ELALLSRERIVLAHAGPLSEAOVLKALAWLLAANPSAPPG-----QGLEVLR 82
QY 96 GVIERGAKPTPVHTWTITPEFMLLLSALTMERTDDDLITFTGVMMFQDNQKGLRDEL 155
Db 83 EVLQ---ARRQPGAQDLREFLSAYFSL-HGRLEDVIGVKDVLQTDQGRKALLDEL 138
QY 156 AEMTAEKLYGVTSQSEINQVLSAASQTKT-NFNLMVLYGYE-SLAKFMEGGEFKLL 213
Db 139 KALTAEKIVSVTSQSQINAAALSAKQIRIDAGGIDLVDPTLYGAVGDPRWKDSPEYALL 198
QY 214 SKMFSDEQVTKAQQDFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIIT 273
Db 199 SNL-----DTFSCK-----LS 209
QY 274 LKTFLESDLKKGSGMGIIEAYKYDKNNKLGNFSTVSDDRPLNDLVSEKTLARLNDV 333
Db 210 IKDFLSCPSQSGELKGLRDEYFPEKDPNPNVGNFATTVSDRSRPLNDKVNKXTLLINDTS 269
QY 334 SRYNAAIEALNRFIOKYDSIMRDILGAI 361
Db 270 SRYNSAVEALNRFIOKYDSVLRDILSAI 297

RESULT 6
US-09-248-588-36
; Sequence 36, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
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; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Versinia peasis
; PUBLICATION INFORMATION:
; AUTHORS: Hill, J.
; AUTHORS: et al.,
; JOURNAL: Infect. Immun.
; VOLUME: 65
; ISSUE: 11
; PAGES: 4476-
; DATE: (1997)
; US-09-248-588-36

Query Match 13.9%; Score 253; DB 2; Length 142;
Best Local Similarity 33.9%; Pred. No. 9.7e-15;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITTTGVMMFQDNQKGLRDELAEMLTAEKLYGVTSQSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVVDSMNHHGDARSKLRELAELTAEKLYSVIQAEINKHLSSSGTINIHKSLNL 60
QY 191 MDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKGSGMGIIEAYKYDKNNKLGNFSTS 310
Db 94 DGS-----EKKIVSIKDFLGSNKRKTGALGNLKNYSYNKDNNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142

RESULT 7
US-09-861-451A-46
; Sequence 46, Application US/09861451A
; Patent No. 6759516
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific & Industrial Research Orga
; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
; FILE REFERENCE: FF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PP7273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone PAD922
US-09-861-451A-46

Query Match 7.0%; Score 127; DB 2; Length 367;
Best Local Similarity 24.0%; Pred. No. 0.0063;
Matches 63; Conservative 46; Mismatches 90; Indels 64; Gaps 13;

QY 132 DLITTTGVMMFQDNQKGLRDELAEMLTAEKLYGVTSQSEINQVLSA-----ASNQT 183
Db 21 DLEMLEKGNFQDFINFQWSRIEKENLAQISTDKITEAKINEFFNSYLLVFEKLQKL 80
QY 184 FKTENLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENVTSTS 243
Db 81 FSSSYNL-----GYENVAKLYD--YFVEVQKIYRQQAQKQVFEFDRSAKKDYEDQLK-- 130
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; ORGANISM: Candida albicans  
US-09-248-796A-20275  
  
Query Match 6.6%; Score 120; DB 2; Length 630;  
Best Local Similarity 19.9%; Pred. No. 0.059;  
Matches 76; Conservative 63; Mismatches 130; Indels 112; Gaps 13;  
  
QY 29 NKNPKLTVELLKGKTTISADSGTALSKE-----OLEKLLAAYLTDPASIN 75  
DB 124 NQIKELSETIKSLKTELKTSGDALKOSQKEYTLKTNSTELKLEKQLE----- 173  
  
QY 76 GWMAGQFGQGDAAIAAIGVIERG---AKQPPPVTH---WTIPFMLSLSALTMERT 129  
DB 174 ---ELEKVKLDLQTADEKLKGITEREIALKSELETVKNSGLSTTSELAALTATKVKLSLEKE 230  
  
QY 130 DDLITTTFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINOVLSAASNOTFTNFN 189  
DB 231 KEEL-----QFLSGNKSKELEDYQK-----HSDISEKLKALTD----- 264  
  
QY 190 LMDYKLYGYESLAKFMEGGEFKLLSKMPSD--EQVTKAQODFTNAKNELE-NVTSTS--- 243  
DB 265 -----ELKKTQKQFDDSKKLTLENDLTSTKKELETEKTQTSKFK 305  
  
QY 244 -----LNPKIQAERAKTDYERKKAIFBEI--VETQITLTKTFLESDLKKSAMS 289  
DB 306 NLEERKDKETIVKLNKELELLKNDNSGAKKELLEKVKLSKEISEIILSKELED--KKSVMKQ 363  
  
QY 290 GIEAEYKYDKNNKLGNFSTSVSDRSRPLNDLYSE-----KTARLNDVSSRY 336  
DB 364 HDELKQOTKEKNQLOKVTQKDYSTTKLKLDELQKELDAALSFKDXKPFETASAKLTQSTSDL 423  
  
QY 337 NAAIEALNRFQKYDSIMRDI 357  
DB 424 EAANKLNILISEKTEQEL 444

RESULT 11  
US-09-710-279-1660  
; Sequence 1660, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1660  
; LENGTH: 885  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-1660

Query Match 6.6%; Score 119.5; DB 2; Length 885;  
Best Local Similarity 22.1%; Pred. No. 0.11;  
Matches 54; Conservative 62; Mismatches 71; Indels 57; Gaps 14;  
  
QY 124 LTMERTDDDLITTTGVMWF-QDNQR-----KGLRDELAEMTAELKIYGVIOSEINOVLS 177  
DB 17 LSKEMEQSDVIVTVSDIDHTEDNQRLDERNLNHLKSQAEKEGQ-----QAQINQLIQ 69  
  
QY 178 AASNOTFTKTNFLN--MDYKLY-----GYESLAKFMEGGEFKLLSKMPSDQVTKA--QQDF 229  
DB 70 KYKQKQNDYDIEKLNLYELVKATENYEQLS-----GKLVLEERKKNQSEINARVEEEL 124  
  
QY 230 TNAKNELENV-TSTSNPKIQARAKTDYERKKAIFBEIVETQITLTKTFLESDLKKSAM 288

DB 125 DNLESQIDSIKNEKAQNEKLLAEK---NKQQLNKEVQE-----LESLLYIS--- 169  
  
QY 289 SGIEAEYKYDKONNKLGN-FSTSVSDRSRPLNDL-----VSEKTAARLNDVSSRYNAAIE 341  
DB 170 -----DEQHDKELEIKNSYYTLMSEQSDVNDNDRPLEHTINEAKKRLDSR---LVE 221  
  
QY 342 ALNR 345  
DB 222 AFNQ 225  
  
RESULT 12  
US-09-134-001C-3159  
; Sequence 3159, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3159  
; LENGTH: 10182  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3159

Query Match 6.6%; Score 119; DB 2; Length 10182;  
Best Local Similarity 21.0%; Pred. No. 4.7;  
Matches 82; Conservative 65; Mismatches 158; Indels 86; Gaps 17;  
  
QY 24 NTLPGKNP---KLTELVELLKGKI-TISADSSSTAL-----SKEOLEKLLAAYLTDPAS 73  
DB 2756 DVLTNDDKPPASVRRYNEAISNIRKELDTAKADASSTLRNTNFSVEQVRDALNKINTVQPK 2815  
  
QY 74 INGWAMGQFGQGDAAIAAIGVIE--RGAKQTPPVTHWTIPEFMLSLSALTMERTDD 131  
DB 2816 VNQAIALLPQKENNELVQAKKRLQDAVNDIPQTQGMTQTTNNYN-----DKQREAE 2868  
  
QY 132 DLITTTFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINOVLSAASNOTFTKTNFLM 191  
DB 2869 RALTSAQRVI---DNGDATTO-----EITSE-----KSKVQEQAMQALNTA--KSNLRAD 2912  
  
QY 192 DYKLY-GYESLAKFMEGGEFKLLSKMPSDEQVTKAQODFTNAKNELENTVSTSLNPKIQ 250  
DB 2913 KNELOTAYNKLJENVSTNGKKPASIROYETAKARIQNQINDAKNEAERILGND-NPQV-S 2970  
  
QY 251 EAKTYERKKAIFEEIVE-----TQIITLTKTFLESDLKKSAMSGI----- 291  
DB 2971 QVTOALNKIKAIQPKLITEAINLQNKENNTLVAKNRLENAVNDTDPHGTQETINNY 3030  
  
QY 292 -----EAELYKYDKNNKLGNFSTSVSDRS-----RPLNDLVSEKTLRNDV 332  
DB 3031 NAKKREAOQNEIOKANMINNGDATQADISSEKSKVEQVLQALQNAKNDRADK-----REL 3086  
  
QY 333 SSRYNAAIEALN-----RFIOKYDSIMRDI 357  
DB 3087 QYAYNKLQNVNTNGKKPSSIQNYKSARRNI 3117

RESULT 13  
US-08-772-270A-5  
; Sequence 5, Application US/08772270A  
; Patent No. 6019984  
; GENERAL INFORMATION:  
; APPLICANT: Macinnes, Janet  
; APPLICANT: Ricciatti, Paul



[illegible]

Search completed: June 16, 2006, 19:28:54  
Job time : 68.6236 secs



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 201.925 Seconds  
(without alignments)  
828.131 Million cell updates/sec

Title: US-10-813-908A-8  
Perfect score: 1816  
Sequence: 1 MSTIPDYNTNPGAFVGLDV.....ALNRFIOKYSIMRDLGAI 361

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA Main.\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pbp.\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pbp.\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pbp.\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pbp.\*
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  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	5	US-10-813-908-8
2	557	30.7	326	5	US-10-987-533-1
3	253	13.9	142	3	US-09-930-915A-11
4	253	13.9	142	4	US-10-082-014-33
5	253	13.9	142	4	US-10-372-076-34
6	253	13.9	142	4	US-10-732-862A-48
7	253	13.9	142	4	US-10-806-006-11
8	253	13.9	142	4	US-10-677-074-34
9	253	13.9	142	4	US-10-805-913-11
10	132	7.3	506	4	US-10-424-539-238728
11	129	7.1	459	4	US-10-702-305A-18
12	129	7.1	1404	5	US-10-732-923-3304
13	129	7.1	2013	6	US-11-097-143-13758
14	128.5	7.1	1939	5	US-10-732-923-3340
15	127	7.0	367	3	US-09-861-451A-46
16	127	7.0	2539	5	US-10-831-070-6
17	125	6.9	643	4	US-10-282-122A-68817
18	121.5	6.7	1196	4	US-10-282-122A-52737
19	121	6.7	366	3	US-09-906-179A-179
20	121	6.7	366	4	US-10-671-403-144
21	121	6.7	366	4	US-10-671-419-144
22	121	6.7	366	4	US-10-670-844-144
23	121	6.7	366	4	US-10-671-134-144
24	121	6.7	366	4	US-10-673-098-144
25	121	6.7	366	4	US-10-672-638-144
26	121	6.7	366	4	US-10-673-127-144
27	121	6.7	366	4	US-10-670-817-144

28	121	6.7	366	4	US-10-673-119-144	Sequence 144, App
29	121	6.7	366	4	US-10-671-207-144	Sequence 144, App
30	121	6.7	366	5	US-10-673-120-144	Sequence 144, App
31	121	6.7	366	5	US-10-671-412-144	Sequence 144, App
32	121	6.7	366	5	US-10-671-859-144	Sequence 144, App
33	121	6.7	366	5	US-10-671-106-144	Sequence 144, App
34	121	6.7	366	4	US-10-282-122A-76864	Sequence 76864, A
35	121	6.7	832	3	US-09-864-636A-446	Sequence 446, App
36	121	6.7	832	3	US-09-864-426A-446	Sequence 446, App
37	121	6.7	832	4	US-10-084-839-446	Sequence 446, App
38	120.5	6.6	980	4	US-10-211-462-145	Sequence 145, App
39	120.5	6.6	989	5	US-10-821-234-975	Sequence 975, App
40	120	6.6	835	3	US-09-864-636A-450	Sequence 450, App
41	120	6.6	835	3	US-09-864-426A-450	Sequence 450, App
42	120	6.6	835	4	US-10-084-839-450	Sequence 450, App
43	120	6.6	1095	4	US-10-128-714-3039	Sequence 3039, Ap
44	120	6.6	1277	4	US-10-128-714-8039	Sequence 8039, Ap
45	119.5	6.6	815	4	US-10-437-963-191043	Sequence 191043,

ALIGNMENTS

RESULT 1

US-10-813-908-8  
; Sequence 8, Application US/10813908  
; Publication No. US20050058662A1  
; GENERAL INFORMATION:  
; APPLICANT: Frey, Joachim Stuber  
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and  
; FILE REFERENCE: MIC01/2315/WO  
; CURRENT APPLICATION NUMBER: US/10/813,908  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US/10/416,902  
; PRIOR FILING DATE: 2003-05-15  
; PRIOR APPLICATION NUMBER: PCT/CA01/01589  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Aeromonas salmonicida  
; US-10-813-908-8

Query Match		100.0%;	Score 1816;	DB 5;	Length 361;
Best Local Similarity		100.0%;	Pred. No. 2.1e-131;		
Matches 361;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	MSTIPDYNTNPGAFVGLDV	VOALNTLPGNKNPKLT	TELVELLKGKITT	SADSSSTALSKEQL 60
Db	1	MSTIPDYNTNPGAFVGLDV	VOALNTLPGNKNPKLT	TELVELLKGKITT	SADSSSTALSKEQL 60
Qy	61	EKLLAAYLTDPASINGWANGQKGGODAAIAA	KGVIERGAKOTPPVTHWT	PEFMLLS 120	
Db	61	EKLLAAYLTDPASINGWANGQKGGODAAIAA	KGVIERGAKOTPPVTHWT	PEFMLLS 120	
Qy	121	LSALTWERTDDDLITFTGVMMFQDNQKRLRDELA	EMTAEKLYGVIQSEINOVLSAAS 180		
Db	121	LSALTWERTDDDLITFTGVMMFQDNQKRLRDELA	EMTAEKLYGVIQSEINOVLSAAS 180		
Qy	181	NOTFKTNFNLMYKLYGYESLAKFMEGGEPKLLSKN	FMDSQVTKAQODFTNAKNELENTV 240		
Db	181	NOTFKTNFNLMYKLYGYESLAKFMEGGEPKLLSKN	FMDSQVTKAQODFTNAKNELENTV 240		
Qy	241	STSLNPKIOAEAKTDYERKKAIFEETIVETQITL	KTFLESDLKSGGMSGIEAEYKYDKD 300		
Db	241	STSLNPKIOAEAKTDYERKKAIFEETIVETQITL	KTFLESDLKSGGMSGIEAEYKYDKD 300		
Qy	301	NNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSR	RYNAALAEALNRFIOKYDYSIMRDLTGA 360		
Db	301	NNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSR	RYNAALAEALNRFIOKYDYSIMRDLTGA 360		

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QY 361 I 361
Db 361 I 361

RESULT 2
US-10-987-533-1
; Sequence 1, Application US/10987533
; Publication No. US20050220797A1
; GENERAL INFORMATION:
; APPLICANT: Chanh, Tran C.
; APPLICANT: Andrews, Gerard P.
; APPLICANT: Adamovics, Jeffrey J.
; APPLICANT: Powell, Bradford S.
; TITLE OF INVENTION: Prophylactic and Therapeutic Monoclonal Antibodies
; FILE REFERENCE: 003/307/SAP
; CURRENT APPLICATION NUMBER: US/10/987,533
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/519,384
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Yersinia Pestis
; FEATURE:
; OTHER INFORMATION: V antigen
US-10-987-533-1

Query Match 30.7%; Score 557; DB 5; Length 326;
Best Local Similarity 37.4%; Pred. No. 1.7e-34;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFWGLDVQALNTLPGNNPKLTVELLKGK-ITIS-----ADSTALSK-- 57
Db 5 YEQNPOHFIEDLEKVRVEQLTGHSSVLELVQVKDKNIDISIKYDPRKDSVFANRVI 64
QY 58 ----EOLKLLAVALTPASINGWAMGQFKGQDAAIAAIGKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKTLAYLPEDALLKGGHVDNLQNG-----IKRVKFLF-----SSPQWEL 115
QY 114 PEFMLLSLALTMTERTDDDLITTTGVMFMFQDNQRKGLRDLAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVHFSLTADRIDDDILKIVDSMNHGHDARSKLREELAEELTAELKIYSVIOAEIN 175
QY 174 QVLASAAN-QTFKTNFNMDYKLYGYESLAKFMWEGGFEKLLSKMFSDEQVTKAQODFTNA 232
Db 176 KHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 223
QY 233 KNELENVTSTSLNPKIOAEAKTDYERKKAIFEIVETQIITLKTFLFESDLKSKGAMSGIE 292
Db 224 -----IQVDS-----EKKIVSIKDFLGSNKRTGALGNL 254
QY 293 AEYKDKNNKLNKFNSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAALRFRIOKYS 352
Db 255 NSYSYKNNKNNELSHFATTCDSKSRPLNDLVSKTTLQSDITSRFNSAIEALNRFIOKYS 314
QY 353 IMRDIL 358
Db 315 VMQRLL 320

RESULT 3
US-09-930-915A-11
; Sequence 11, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
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; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-09-930-915A-11

Query Match 13.9%; Score 253; DB 3; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITTTGVMFMFQDNQRKGLRDLAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVDSMNHGHDARSKLREELAEELTAELKIYSVIOAEINKHLSSSGTINIHDKSINL 60
QY 191 MDYKLYGYESLAKFMWEGGFEKLLSKMFSDEQVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEIVETQIITLKTFLFESDLKSKGAMSGIEAEYKYDKNNKLNKFNST 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNKNSYSYNKNNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142

RESULT 4
US-10-082-014-33
; Sequence 33, Application US/10082014
; Publication No. US2003018585A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C-
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-082-014-33

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITTTGVMFMFQDNQRKGLRDLAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVDSMNHGHDARSKLREELAEELTAELKIYSVIOAEINKHLSSSGTINIHDKSINL 60
QY 191 MDYKLYGYESLAKFMWEGGFEKLLSKMFSDEQVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEIVETQIITLKTFLFESDLKSKGAMSGIEAEYKYDKNNKLNKFNST 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNKNSYSYNKNNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142
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US-10-372-076-34  
RESULT 5  
; Sequence 34, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS  
; FILE REFERENCE: 4564/87179  
; CURRENT APPLICATION NUMBER: US/10/372,076  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 10/080,299  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 10/082,014  
; PRIOR FILING DATE: 2002-02-22  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-372-076-34  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-372-076-34  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-372-076-34  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-372-076-34

US-10-732-862A-48  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-806-006-11  
RESULT 7  
US-10-806-006-11  
; Sequence 11, Application US/10806006  
; Publication No. US20040152876A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED  
; TITLE OF INVENTION: STABILITY  
; FILE REFERENCE: 4564/91644 ICC-102.2 DV I  
; CURRENT APPLICATION NUMBER: US/10/806,006  
; CURRENT FILING DATE: 2004-03-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: PCT/US01/41759  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/226,867  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,843  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-806-006-11  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-806-006-11  
Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
Qy 132 DLITFTGVMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEALTAELKIYSVIOAEINKHLSSTGTTINIHDKSINL 60  
Qy 191 MDYKLYGYESLAKFMEGEFKLLSKMFSDEOVTKAQODFTNAKNELENTVSTSLNPKIOA 250  
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEABYKYDKONNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139  
Qy 311 VSD 313  
Db 140 CSD 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-677-074-34  
RESULT 8  
US-10-677-074-34

; Sequence 34, Application US/10677074  
; Publication No. US20040156863A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Schmidt, Annette Elisabeth  
; APPLICANT: Stober, Detlef  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS  
; FILE REFERENCE: 4564/87179  
; CURRENT APPLICATION NUMBER: US/10/677,074  
; CURRENT FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: 10/372,076  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 10/080,299  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 10/082,014  
; PRIOR FILING DATE: 2002-02-22  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-677-074-34

Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
  
Qy 132 DLITFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHCDAKRLRELAELTAELKIYSVIOAEINKHLSSSGTINTHDKSINL 60  
  
Qy 191 MDYKLYGESLAKPMEGEFLKLSKMFSDQVTKAQOFTNAKNELENVTSTSLNPKIQ 250  
Db 61 MDKNLYGTYDEEIFKASAEYKILEKM---PQTT-----IQV 93  
  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKXGMSGIEAEYKYDKNNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKDNLSHPATT 139  
  
Qy 311 VSD 313  
Db 140 CSD 142

RESULT 9  
US-10-805-913-11  
; Sequence 11, Application US/10805913  
; Publication No. US20040156864A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED  
; TITLE OF INVENTION: STABILITY  
; FILE REFERENCE: 4564/91645 ICC-102.2 DV II  
; CURRENT APPLICATION NUMBER: US/10/805,913  
; CURRENT FILING DATE: 2004-03-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: PCT/US01/41759  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/226,867  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,843  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Yersinia pestis  
US-10-805-913-11

Query Match 13.9%; Score 253; DB 4; Length 142;  
Best Local Similarity 33.9%; Pred. No. 1.4e-11;  
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;  
  
Qy 132 DLITFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190  
Db 1 DILKVIIVDSNMNHCDAKRLRELAELTAELKIYSVIOAEINKHLSSSGTINTHDKSINL 60  
  
Qy 191 MDYKLYGESLAKPMEGEFLKLSKMFSDQVTKAQOFTNAKNELENVTSTSLNPKIQ 250  
Db 61 MDKNLYGTYDEEIFKASAEYKILEKM---PQTT-----IQV 93  
  
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKXGMSGIEAEYKYDKNNKLGNFSTS 310  
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKDNLSHPATT 139  
  
Qy 311 VSD 313  
Db 140 CSD 142

RESULT 10  
US-10-424-599-238728  
; Sequence 238728, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 238728  
; LENGTH: 506  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(506)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_57597C.1.pep  
US-10-424-599-238728

Query Match 7.3%; Score 132; DB 4; Length 506;  
Best Local Similarity 23.1%; Pred. No. 0.17;  
Matches 85; Conservative 73; Mismatches 132; Indels 78; Gaps 18;  
  
Qy 33 KLTELVELLKGKITISADSSTALSKEQLEKLLAA-----YLTDPASINGWGMQFGK 85  
Db 30 KYSELESVLEAEKYSQNSLNOIS--TLEEKGASEGQANKYLDVDSNUTS--ELEAIQA 85  
  
Qy 86 QODAAIAAKGVIERGAKQTPVTHWTIPEFMLLSLSLTMBRTD--DDLITFTGYMMFQ 144  
Db 86 RASTLETTLQAANERKGELED-----SLNAVTEKKNELEDASISLNKLAEK 132  
  
Qy 145 DNQRKGLRDE-----LAEMTAELKIYGVIOSEINQVLSAASNQTF-----KTNFNL 190  
Db 133 ENLLEILRDDNLNTQDKLQSTEDLREAEFLRESEIEIKLKASEENLWVRGRDIEETAARH 192  
  
Qy 191 MDYKLYGESLA-----KFMEGE-----FKLLSKM-FSDEQVTKAQOFTNAKNE 235  
Db 193 SELQLL-HESLTRDSEQKFOEAIEKFNKNDSEVQSLLEKIKILEQIAKAGEQSTLKNE 251  
  
Qy 236 LENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKXGMSGIEAEY 295  
Db 252 FEE-----SLSKLASLESENEIDLKRG-----ILEAESKSSQSPSENELLVG---TNIQLKT 299

QY 296 KYDKNNKLGNFSTSVDRSRPLNDLVSEKTA--RLNDV---SSRYNAIAEALNRFIOKY 350  
Db 300 KIDELEESLNH---ALSEKEAAAQELVSHKNSITSLNDLQSKSSEIQCANEAAL---ILKV 353  
QY 351 DSIMRDIL 358  
Db 354 ESQLEAL 361

## RESULT 11

US-10-702-305A-18  
; Sequence 18, Application US/10702305A  
; Publication No. US20040213803A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael C. Chen  
; APPLICANT: Chung-Jiun Chiou  
; APPLICANT: Zhongming Li  
; APPLICANT: Dong-Sheng Chen  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR  
; TITLE OF INVENTION: PREVENTING PNEUMOCOCCAL INFECTION  
; FILE REFERENCE: 12844-002001  
; CURRENT APPLICATION NUMBER: US/10/702,305A  
; CURRENT FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: US 60/424,497  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence  
US-10-702-305A-18

Query Match  
Best Local Similarity 22.7%; Pred. No. 0.25; Length 459;  
Matches 80; Conservative 63; Mismatches 127; Indels 82; Gaps 15;  
QY 19 DVQALNTLPGNKPKLTTEL-VLLKGGKITISADSSSTALSKEQ---LEKLLAAYLTDP--- 71  
Db 154 DYATLKVALAKVEAKELEIEKLQYEIS-LEQEVAlAQHQVNLNKKLAG--ADPDG 210  
QY 72 -----ASINGWANGQFGGQDAALAAIKGVIERGAKOTPPVTHWTIPEFMLLSALTM 126  
Db 211 TKVTEAKLN-----KGEALNAKQAEALAKKQTELEKLLSLD--PE 249  
QY 127 ERTDDDLITFTGVMMFODNOKGLRDELAEMLTAELKIYGVIOSEINQVLSAASNQTFKT 186  
Db 250 GKTDQLDKKAAEAEL--DKKADLQNKVADLEKGIAPYQIKVAELNKEITA-----RL 300  
QY 187 NFNLMYKLYGYESLAKFMGEGFKLLSK---MFSDEQVTKAQDFTNAKNELENTVST 242  
Db 301 QSDLKDAEENNVEDIK--EGLEQAIADKKAELATTQKNIDKTQKDLDAELEKELVAT 358  
QY 243 SLNPKIOAEAKTYDERKKAIFEEIVEQIITLK-----TFLESCLKSGMAGSIE 292  
Db 359 -LDPEGTQDELKAEAEADANIERALQNKVADLNKVAELDKVEVRLQSDLK-----D 409  
QY 293 AEYKYDKNNKLGNFSTSVDRSRPLNDLVSEKTAARLNDVSSRYNAIAEALN 344  
Db 410 AEENNVEDYKEG-----LDKALTDKKVNLNTQKALDTAQKALD 449

## RESULT 12

US-10-732-923-3304  
; Sequence 3304, Application US/10732923  
; Publication No. US2005010879A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 3304  
; LENGTH: 1404  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-10-732-923-3304

Query Match  
Best Local Similarity 22.6%; Pred. No. 1.2; Length 1404;  
Matches 88; Conservative 57; Mismatches 136; Indels 108; Gaps 18;  
QY 29 NKNPKLTVELLKKG-----ITISADSSSTALSKEQ-LEKLLAAYLTDPASING----- 76  
Db 598 NTNPNYATLIQKLOAKLDKNSITKSSNKSIDIATNQALQALAEKTEKESANSQNAV 657  
QY 77 ----GWANGQPK-----GGQDAALAAIKGVIERGAKOTPPVTHWTIPEFMLLSLS 122  
Db 658 KNTLNETIGKAKELDKNLTDSDGEIQQAKAELTNEIEK-ANQT-----IASNN 704  
QY 123 ALTWERTDDDLITFTGVMMFQD---NORKGLRDELAEMTAELKIYGVIOSEINQVLSAA 179  
Db 705 TALMENSNTSLNKISEVQNKLDKFNNDKKAEFNKLOE-----LNKIDDFEKN 754  
QY 180 SNOTFKTNFN---LMDYKLYGYESLAKFMGEGFK-----LLSKMFSDEQ 221  
Db 755 KNEIYKFNLDLDELINKSVQIKNSLGSINSSNKKDIVDANKKQDALNELQAKM--AEI 812  
QY 222 VTKAQDFTNAKNELENTVSTSLNPKIOAEAKTYDERKKAIFEEIVEQIITLKTFLES 281  
Db 813 HKKTFQEFNEHKNELENL---IKKEDAKEVGTD-EANTAI-----TNND 852  
QY 282 LKXSGAMSGI-----EAERYKYD-KNNKLGNFSTSVDRSRPLNDLVSEKTAARLNDV 332  
Db 853 VKENSIEETTKATKALDEAKSLDKQKINTQKATELSLNESEKELANNLI---TSSNQV 909  
QY 333 S-----SRYNAAIEALNRFIOKYSIMRDI 357  
Db 910 SAEISKAKKVLBEINNLNLNNDSSIKSL 938

## RESULT 13

US-11-097-143-13758  
; Sequence 13758, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13758

; LENGTH: 2013

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-13758

Query Match

Best Local Similarity 7.1%; Score 129; DB 6; Length 2013;

Matches 83; Conservative 78; Mismatches 138; Indels 94; Gaps 17;

Qy 33 KLTELVELLKGKI-----TISADSTSLKSEQLKLAAYLTDPASINGWAMQFGQGD 88

Db 1251 KLNQLLNAAKDELHDVRRIKDDEISALRMEFLLIQIETNEKENQAKFYA--ELQETKDRYE 1308

Qy 89 AATAAKGVTERGAKQTPPTHWTIPFMLL-----SLSALTWERTDDDLITFTGVMM 142

Db 1309 SNVAELKEKLQVEETLSSVTVRCAELEALKSAHNENISQAVEER--NNLIVQHOAEM- 1365

Qy 143 FQNRQKGLRDLAE-MTAEKIVGVIOSEINOVLSAASNOTFTKN-----FNLMDYK 194

Db 1366 --ETIRETLKNKLAESTQSKMEDAFRAINEVRATLMEQLNOTKEDRDKGASKLEEVK 1423

Qy 195 LYGVESLAKPMEGEFKLLSKMFSDEQVTKAQQDF-----TNAKNEL 236

Db 1424 ---KTLQWINGG--RVMSDTIAELEKTKAEQDLAVNKLTKDNIELEKQCSKTQBOLOM 1477

Qy 237 ENVTSTSLNPKIOAEAK-----TDYERKKAI-FEEIVETQIITL-----KTFLESDLKK 284

Db 1478 ESLTRDQISFEIHAHTKKLELIVASSKKRIIELEKCDQOQVLELDKCRLEKLSLESEIQ 1537

Qy 285 SGA-----MSGIEAEYKYDKN-----KLGNFSTSVSRSRPL-----318

Db 1538 ANSEHSCTMKELQLOAEKVLNREKEKCDFTKLETFTKITLDEEVILKEAOKHVL 1597

Qy 319 -NDLVSEK-----TARLNDVSSRYNAEALN 344

Db 1598 YDDLVSQHERLKICLAEANELSSNLQKVMSLH 1630

RESULT 14

US-10-732-923-3340

; Sequence 3340, Application US/10732923

; Publication No. US20050108791A1

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149

; SEQ ID NO 3340

; LENGTH: 1939

; TYPE: PRT

; ORGANISM: Plasmodium chabaudi

US-10-732-923-3340

Query Match

Best Local Similarity 7.1%; Score 128.5; DB 5; Length 1939;

Matches 59; Conservative 46; Mismatches 103; Indels 63; Gaps 11;

Qy 119 LLSALTWERTDDDLITFTGVMMFQDNQKGLRDELAEMTAEKIVGVIOSEINQVLSA 178

Db 193 MSLDKLTCE-----VOEKDNLEK-INKKVIEKENNLRELKFMKERNIEIES 239

Qy 179 ASNOTFKTNFNLMDYKLYGVESLAKFMEGEFKLLSKMFSDEQVTKAQQDFTN--AKNEL 236

Db 240 LDG-TINDKKNAYEKLKLEISFEERKKMIEMLDLSKLEK-----EENFANKQAKLEK 288

Qy 237 ENVTSTSLNPKIOAEAKTDYERKKAI-FEEIVETQIITLKTFLSDDLKSGMMSGI-----291

Db 289 ENELIIIEKLKDIESREK-DFKSKKEKFAS-MENELNTLK-----SDLSKNACQMEVYKLEI 342

Qy 292 -----EAEYKYDKNNKLGNFSTSVSDR-----SRPLNDLYSEKT 326

Db 343 KOLSQSLVEKEREIFEIKNEYDDKINNKKKUSSINDKIGDINTVLHSEBEKINKLLKEKE 402

Qy 327 ARLNDVSSRYNAEAL-NRFIOKYDSIMRD 356

Db 403 TELNEIHKYKNLEIETIKNELNEKEELEEKN 433

RESULT 15

US-09-861-451A-46

; Sequence 46, Application US/09861451A

; Patent No. US20020068289A1

; GENERAL INFORMATION:

; APPLICANT: Commonwealth Scientific & Industrial Research Orga

; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences

; FILE REFERENCE: PF34033/01

; CURRENT APPLICATION NUMBER: US/09/861,451A

; CURRENT FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: PF7273

; PRIOR FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 46

; LENGTH: 367

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein

; OTHER INFORMATION: sequence from clone PAD922

US-09-861-451A-46

Query Match

Best Local Similarity 7.0%; Score 127; DB 3; Length 367;

Matches 63; Conservative 24.0%; Pred. No. 0.26;

Mismatches 46; Mismatches 90; Indels 64; Gaps 13;

Qy 132 DLITFTGVMMFQD--NORKGLRDELAEMTAEKIVGVIOSEINQVLSA-----ASNQT 183

Db 21 DLEMLEKGNFEFQDFINFQWSRIEKIEENLAQLSTDKITEAKINEFFNSLYLFEKLOKL 80

Qy 184 FKTNFNLMDYKLYGVESLAKFMEGGEFFKLLSKMFSDEQVTKAQQDFTNARNELENTSTS 243

Db 81 FSSSYNL-----GYENVAKLYD--YFYEYQKIYRQKQAKVEFDYRSAKKDVEDQLK-- 130

Qy 244 LNPKIQAEAKTDYERKKAI-FEEIVETQIITLKTFLSDDLKSGMMSGI-----EAEYKY 297

Db 131 ---KIKQE-----KAFFIKTLNVKALNLKKEAQLEIDKDKFTAQHNLLTSYIDFNFYEY 179

Qy 298 DXDNKK-----LGNFS-----TSVSDRSRPLNDLVSEKT--ARLNDVSSRYN 337

Db 180 KIANNKALVTTLQKNYSPFKQAIINKEIAKFLDRR---NILLEKNLFSFLN--ISEIE 234

Qy 338 AAIEALNRF----IQYDSIMRD 356

Db 235 KLFEIMNPFKKSQIEKYKSLTFD 257

Search completed: June 16, 2006, 20:24:51

Job time : 203.925 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 15.5553 Seconds  
(without alignments)  
523.484 Million cell updates/sec

Title: US-10-813-908A-8  
Perfect score: 1816  
Sequence: 1 MSTIPDYNTNPGAFVGLDV.....ALNRFIOKYDSIMRDLGAI 361

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pbp:\*  
2: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pbp:\*  
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8: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pbp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.5	6.6	980	7	US-11-289-102-296
2	117.5	6.5	9535	6	US-10-471-571A-4496
3	113.5	6.2	515	6	US-10-953-349-17060
4	113.5	6.2	541	6	US-10-953-349-17059
5	109	6.0	2478	6	US-10-471-571A-2278
6	107.5	5.9	720	6	US-10-449-902-51542
7	106.5	5.9	1169	6	US-10-527-411-20
8	106	5.8	686	6	US-10-449-902-45659
9	105	5.8	2871	6	US-10-505-928-100
10	104.5	5.8	972	6	US-10-480-962-4
11	104.5	5.8	1234	7	US-11-327-900-6
12	104	5.7	578	6	US-10-471-571A-1920
13	103.5	5.7	1224	6	US-10-449-902-41406
14	103	5.7	872	6	US-10-449-902-53872
15	103	5.7	971	6	US-10-449-902-45697
16	102	5.6	888	6	US-10-527-411-112
17	102	5.6	1056	6	US-10-449-902-45516
18	101.5	5.6	432	6	US-10-449-902-50904
19	101.5	5.6	677	7	US-11-165-586-44
20	101.5	5.6	844	6	US-10-449-902-56744
21	101.5	5.6	880	6	US-10-449-902-56394
22	101	5.6	311	6	US-10-953-349-17061
23	100.5	5.5	491	6	US-10-449-902-44584
24	100.5	5.5	561	6	US-10-953-349-20041
25	99.5	5.5	432	6	US-10-449-902-31206

26	99	5.5	466	6	US-10-953-349-33042	Sequence 33042, A
27	99	5.5	496	6	US-10-953-349-33041	Sequence 33041, A
28	99	5.5	562	6	US-10-953-349-33040	Sequence 33040, A
29	99	5.5	858	6	US-10-527-411-22	Sequence 22, Appl
30	99	5.5	860	6	US-10-527-411-175	Sequence 175, Appl
31	99	5.5	862	6	US-10-527-411-94	Sequence 94, Appl
32	99	5.5	862	6	US-10-527-411-171	Sequence 171, Appl
33	99	5.5	862	6	US-10-527-411-173	Sequence 173, Appl
34	99	5.5	864	6	US-10-527-411-102	Sequence 102, Appl
35	99	5.5	865	6	US-10-527-411-100	Sequence 100, Appl
36	99	5.5	866	6	US-10-527-411-88	Sequence 88, Appl
37	99	5.5	866	6	US-10-527-411-104	Sequence 104, Appl
38	99	5.5	867	6	US-10-527-411-80	Sequence 80, Appl
39	99	5.5	867	6	US-10-527-411-96	Sequence 96, Appl
40	99	5.5	867	6	US-10-527-411-98	Sequence 98, Appl
41	99	5.5	870	6	US-10-527-411-92	Sequence 92, Appl
42	99	5.5	871	6	US-10-527-411-84	Sequence 84, Appl
43	99	5.5	871	6	US-10-527-411-86	Sequence 86, Appl
44	99	5.5	871	6	US-10-527-411-90	Sequence 90, Appl
45	99	5.5	876	6	US-10-527-411-82	Sequence 82, Appl

## ALIGNMENTS

## RESULT 1

US-11-289-102-296  
; Sequence 296, Application US/11289102  
; Publication No. US20060121511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Hyerim  
; APPLICANT: Shaw, Peter M.  
; APPLICANT: Clark, Edwin  
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO MICROBUTULE-STABILIZING AGENTS  
; FILE REFERENCE: 10338 NP  
; CURRENT APPLICATION NUMBER: US/11/289,102  
; CURRENT FILING DATE: 2005-11-29  
; PRIOR APPLICATION NUMBER: US 60/631,993  
; PRIOR FILING DATE: 2004-11-30  
; NUMBER OF SEQ ID NOS: 395  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 296  
; LENGTH: 980  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-289-102-296

Query Match	6.6%	Score 120.5;	DB 7;	Length 980;
Best Local Similarity	20.2%	Pred. No. 1.1;		
Matches	79;	Conservative	67;	Mismatches 151; Indels 95; Gaps 16;
QY	36	ELVELLKGKITISADSTALSKEOLEKLAAYLTDPASINGWAMGQFGQDAAIAIK	95	
Db	347	DLUSLQAKVA-----SLTHNKLQDKLQA---KSPKEAEADLSFDSYHSTQ-----TDLG	395	
QY	96	GVIERGAKQPPVTHWTIPFELLSLSALMTERTDD-----LITTFGVMMFDNQ	147	
Db	396	PSLGKPGCTSPDPK-SSPSVLHSLGKST---TDNVRIOQLQOEILQKRLSEAE	451	
QY	148	RKGLRDLAMTAEKLYGVIOSEINQVLSAANQTKTNFNL-----MDYK	194	
Db	452	RKQLOVELOSRRAELVCLN--NTEISENSDLSQKLKETQSKYEAMKEVLSVQKQMKLG	509	
QY	195	LYGESLAKMEGEGEFKLLSKMFSDQVTKAQODFTNAKNE-----LENV	239	
Db	510	LVSPEMDNYSHFHELRV-----TEBEINVLODKLQNALEESERNKEKVELKEKLVRE	564	
QY	240	TSTSLNPKIO--AEAKTDY-----ERKKAIFEIVETQ--IITLKTFLSDLKSGA	287	
Db	565	KGVIVKPPVEEYEMKSSYVLENKNKKAFLFEKYQEAQAEIMKLKDTLKSQMTQ--	622	
QY	288	MSGIEAEYKDKNNKLGNFSTSVSRPLNDLVSE-----KTARLNDVSSRY-----	336	





Db 263 LKQFELALGEASKSQI-VIADLSQERDDLKEALDNE--SSKVHKLQELQVTLLENLAKS 319  
QY 289 SGIEAEY-----KYDKNNKLGNFSTVSDDR-SRPLND-----LVSEKT-- 326  
Db 320 RNESAELNLLTSLNKLCKELEVSKLSSELTEVNESLQRLNLDADKAEAWLASLTTA 379  
QY 327 -----ARLNDVSSRYNAIAEALNRFIQYDSIMRDIL 358  
Db 380 KEHLKEAQELQGVSKELTALE-----KNDLSQKELV 412

## RESULT 5

US-10-471-571A-2278  
; Sequence 2278, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 2278  
; LENGTH: 2478  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(2478)  
; OTHER INFORMATION: FmtB protein [Staphylococcus  
US-10-471-571A-2278

Query Match 6.0%; Score 109; DB 6; Length 2478;  
Best Local Similarity 19.3%; Pred. No. 23;  
Matches 90; Conservative 64; Mismatches 146; Indels 166; Gaps 20;  
QY 6 DYNTPGAFVGLDVQALNTLPG-----NKNPKLTVEL-----LKGKIT 46  
Db 454 DONANKVTFTS---QGVTTARGTHKEVLPDPKSLKSYKVNVANIDTPKNIDFNEKLT 509  
QY 47 ISADSSTALSKEQLEKLLAAYLTDPASINGGWAMQFGGQDAIAIAKGVIERGAKQTP 106  
Db 510 YRTASDVVINNAQPEVTLTA---DPFSV-----AVENMKDALQQQVNSQV 551  
QY 107 PVTHWT---IPEFMLLSLSALTMERTD-----DDLITFTGVMMFQDNO- 147  
Db 552 DNSHYTTASIAEYNKLLKQADTILNEDANHVKTANRASQADIDGLVTKLQAALI--DNQA 609  
QY 148 -----RKGLRDE-----LAEMTAELKIYGV----- 167  
Db 610 AIAELDTKAQEKVTAAGQSKVQDVAALVTKINNDKNAIAEINKQTTAQGVTEKDN 669  
QY 168 -----IQSEINQVLGAASNQTFKTNFNLMDYKLYGVESLAKMEGGEF 210  
Db 670 GIAVLEQDVITPTVPKQAKQDIIQAVTTKQKQIKKSNASLQDEKDVANDKIGKI-----ET 725  
QY 211 KLSKMFSDQVTKAQODF--TNAKNELENVTSTSLNPKIOAEAKTDYERKKAFFESIVE 268  
Db 726 KAIKDI--DAATTNAQVEAIKTRAINDINQFT-----PATTAKAAALEE-----FDEWVQ 773  
QY 269 TQI-----ITLTKTFLDLKKSQA--MSGIEA-----EYKDYKDNKNKLGNFST 309  
Db 774 AQIDQAPLNPDTTNEEVAEAIERINAAKVSQVKAIEATTTAQDLERKVNKEISKIENTID 833  
QY 310 SVSDRSRPLNDLVSEKTAR-----LNDVSSRYNAIAEALNR 345  
Db 834 STQTKMDAYNEVKQAATARKAQNATVSNATNEEVAEADAADVAQAQ 879

## RESULT 6

US-10-449-902-51542  
; Sequence 51542, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51542  
; LENGTH: 720  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-51542

Query Match 5.9%; Score 107.5; DB 6; Length 720;  
Best Local Similarity 21.0%; Pred. No. 5.3;  
Matches 85; Conservative 72; Mismatches 130; Indels 117; Gaps 20;  
QY 33 KLTVELLLKQKJ--TISADSTALSKEQLEK-----LAAYLTD 70  
Db 148 KIGELETQLKKEIDSRITAESSASAKESVKELEGNLQRLSENREKKAUKKLSYLQD 207  
QY 71 PASINGGWAMQFQK-----GGQDAA-----IAAIKGVIERGAKQTPPVTHWTIDEFM 117  
Db 208 DTKLISIKLNAELERMELRALNSEDEAKLNEQLEDLKKQLDSESVNENMEH-----R 261  
QY 118 LLSLSALTMERTDD-----LITPTGVMMFQDN--QRKGL 151  
Db 262 LINCSSLSYERTSPDDQKLIKLOEELRNYEKEVDEARLKSSTNTVELLKEKILEEQGC 321  
QY 152 RDELAEMTAELKIYGVITQSEINQV--LSAASNQTFKTNFNLMDYKLYGVESLAKMEGGEF 210  
Db 322 R-ERAEW--ELSKLOEIEAKQAQKLELASCALLS--NIPDVSSFGD----- 364  
QY 211 KLSKMFSDQVTKAQODFTNAKNELENVTSTSLNPKI-----QAEAKTDYER 258  
Db 365 --IPQKIADI-Q---KQALTNL-NKYGEVTSQKELKVALEFADLSKQRAEGEATLAKER 417  
QY 259 KKAIFBEIVTQIITLTKTFLESD-LKXSGAMS-----GIEAEYK-YDKNNKLGNFSTSVS 312  
Db 418 AESATREIKLELLELLAAISEERDLRKDHAVSKSRDGDASSKNMESDLSRMEKVVTELE 477  
QY 313 DRSRPLNDLVSEKTARLNDVSSRYNAIAEALNRFIQYDSIMRD 356  
Db 478 STTDRDELISQOQTELNLMNEK--LSIES-----RKAKSLERD 514

## RESULT 7

US-10-527-411-20  
; Sequence 20, Application US/10527411  
; Publication No. US20060110410A1  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford  
; APPLICANT: Foster, Keith Alan  
; APPLICANT: Chaddock, John  
; APPLICANT: Marks, Philip  
; APPLICANT: Sutton, J. Mark  
; APPLICANT: Stancombe, Patrick  
; TITLE OF INVENTION: Recombinant Toxin Fragments  
; FILE REFERENCE: 1581.0130005  
; CURRENT APPLICATION NUMBER: US/10/527,411  
; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: PCT/GB2003/003824
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 10/241,596
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-527-411-20

Query Match
Best Local Similarity 5.9%; Score 106.5; DB 6; Length 1169;
Matches 81; Conservative 59; Mismatches 135; Indels 93; Gaps 20;

QY 12 GAFVGLDVQALNTLPQGNKPKLTVELLKGKITISADSSTALSKEQLEKLAAYLTDP 71
Db 588 GLFAGM-----VKQIVNDFVIEANKSNTMDKIADISLIVPYIGLA 627

QY 72 ASINGWAMQFQKGGODAAIAIKGVIERGAKQTPPVTHWTIPFMLLSLSALTMERTDD 131
Db 628 LNVGNETAKGNFENAEIAGAST--LLE-----FPELLIPVVGAFLLSEYID 673

QY 132 D---LITFTGVMMFQDNQKGLRDELAEMTAEIKYVGIQSEINQVLSAASNQ--TFKT 186
Db 674 NKNKIITKTI-----DNALTKNEKWSDM-----YGLI---VAQWLSTVNTQFYTIKE 717

QY 187 N-FNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDQVTKAQODFT--NAK-NLELVNTST 242
Db 718 GMYKALNYQAQALEERIKYR-----YNIYSEKEKSNINIDFNDSKLNQEGINQAID 769

QY 243 SLNPKIQAEAKTDYERKKAIF--FEIIVETQIITLTKTFL-----ESDLKXGMSGIEAEV 295
Db 770 NINNFING-CSVSYLWKKMIPLAVERKLDLFDNTLKNLNYIDENKLYLIGS-----AEY 823

QY 296 KYDKNNKLNSTSVDSRSRPLNDLVSEKTLRNDVSSRYNAALRNFI---QKYDS 352
Db 824 EKSXVKNYLTIMP--FDLSIYNTDI-----LIEMFNKYS--EILNIIILNRYKDN 873

QY 353 IMRDIIG 359
Db 874 NLIDLSG 880

RESULT 8
US-10-449-902-45659
; Sequence 45659, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45659
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45659

Query Match
Best Local Similarity 5.8%; Score 106; DB 6; Length 686;
Matches 79; Conservative 63; Mismatches 130; Indels 110; Gaps 17;

QY 6 DYTNPAGFVGLDVQALN-----TLPGNKPKLTVELLKGKITISADSSTALSKEQ 59
Db 338 DGHSTQEQFTG-LDQQLLYDMAQIILPADQRPKLTLL-----ISMDRRQVTKATD 388

QY 60 LEKLLAAYLTDPASINGWAMQFQKGGODAAIAIKGVIERGAKQTPPVTHWTIPFMLL 119
Db 389 MEDLI-----ARLNQEVAVKEYLA---TKVKDLEVELEATKKDKKEILHQAV----- 432

QY 120 SLSALTMERTDDDLITFTGVMMFQDNQKGLRDEL-----ABMTAEIKYVGIQSEINQV 175
Db 433 -----LTEREKIT-----QLQWDKDELYRYKSEMSLNKIE---QNEKTRV 470

QY 176 LSAASNOTFKTNFNL--MDYKLYGYESLAKFMEGGEFKLLSK-----MFSDE 220
Db 471 QSEKTTASEKEMLLEETKKEVESLQOHI--GEFEAKSKADIKVLVKEVKSLSNSQK 528

QY 221 QYTKAQODFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFE----- 264
Db 529 EMKKVLNQYHEEKTELERI-----VNRQKORSTRARFSREKILHECRLLRERLQECTAKFV 584

QY 265 -EIVETQIITLTKTFL-----SD-----LKXGMSGIEAEYKYDKNNKLNSTSV 310
Db 585 ADEQDQTMITDLSLFDALDLVTSDNRIRLVAEQALLSRDDEQGSDDGDGNSDGKSSVT 644

QY 311 VDSRSRPLNDLVSEKTLRNDV 332
Db 645 MSEDAYVTD--EETTKMLSDL 664

RESULT 9
US-10-505-928-100
; Sequence 100, Application US/10505928
; Publication No. US2006008832A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 100
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-100

Query Match
Best Local Similarity 5.8%; Score 105; DB 6; Length 2871;
Matches 53; Conservative 42; Mismatches 96; Indels 44; Gaps 9;

QY 135 TTTFTGVMMFQDNQKGLRDELAEMTAEIKYVGIQSEI---NOVLSAASNOTFKTNFNL 191
Db 1219 TTIKEISMOKEDDSKNLRNQLDRLSREN---DLKDEIVRLNDSILQATEQRRRAENAL 1275

QY 192 DYKLYGYESLAKFMEGGEFKLLSKMFSDQVTKAQODFTNAKNELENVTST----- 242
Db 1276 QQKACGSGEIMQK-KQHLETELKQVM-----QQRSEDNARHKQSLEEAATTIQDKNKEIE 1328

QY 243 SLNPKIQAEAKTDYERKKAIF-----EIVY-----ETQI--ITLKTFLSDLKXGMS 288
Db 1329 RLKAEFQBEAKRWEYENELSKVRNNYDEEIIISLNQFETENITKTTIHLTMQKEEDT 1388

QY 289 SGIEAEY-----KYDKNNKLNSTSVDSRSRPLNDLVSEKTLRNDVSSR 335
Db 1389 SCVRAQIDNLTRENSLSLEEIKRLKNTLTQTENLRREEDIQQKATGSEVSQR 1443

RESULT 10
US-10-480-962-4

Sequence 4, Application US/10480962  
Publication No. US20060115813A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Junming; EMERLING, Brooke M.;  
APPLICANT: TANG, Y. Tom; BAUGHN, Mariah R.;  
APPLICANT: LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;  
APPLICANT: YUE, Henry; GRIFFIN, Jennifer A.;  
APPLICANT: CHAWLA, Narinder K.; TRAN, Bao  
APPLICANT: NGUYEN, Danna B.; KHAN, Farrah A.;  
APPLICANT: GANDHI, Aneena R.; HAFALIA, April J.A.;  
APPLICANT: SWARNAKER, Anita; GURURAJAN, Rajagopal;  
APPLICANT: POLICKY, Jennifer L.; YAO, Monique G.;  
APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.;  
APPLICANT: ELLIOTT, Vicki S.; LEE, Soo Yeun;  
APPLICANT: SANJANWALA, Bharati; HONCHELL, Cynthia D.;  
APPLICANT: FORSYTHE, Ian J.; GORVAD, Ann E.;  
APPLICANT: RICHARDSON, Thomas W.; LEE, Sally;  
APPLICANT: BARROSO, Ines  
TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES  
FILE REFERENCE: PF-1002 USN  
CURRENT APPLICATION NUMBER: US/10/480,962  
CURRENT FILING DATE: 2003-12-04  
PRIOR APPLICATION NUMBER: PCT/US02/17955  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/297,010  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/298,706  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: US 60/299,998  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: US 60/300,377  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301,871  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/303,349  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: US 60/303,403  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: US 60/351,927  
PRIOR FILING DATE: 2002-01-25  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PERL Program  
SEQ ID NO 4  
LENGTH: 972  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 3418524CD1  
US-10-480-962-4

Query Match 5.8%; Score 104.5; DB 6; Length 972;  
Best Local Similarity 21.3%; Pred. No. 13;  
Matches 81; Conservative 50; Mismatches 127; Indels 123; Gaps 18;

Qy 46 TISADSTALSKEOLEKLLAAYLTD-----PASI-----NGG----- 77  
Db 45 SVGGGSGKTLMSMENIOSLNAAYATSPGMYLSDHENVGSETPKSTMTLGRSGRGLPYGVRM 104

Qy 78 WAMQFQGGQDAATAAIAKGVIERGAKOTPPVT-HWTIPFEMLLSLSALTMTERTDDDLITT 136  
Db 105 TAMGSSPNIASSGVAS--DTAFGEHLLPPVSMASVTPHSL-----ROADNTIMDLQ 157

Qy 137 FTGYMFQDNQKGL-----RDELAEMTAELKIYGV 167  
Db 158 LKEVLRENDLLRKDVEKESKLSMNSIKTFWSPELKKERALKDEASKITTIWKEQYRV 217

Qy 168 IQSE-----INQVLSAASH-----QTFKTNFNLMDYKUYG 198  
Db 218 VQEEENOHQMTQIALQDELRIQRLNQLFQDSSRTGEPVCAELTEENFORLHAE---H 274

Qy 199 ESLAKFMGEGFKLLSKWFSDEQV-TKAQDFTNAKNE-----LENTVSTSLNPKIOAEA 252

Db 275 ERQAK-----ELFLLRKTLEEMELRIETQKOTLNARDESIKKLEMLQSKGLSAKATEE- 328  
Qy 253 KTDYERKKAIFEEIVETQIITLKTFLFESDLKSGAMSGIAEAYKYDK--DNNKLGNFST- 309  
Db 329 --DHERTERLAE--AEMHVHLESLLLEQK-EKENSMLREEMHRRFENAPDSAKTKALQTV 383  
Qy 310 -----SVRSRSLPLNDLVSE 324  
Db 384 IEMKDSKISSMERGLRDLLEE 404

RESULT 11  
US-11-327-900-6  
Sequence 6, Application US/11327900  
Publication No. US20060099174A1  
GENERAL INFORMATION:  
APPLICANT: PHARMA PACIFIC  
APPLICANT: Meritet, Jean Francois  
APPLICANT: Dron, Michel  
APPLICANT: Tovey, Michael Gerard  
TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE  
FILE REFERENCE: 46658/250044  
CURRENT APPLICATION NUMBER: US/11/327,900  
CURRENT FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/10/203,311  
PRIOR FILING DATE: 2002-12-30  
PRIOR APPLICATION NUMBER: GB 0002979.3  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: GB 0002980.1  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: GB 0002982.7  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: GB 0002981.9  
PRIOR FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1234  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-327-900-6

Query Match 5.8%; Score 104.5; DB 7; Length 1234;  
Best Local Similarity 18.8%; Pred. No. 18;  
Matches 78; Conservative 71; Mismatches 150; Indels 117; Gaps 16;

Qy 19 DVQALNTLPCKNPKLTVE-----LLKGKITI 47  
Db 404 EIEDVNTLQGGQGPVVTSPVQSLQPAHPALPQWTSQAQPSVTGLQAPSAALMQ---VS 460

Qy 48 SADSSTALS-----KEQLEKLLAAY---LTDPAISINGWAMG 81  
Db 461 SLDSHSAVSGNAQSFPYAGMQAYAYQASAVTSQLOPVPLYPAPLSQPPHFGSGDMA 520

Qy 82 QFQGGQ-----DAAIAAKGVIERGAKOTPPVTHWTIPFEMLLSLSALTMTERTDDDL 133  
Db 521 SPLMTEARQHTNIRMAVSKVADKMDHLMTKVELOKHSAGNSMLIPMSMTVE----- 574

Qy 134 ITTFTFGVM-----FQDNORKGLRDELAEMTAELKIYGVIOSEINQVLS--AASNOTFK 185  
Db 575 -----TSMIMNSNIQRIIOENER--LKOILEKSNRIE-----EQNDKISELIERNORYV 621

Qy 186 TNFNLMYKLYGVESLAKFMGEGFKLLSKWFSDEQVTKAQDFTNAKNELENTS--TS 243  
Db 622 EQSNLWMEK--RNSLOTATENTQARVL-----HAEQEKAKVTEELAAATAQVSH 669

Qy 244 LNPKIOAEAKTYVERKKAIFEEIVETQI-----ITLKTFLFESDLKSGAMSGIAEAYKYDK 299  
Db 670 LQLKMTAHQKTELOMQLTESLKTDLRLGQLTKVQAKLSELQETSEQA--QSKPKSEK 727

Qy 300 DNNKLGNFSTVSDDRPLNDLVSEKTAERLNDVSSRYNAEALNRFIOKYDSIMR 355  
Db 728 QNRK--OLELKVTSLEELTDLRVEKESLEKNLSEKRSKSAQERSQAEEIDEIRK 781



Qy		98	IERGAKOTPPVTHWTIPEFMILLSALSALTWERTDDLLITTFGTGMVFQDNQRKGLRD---E	154
Dd	:	460	LKRSLQSTEP---FDPV--MTDSVRAGSPKIDDEVAKEWEHTML-ODSMGKELNELNQ	513
Qy	:	155	LAEMTAELKIYG-----VIQSEINQVLSA-----ASNQTFFKTN	187
Dd	:	514	LEQEKESMKYGSdTVALKHQFKGLLEBEKBRAVQQERDRLLAEVESLNDAGQTHK--	571
Qy	:	188	ENLMWDYKLYGVYESL-----AKFMEGGEFKLL-SKMFSDEQVTKAQODFTNAKNELVNT	240
Dd	:	572	--LRDAQIOUKLTLEAQILDULKKOENQVQLLKREKOKSDEAAKUQEETHSKAQ-----	624
Qy	:	241	STSLNPKIQAEB-----KTDYERKKAIPEEVIVETQIIILTKTEL	278
Dd	:	625	KVOLQHKKIQEAEQFRWKATREKELLQLRKEGRNERHERK--LQALNQORKVLQRTK	682
Qy	:	279	ESDLKKSAMSG-TIAEAYKYDKDNNKL-----GNFSTSVSDRSRPLNDLVSEKTRANDV	332
Dd	:	683	EBAAMATKRLKELLEARKSSGRDNSGMNGTSPGSHMTEKSLQKWLEQDDL--EVMVHVHEV	740
Qy	:	333	SSRY	336
Dd	:	741	RNEY	744

RESULT 15

```

US-10-449-902-45697
; Sequence 45697, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45697
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45697

```

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Query Match      5.7%; Score 103; DB 6; Length 971;
Best Local Similarity 20.3%; Pred. No.16;
Matches 86; Conservative 67; Mismatches 129; Indels 142; Gaps 22;

QY      21 QALNTLP-----GNKVP-----KLTELVELLKGKTIISADSTALSK----- 57
      : ||||| : ||| : : || : : || :
Db      291 ETLNTLYANRARNIONKPIVNRNPVADMKRMRCQIEYLAEL-VSARGGWLLDDVQGL 349
      : ||||| : ||| : : || : : || :

QY      58 -----EOLEKLLAAYL-----TDPA-----SINGGWAMQCFKGQDAAATIKGV 97
      : ||| : ||| : ||| :

Db      350 RERISMLEQKNEDLCRLYDLRNHGYTDPCEPELOKIGTGYTKGE-----G 395
      : ||| : ||| : ||| :

QY      98 IERGAKOTPPVTHWTIPEFLLLSALTMTDDDLITTTGVMVFODNQKGLRD--E 154
      : ||| : : ||| : : ||| : : ||| :

Db      396 LKRSLSQSTEP---FDVP--MTDSVRAGSPKDIIDDEVAKEWHTWL-QDSMGKELNELNRQ 449
      : ||| : : ||| : : ||| : : ||| :

QY      155 LAEMTAEKLYIG-----VIQSEINQVLSA-----ASNQTFKTN 187
      : ||| : ||| : ||| :

Db      450 LEQKESEMKMGSDTVALKQHFGKLLLEEEKRAVQOERDRLAELVESLNADQTHK-- 507
      : ||| : ||| : ||| :

QY      188 FNLMDYKLYGVESI-----AKFWEGGEFKLL-SKMFSDQVTKAQODFTNAKNELENV 240
      : ||| : ||| : ||| :

Db      508 --LRDAQOLKLTLEAQIDLLKKQENOVOLLKEKOKSDSAAKKLOEIIHSIKAO----- 560
      : ||| : ||| : ||| :

```

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 105.354 Seconds  
(without alignments)  
690.032 Million cell updates/sec

Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTITPVEAELEAFMA.....QADLAASAKVMLEAIRRD 159

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Geneseqp1980s:\*  
2: Geneseqp1980s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	827	100.0	159	5 ABB80777	Abb80777 A. salmon
2	596	72.1	168	6 ABM69523	Abm69523 Photorhab
3	549	66.4	167	6 ABU38392	Abu38392 Protein e
4	548	66.3	239	7 ABO81217	Abu81217 Pseudomon
5	177	21.4	171	6 ABU22325	Abu22325 Protein e
6	169.5	20.5	172	6 ABU40949	Abu40949 Protein e
7	167	20.2	161	3 AAB14112	Aab14112 Bordetell
8	166.5	20.1	165	6 ABU45583	Abu45583 Protein e
9	166.5	20.1	165	6 ABU48112	Abu48112 Protein e
10	166.5	20.1	165	9 ADW28241	Adw28241 Amino aci
11	165	20.0	151	7 ADC00814	Adc00814 Enterohae
12	163.5	19.8	182	7 ADF06293	Adf06293 Bacterial
13	151	18.3	156	6 ABM70111	Abm70111 Photorhab
14	125.5	15.2	157	3 AAY70581	Aay70581 Salmonell
15	125.5	15.2	157	6 ABU47399	Abu47399 Protein e
16	121.5	14.7	158	3 ABM94434	Abm94434 M. xanthu
17	118	14.3	144	3 AAY70582	Aay70582 Salmonell
18	116.5	14.1	154	9 ABM96865	Abm96865 M. xanthu
19	109	13.2	246	6 ABU27402	Abu27402 Protein e
20	107.5	13.0	163	4 AAG98281	Aag98281 Escherich
21	107.5	13.0	163	6 ABU14803	Abu14803 Protein e
22	107.5	13.0	227	10 AEB60329	Aee60329 Cat chlam
23	105	12.7	210	2 AAY35451	Aay35451 Chlamydia

24	105	12.7	231	6 ABU27062	Abu27062 Protein e
25	105	12.7	231	9 AEC95744	Aec95744 C. pneumo
26	101.5	12.3	234	2 AAY37634	Aay37634 Protein w
27	100	12.1	172	9 AEC95749	Aec95749 C. pneumo
28	100	12.1	191	2 AAY35677	Aay35677 Chlamydia
29	90	10.9	172	2 AAY37895	Aay37895 Amino aci
30	90	10.9	304	8 ADS29906	Ads29906 Bacterial
31	88.5	10.7	280	8 ADS22934	Ads22934 Bacterial
32	87	10.5	153	3 AAB14140	Aab14140 Bordetell
33	86	10.4	172	10 AEB60330	Aee60330 Cat chlam
34	86	10.4	264	3 AAG42356	Aag42356 Arabidops
35	86	10.4	341	3 AAG42355	Aag42355 Arabidops
36	86	10.4	342	3 AAG42354	Aag42354 Arabidops
37	84.5	10.2	1564	8 ADL12580	Adl12580 Human ste
38	83	10.0	639	9 ABM92892	Abm92892 M. xanthu
39	80.5	9.7	562	9 AEB27261	Aeb27261 Pinus rad
40	80.5	9.7	579	6 ABU20545	Abu20545 Protein e
41	80.5	9.7	676	8 ADN20615	Adn20615 Bacterial
42	80	9.7	458	2 AAR41781	Aar41781 Rabbit HB
43	79	9.6	315	4 AAB60367	Aab60367 Xenopus l
44	79	9.6	315	6 AAO30937	Aao30937 Frog aton
45	79	9.6	574	9 AEB27139	Aeb27139 Pinus rad

#### ALIGNMENTS

##### RESULT 1

ABB80777  
ID ABB80777 standard; protein; 159 AA.  
XX  
AC ABB80777;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE A. salmonicida type III secretion protein acrH sequence.  
XX  
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;  
KW acrV; acrH; antibiotic; vaccine; fish.  
XX  
OS Aeromonas salmonicida.  
XX  
PN WO2002040514-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 15-NOV-2001; 2001WO-CA001589.  
XX  
PR 15-NOV-2000; 2000US-0248864P.  
XX  
(FREY/) FREY J.  
(STUB/) STUBER K.  
PA (THOR/) THORNTON J C.  
PA (KUZY/) KUZYSK M A.  
PA (BURI/) BURIAN J.  
XX  
Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;  
PI WPI: 2002-537338/57.  
XX  
DR N-PSDB; ABN86172.  
XX  
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the  
PT protein, useful for reducing susceptibility of fish to infection by a  
XX virulent strain of Aeromonas salmonicida.  
XX  
PS Claim 13; Page 29; 39pp; English.  
XX  
CC The invention relates to A. salmonicida type III secretion genes and  
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.  
CC A. salmonicida type III secretion apparatus is useful for producing  
CC selected products, especially Aext. AcrV in vaccine, epitope or epitopic  
CC region of AcrV or any other protein of A. salmonicida type III secretion  
CC apparatus is useful for reducing the susceptibility of fish to infection





the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

XX Sequence 167 AA;

Query Match 66.4%; Score 549; DB 6; Length 167;

Best Local Similarity 64.8%; Pred. No. 4.6e-54;

Matches 103; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 1 MQTDTTLTPEVEALEAFMADGGTLMLODLSGTLEQLYALAFSQYQAGKWDAAHKIFQ 60

Db 1 MNQTPSDTDQQQALEAFRLDGGTLMRLGLSEDTLEQLYALGFNQYQAGKWDAAQKIFQ 60

QY 61 ALCLMDHYEPYFLGLGACROAMGEFFETAVOSYSGAMLDLKDPRFPFHAGECRLQOQGLD 120

Db 61 ALCLMDHYDARYFLGLGACROSLGLYEQALQSYSGALMDINEPRFPFHAAEHLQGLD 120

QY 121 NGAESGFHSARLLADTDPQQAADLAASAKVMLEAIAIRRD 159

Db 121 DGAESGFYSARALAAQPAHEALAAARAGMLEAVTARKD 159

RESULT 4

ABO81217

ID ABO81217 standard; protein; 239 AA.

AC ABO81217;

XX ABO81217;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #13392.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

KW Pseudomonas aeruginosa.

OS US6551795-B1.

PN 22-APR-2003.

PD 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD14788.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 29963; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences ABO67896-ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 239 AA;

Query Match 66.3%; Score 548; DB 7; Length 239;

Best Local Similarity 65.2%; Pred. No. 9.8e-54;

Matches 103; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 2 QDTDTTLTPEVEALEAFMADGGTLMLODLSGTLEQLYALAFSQYQAGKWDAAHKIFQ 61

Db 74 QQTTPSDTDQQQALEAFRLDGGTLMRLGLSEDTLEQLYALGFNQYQAGKWDAAQKIFQ 133

QY 62 LCMLDHYEPYFLGLGACROAMGEFFETAVOSYSGAMLDLKDPRFPFHAGECRLQOQGLD 121

Db 134 LCMLDHYDARYFLGLGACROSLGLYEQALQSYSGALMDINEPRFPFHAAEHLQGLD 193

QY 122 GAESGFHSARLLADTDPQQAADLAASAKVMLEAIAIRRD 159

Db 194 GAESGFYSARALAAQPAHEALAAARAGMLEAVTARKD 231

RESULT 5

ABU22325

ID ABU22325 standard; protein; 171 AA.

XX ABU22325;

AC ABU22325;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #7852.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.



Db	9	EKELDQLANYIVISVONGASIKDESEIPDGFMEGIYSFAYDFYQYQKLDDEAEIFKFLCL	68
QY	65	LDHYEPRYFLGIGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDNGAE	124
Db	69	YDFYNVDYIMGLAAVNQLKKQYQAIDLYALAYLNAKNDRPVPFVAGQCNLSIGEKEKAK	128
QY	125	SGFH	128
Db	129	YCFH	132
RESULT 7			
ID	AAB14112	standard; protein; 161 AA.	
XX	AC	AAB14112;	
XX	DT	02-FEB-2001 (first entry)	
XX	DE	Bordetella pertussis class I gene protein BcrH.	
XX	KW	BcrH; bacterial infection; anti-bacterial; vaccine; whooping cough;	
XX	KW	type III secretion system; virulence factor; pathogenicity island.	
XX	OS	Bordetella pertussis.	
XX	PN	WO200037493-A2.	
XX	PD	29-JUN-2000.	
XX	PF	21-DEC-1999; 98WO-EP010297.	
XX	PR	21-DEC-1998; 98GB-00028217.	
XX	PA	(ULBR ) UNIV LIBRE BRUXELLES.	
XX	PI	Bollen A, Fauconnier A, Godfroid E;	
XX	DR	WPI; 2000-452178/39.	
XX	DR	N-PSDB; AAA64850, AAA64890.	
XX	PT	Novel polypeptides derived from Bordetella pertussis, useful for treating	
XX	PT	and diagnosing Bordetella infection.	
XX	PS	Example 2; Page 87-88; 165pp; English.	
XX	CC	Bordetella pertussis possesses a type III secretion system. Type III	
XX	CC	secretion systems allow bacteria to target virulence factors directly at	
XX	CC	host cells. The present sequence is the BcrH protein of B. pertussis. The	
XX	CC	present protein is encoded by a Class I type gene and is involved in the	
XX	CC	type III secretion system of B. pertussis i.e. a Bordetella pathogenicity	
XX	CC	protein. The gene of the present protein is located within a	
XX	CC	pathogenicity island (see AAA64890). A pathogenicity island is a compact,	
XX	CC	distinct genetic unit carrying virulence genes. The present protein may	
XX	CC	be used to treat or diagnose B. pertussis infection, e.g. as a vaccine.	
XX	CC	Whooping cough is a disease caused by infection by B. pertussis	
SQ	Sequence 161 AA;		
Query Match			
Best Local Similarity 20.2%; Score 167; DB 3; Length 161;			
Matches 47; Conservative 24; Mismatches 81; Indels 2; Gaps 2;			
QY	2	QTDTTLTPEYEAELFAFWADGGTGLAMLODISGDTLEQLVALAFSQYQAGKVEDAHKIFQA	61
Db	7	QGGSPASASHEA-LRHIIIDAGSMGGLQGLDEAQQQALYALGHGAYEQGRVADAKMFCL	65
QY	62	LCMLDHYPRYFLGIGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDNLN	121
Db	66	LVACDPLEARYLLALGAAQAQELGLYEHALQQYAAAAALQDLSRPLLHGAECCLVALGRRR	125
QY	122	GAESGFHSARLLADTDPOQADLAASAKVNLRAIA	155

Db	126	DALDTLDMVLELQGS-PERAAALRERAEELRRSYA	158
RESULT 8			
ID	ABU45583	standard; protein; 165 AA.	
XX	AC	ABU45583;	
XX	DT	19-JUN-2003 (first entry)	
XX	DE	Protein encoded by Prokaryotic essential gene #31110.	
XX	KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.	
XX	OS	Salmonella paratyphi.	
XX	PN	WO200277183-A2.	
XX	PD	03-OCT-2002.	
XX	XX	21-MAR-2002; 2002WO-US009107.	
XX	PR	21-MAR-2001; 2001US-00815242.	
XX	PR	06-SEP-2001; 2001US-00948993.	
XX	PR	25-OCT-2001; 2001US-0342923P.	
XX	PR	08-FEB-2002; 2002US-00072851.	
XX	PR	06-MAR-2002; 2002US-0362699P.	
XX	PA	(ELIT-) ELITRA PHARM INC.	
XX	PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;	
XX	PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX	DR	WPI; 2003-029926/02.	
XX	DR	N-PSDB; ACA49453.	
XX	PT	New antisense nucleic acids, useful for identifying proteins or screening	
XX	PT	for homologous nucleic acids required for cellular proliferation to	
XX	XX	isolate candidate molecules for rational drug discovery programs.	
XX	PS	Claim 25; SEQ ID NO 73507; 1766pp; English.	
XX	CC	The invention relates to an isolated nucleic acid comprising any one of	
XX	CC	the 6213 antisense sequences given in the specification where expression	
XX	CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
XX	CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
XX	CC	encoding a polypeptide whose expression is inhibited by the antisense	
XX	CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
XX	CC	polypeptide or its fragment whose expression is inhibited by the	
XX	CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
XX	CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
XX	CC	proliferation or the activity of a gene in an operon required for	
XX	CC	proliferation; (7) identifying a compound that influences the activity of	
XX	CC	the gene product or that has an activity against a biological pathway	
XX	CC	required for proliferation, or that inhibits cellular proliferation; (8)	
XX	CC	identifying a gene required for cellular proliferation or the biological	
XX	CC	pathway in which a proliferation-required gene or its gene product lies	
XX	CC	or a gene on which the test compound that inhibits proliferation of an	
XX	CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
XX	CC	compound's activity; (11) a culture comprising strains in which the gene	
XX	CC	product is overexpressed or underexpressed; (12) determining the extent	
XX	CC	to which each of the strains is present in a culture or collection of	
XX	CC	strains; or (13) identifying the target of a compound that inhibits the	
XX	CC	proliferation of an organism. The antisense nucleic acids are useful for	
XX	CC	identifying proteins or screening for homologous nucleic acids required	
XX	CC	for cellular proliferation to isolate candidate molecules for rational	
XX	CC	drug discovery programs, or for screening homologous nucleic acids	
XX	CC	required for proliferation in cells other than S. aureus, S. typhimurium,	
XX	CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of	
XX	CC	the target prokaryotic essential genes. Note: The sequence data for this	
XX	CC	patent did not form part of the printed specification, but was obtained	

CC	in electronic format directly from WIPO at									
CC	ftp.wipo.int/pub/published_pct_sequences									
XX										
SQ	Sequence 165 AA;									
	Query Match	20.1%;	Score 166.5;	DB 6;	Length 165;					
	Best Local Similarity	30.8%;	Pred. No. 2.4e-10;							
	Matches	48;	Conservative	25;	Mismatches 76;	Indels	7;	Gaps	3;	
QY	1	MQTDTTLTPEYAEAL--EAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEDAHKI	58							
DB	1	MDYQNNVSEERVAEMIWDA-VSEGATLKDVHGIPQDMMDGLYAHAYEFYNQGRLEDEATF	59							
QY	59	FOALCMLDHYEPRYFLGLGACRQMGFEFETAVQSYSGAMLDLKDPRFPFHAGECRLOQG	118							
DB	60	FRFLCIYDFNPDYTMGLAAVCQKKQFQKACDLYAVATLLKNDYRPVFTFGCQQLMR	119							
QY	119	DLNGAESGFHSARLLADTPQADLAASAKVMLEAI	154							
DB	120	KAAKARQCFE---LVNRTEDESLRAKALVYLEAL	151							
RESULT 9										
ABU48112										
ID	ABU48112	standard; protein; 165 AA.								
XX										
AC	ABU48112;									
XX										
DT	19-JUN-2003	(first entry)								
XX										
DE	Protein encoded by Prokaryotic essential gene #33639.									
XX										
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.									
XX										
OS	Salmonella typhi.									
XX										
PN	WO200277183-A2.									
PD	03-OCT-2002.									
XX										
PF	21-MAR-2002;	2002WO-US009107.								
XX										
PR	21-MAR-2001;	2001US-00815242.								
PR	06-SEP-2001;	2001US-00948993.								
PR	25-OCT-2001;	2001US-0342923P.								
PR	08-FEB-2002;	2002US-00072851.								
PR	06-MAR-2002;	2002US-0362699P.								
XX										
PA	(ELIT-) ELITRA PHARM INC.									
XX										
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;									
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;									
XX										
DR	WPI; 2003-029926/02.									
DR	N-PSDB; ACAS1982.									
XX										
PT	New antisense nucleic acids, useful for identifying proteins or screening									
PT	for homologous nucleic acids required for cellular proliferation to									
PT	isolate candidate molecules for rational drug discovery programs.									
XX										
PS	Claim 25; SEQ ID NO 76036; 1766pp; English.									
XX										
CC	The invention relates to an isolated nucleic acid comprising any one of									
CC	the 6213 antisense sequences given in the specification where expression									
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:									
CC	(1) a vector comprising a promoter operably linked to the nucleic acid									
CC	encoding a polypeptide whose expression is inhibited by the antisense									
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated									
CC	polypeptide or its fragment whose expression is inhibited by the									
CC	antisense nucleic acid; (4) an antibody capable of specifically binding									
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular									
CC	proliferation or the activity of a gene in an operon required for									
CC	proliferation; (7) identifying a compound that influences the activity of									

CC	the gene product or that has an activity against a biological pathway									
CC	required for proliferation, or that inhibits cellular proliferation; (8)									
CC	identifying a gene required for cellular proliferation or the biological									
CC	pathway in which a proliferation-required gene or its gene product lies									
CC	or a gene on which the test compound that inhibits proliferation of an									
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a									
CC	compound's activity; (11) a culture comprising strains in which the gene									
CC	product is overexpressed or underexpressed; (12) determining the extent									
CC	to which each of the strains is present in a culture or collection of									
CC	strains; or (13) identifying the target of a compound that inhibits the									
CC	proliferation of an organism. The antisense nucleic acids are useful for									
CC	identifying proteins or screening for homologous nucleic acids required									
CC	for cellular proliferation to isolate candidate molecules for rational									
CC	drug discovery programs, or for screening homologous nucleic acids									
CC	required for proliferation in cells other than S. aureus, S. typhimurium,									
CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of									
CC	the target prokaryotic essential genes. Note: The sequence data for this									
CC	patent did not form part of the printed specification, but was obtained									
CC	in electronic format directly from WIPO at									
CC	ftp.wipo.int/pub/published_pct_sequences									
XX										
SQ	Sequence 165 AA;									
	Query Match	20.1%;	Score 166.5;	DB 6;	Length 165;					
	Best Local Similarity	30.8%;	Pred. No. 2.4e-10;							
	Matches	48;	Conservative	25;	Mismatches 76;	Indels	7;	Gaps	3;	
QY	1	MQTDTTLTPEYAEAL--EAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEDAHKI	58							
DB	1	MDYQNNVSEERVAEMIWDA-VSEGATLKDVHGIPQDMMDGLYAHAYEFYNQGRLEDEATF	59							
QY	59	FOALCMLDHYEPRYFLGLGACRQMGFEFETAVQSYSGAMLDLKDPRFPFHAGECRLOQG	118							
DB	60	FRFLCIYDFNPDYTMGLAAVCQKKQFQKACDLYAVATLLKNDYRPVFTFGCQQLMR	119							
QY	119	DLNGAESGFHSARLLADTPQADLAASAKVMLEAI	154							
DB	120	KAAKARQCFE---LVNRTEDESLRAKALVYLEAL	151							
RESULT 10										
ADW28241										
ID	ADW28241	standard; protein; 165 AA.								
XX										
AC	ADW28241;									
XX										
DT	07-APR-2005	(first entry)								
XX										
DE	Amino acid sequence of Sica protein from Salmonella typhimurium.									
XX										
KW	gastrointestinal-Gen.; dermatological; cardiovascular-Gen.; vasotropic;									
KW	vulnary; ophthalmological; neuroprotective; antidiabetic; antidiabetic;									
KW	antiinflammatory; cardiac; antimicrobial;									
KW	matrix metalloproteinase inhibitor; elastase inhibitor;									
KW	apoptosis inhibitor; cell damage; tissue damage; protective protein;									
KW	cationic antimicrobial proteolysis; matrix metalloproteinase; elastase;									
KW	wound healing; corneal damage; keratitis; meningitis; apoptosis;									
KW	necrosis; burn; scar tissue; inflammation; heart valve disease;									
KW	varicose vein; rash; incision; ulcer; valve stenosis; gingivitis;									
KW	endocarditis; cardiac tissue calcification; injury; antimicrobial;									
KW	neurological disease; ocular disease; infection; cardiovascular disease;									
KW	antiulcer; inflammation; mouth disease; Sica.									
XX										
OS	Salmonella typhimurium.									
XX										
PN	WO2005004894-A2.									
XX										
XX	20-JAN-2005.									
XX										
PF	12-MAY-2004;	2004WO-US014920.								
XX										
PR	12-MAY-2003;	2003US-0469869P.								
PR	21-JAN-2004;	2004US-0537814P.								

the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 165 AA;

Query Match 20.1%; Score 166.5; DB 6; Length 165;  
Best Local Similarity 30.8%; Pred. No. 2.4e-10;  
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;  
  
QY 1 MQTDTLTPEYAEAL--EAFMADGGTTLAMLODISGDTLEQLYALAFSQYQAGKWEDAHKI 58  
DB 1 MDYQNNVSEERVAEMIWDA-VSEGATLKDVHGIPQDMMDGLYAHAYEFYNQGRUDEATF 59  
  
QY 59 FOALCMLDHYEPRYFLGLGACRQMGFEFETAVQSYSGAMLDLKDPRFPFHAGECRLOQG 118  
DB 60 FRFLCIYDFYNDPTMTGLAAVCQKKQFQKACDLYAVAFLLKNDKDYRPVFTGCQQLMR 119  
  
QY 119 DLNGAESGFHSARLLADTPQADLAASAKVMLEAI 154  
DB 120 KAAKARQCFE---LVNRTEDESLRKALVYLEAL 151

RESULT 10  
ADW28241  
ID ADW28241 standard; protein; 165 AA.  
XX  
AC ADW28241;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Amino acid sequence of Sica protein from *Salmonella typhimurium*.  
XX  
KW gastrointestinal-Gen.; dermatological; cardiovascular-Gen.; vasotropic;  
KW vulnery; ophthalmological; neuroprotective; antiapoptotic;  
KW antiinflammatory; cardiant; antimicrobial;  
KW matrix metalloprotease inhibitor; elastase inhibitor;  
KW apoptosis inhibitor; cell damage; tissue damage; protective protein;  
KW cationic antimicrobial proteolysis; matrix metalloprotease; elastase;  
KW wound healing; corneal damage; keratitis; meningitis; apoptosis;  
KW necrosis; burn; scar tissue; inflammation; heart valve disease;  
KW varicose vein; rash; incision; ulcer; valve stenosis; gingivitis;  
KW endocarditis; cardiac tissue calcification; injury; antimicrobial;  
KW neurological disease; ocular disease; infection; cardiovascular disease;  
KW antiulcer; inflammation; mouth disease; Sica.  
XX  
OS *Salmonella typhimurium*.  
XX  
PN WO2005004894-A2.  
XX  
PD 20-JAN-2005.  
XX  
PF 12-MAY-2004; 2004WO-US014920.  
XX  
PR 12-MAY-2003; 2003US-0469869P.  
PR 21-JAN-2004; 2004US-0537814P.



XX The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
SQ Sequence 182 AA;  
  
Query Match 19.8%; Score 163.5; DB 7; Length 182;  
Best Local Similarity 29.8%; Pred. No. 6e-10;  
Matches 37; Conservative 25; Mismatches 55; Indels 7; Gaps 1;  
  
QY 12 EAELE-----AFMADGGT LAMLDISGDTLEQLYALAFSQYQAGKWE DAHKIFQALCM 64  
Db 19 EKELDQLANIVISVQNGASIKDESELPDGFMEGDYSFAYDFYQKGLDEAEAIKPLCL 78  
  
QY 65 LDHYEPYRFLGACRQAMGEFFETAVQSYSGFAMLDLKDPRFPFHAGECRLOQGD LNGAE 124  
Db 79 YDFYNDYINGLAANVLKQYQAAIDLVALALNAKNDRYPVYAGQCNLSIGEKAK 138  
  
QY 125 SGFH 128  
Db 139 YCFH 142  
  
RESULT 13  
ABM70111  
ID ABM70111 standard; protein; 156 AA.  
XX  
AC ABM70111;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
XX Photorhabdus luminescens protein sequence #3208.  
XX  
DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
KW detection; food; gene expression; plant; animal; microorganism; toxin;  
KW antibiotic; biopesticide; virulence factor; disease model; plague;  
KW whooping cough.  
XX  
OS Photorhabdus luminescens.  
XX  
PN W0200294867-A2.  
XX  
PD 28-NOV-2002.  
XX  
XX 07-FEB-2002; 2002WO-IB003040.  
XX  
XX 07-FEB-2001; 2001FR-00001659.  
XX  
XX (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
PI Buchrieser C;  
XX  
XX WPI; 2003-148459/14.  
DR  
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX  
XX Claim 2; SEQ ID NO 3208; 1205pp; French.  
XX  
XX The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX  
SQ Sequence 156 AA;  
  
Query Match 18.3%; Score 151; DB 6; Length 156;  
Best Local Similarity 32.6%; Pred. No. 1.3e-08;  
Matches 31; Conservative 17; Mismatches 47; Indels 0; Gaps 0;  
  
QY 22 GGT LAMLDISGDTLEQLYALAFSQYQAGKWE DAHKIFQALCM LDHYEPYRFLGACRQ 81  
Db 22 GATLKDINAIPDDMMDDIYSAYDFYNKGRIBEA EVFFRFLCYDFYNVDYINGLA AIYQ 81  
  
QY 82 AMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLO 116  
Db 82 IKEQFQQAADLYAVAFALGKNDRYTPVFTGQCQLR 116  
  
RESULT 14  
AAY70581  
ID AAY70581 standard; protein; 157 AA.  
XX  
AC AAY70581;  
XX  
DT 04-JUL-2000 (first entry)  
XX  
XX Salmonella Pathogenicity Island 2 (SPI2) SsCA protein.  
DE  
XX Salmonella Pathogenicity Island 2 locus; SPI2 locus; antigen carrier;  
KW attenuation; gram-negative cell; vaccine; cytostatic; virucide; tumour;  
KW anti-arteriosclerotic; anti-Alzheimer's; bactericide; hepatotropic;  
KW antiinflammatory; microbial infection; therapeutic; Salmonella infection;  
KW Helicobacter pylori; stomach cancer; Herpes virus; Chlamydia pneumoniae;  
KW Alzheimer's disease; arteriosclerosis; viral pathogen; Hepatitis virus;  
KW cervical cancer; ssca; chaparon; type III secretion system.  
XX  
OS Salmonella typhimurium.  
XX  
XX W0200014240-A2.  
XX  
XX 16-MAR-2000.  
XX  
XX 03-SEP-1999; 99WO-EP006514.  
XX  
XX 04-SEP-1998; 98EP-00116827.  
XX  
XX (CREA-) CREATOGEN BIOSCIENCES GMBH.  
XX  
XX Hensel M, Guzman CA, Medina E, Apfel H, Hueck C;  
PI  
XX WPI; 2000-256988/22.  
DR  
DR N-PSDB; AA251993.  
XX  
PT Attenuated gram-negative Salmonella cells, comprising inactivated genes  
CC in the SPI2 locus and useful for vaccinating against a range of disorders  
PT associated with microbial infections such as stomach and cervical

PT cancers.  
PS Claim 18; Fig 23H; 180pp; English.  
XX  
CC The patent discloses attenuated gram-negative cells, especially  
CC Salmonella, in which at least 1 gene in the Salmonella Pathogenicity  
CC Island 2 (SPI2) locus has been inactivated resulting in attenuation/  
CC reduction of virulence compared to the wild type cell. The attenuated  
CC cells are used as carriers for presenting bacterial, viral or tumour  
CC antigens to a host and are capable of expressing the antigen in a target  
CC cell, especially a macrophage. The cells may therefore be used for the  
CC preparation of a prophylactic or therapeutic composition for the  
CC treatment of a chronic disease caused by a bacterium or virus, e.g.  
CC Salmonella infection or a tumour. The cells may also be used to vaccinate  
CC against a range of bacterial and viral pathogens e.g. Helicobacter pylori  
CC (associated with stomach cancer), Chlamydia pneumoniae (associated with  
CC arteriosclerosis and Alzheimer's disease), Borrelia burgdorferi,  
CC Nanobacteria (found in the chronically diseased kidneys of patients with  
CC crystalline deposits), Hepatitis virus (causative agent of Hepatitis B  
CC and C and associated with liver cancer), Human papilloma virus (HPV)  
CC (associated with cervical cancer) or Herpes virus. The present sequence  
CC is the SCA protein, a chaperon protein of type III secretion system,  
CC from the SPI2 locus of Salmonella. Inactivation of the ssc gene is useful  
CC for producing the attenuated cells  
XX  
SQ Sequence 157 AA;

Query Match 15.2%; Score 125.5; DB 3; Length 157;  
Best Local Similarity 27.0%; Pred. No. 1.1e-05;  
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;  
Qy 1 MQTDTLTPEYAELEAFMADGGTLLAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59  
Db 1 MKKQPTLQQAHD--MRFFRRGSLRMLLDDDDVTQPLNTLYRYATQLMVEKFEFAGARLF 58  
Qy 60 QALCMLDHYEPRYFLGIGACQRMGEFETAVQSISFGMLDLKDPFFPHAGECRLOQGD 119  
Db 59 QLLTIYDAWSFDYFRLGECQQAQKHGEAIYAGRAAQIKIDAPQAPMAAECYLACDN 118  
Qy 120 LNGAESGFHS--ARLLADTDPQADLAASAKVMLEAIAIR 157  
Db 119 VCVAIKALKAVVRICGEVSEHQI-LRQRAEKMLQQLSDR 156

RESULT 15  
ABU47399  
ID ABU47399 standard; protein; 157 AA.  
XX  
AC ABU47399;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #32926.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmonella typhimurium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA51269.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 75323; 1766pp; English.  
XX

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than S. aureus, S. typhimurium,  
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 157 AA;  
Query Match 15.2%; Score 125.5; DB 6; Length 157;  
Best Local Similarity 27.0%; Pred. No. 1.1e-05;  
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;  
Qy 1 MQTDTLTPEYAELEAFMADGGTLLAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59  
Db 1 MKKQPTLQQAHD--MRFFRRGSLRMLLDDDDVTQPLNTLYRYATQLMVEKFEFAGARLF 58  
Qy 60 QALCMLDHYEPRYFLGIGACQRMGEFETAVQSISFGMLDLKDPFFPHAGECRLOQGD 119  
Db 59 QLLTIYDAWSFDYFRLGECQQAQKHGEAIYAGRAAQIKIDAPQAPMAAECYLACDN 118  
Qy 120 LNGAESGFHS--ARLLADTDPQADLAASAKVMLEAIAIR 157  
Db 119 VCVAIKALKAVVRICGEVSEHQI-LRQRAEKMLQQLSDR 156

Search completed: June 16, 2006, 19:06:50  
Job time : 108.354 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 16.1585 Seconds  
(without alignments)  
946.773 Million cell updates/sec

Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTTLTPEYEAELEAFMA.....QADLAASAKVMLEAIAIRRD 159

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	66.4	167	2 H83432	regulatory protein
2	517	62.5	168	2 C37314	regulatory protein
3	509	61.5	168	2 C33601	low calcium respon
4	166.5	20.1	165	2 A80851	hypothetical prote
5	166.5	20.1	165	2 S70217	sipB protein - Sal
6	166.5	20.1	165	2 A57357	sicA protein - Sal
7	165	20.0	151	2 H91200	type III secretion
8	165	20.0	151	2 D86047	cesD (imported) -
9	151	18.3	155	2 S15576	ipp1 protein - Shi
10	151	18.3	155	2 C24965	hypothetical 17K p
11	124.5	15.1	157	2 A80699	probable type III
12	116.5	14.1	172	2 F81723	type III secretion
13	115.5	14.0	163	2 H85937	hypothetical prote
14	115.5	14.0	163	2 D91092	hypothetical prote
15	114	13.8	596	2 G75457	tetratricopeptide
16	113	13.7	144	2 A10698	probable pathogeni
17	109	13.2	246	2 D81655	type III secretion
18	108	13.1	198	2 E71461	probable low calci
19	107.5	13.0	163	2 D65068	hypothetical prote
20	105	12.7	231	2 A86592	low calcium respon
21	105	12.7	231	2 H72031	type III secretion
22	103.5	12.5	232	2 B71497	probable low calci
23	100	12.1	172	2 B86618	low calcium respon
24	100	12.1	172	2 C72007	type III secretion
25	98	11.9	403	2 S42532	hypothetical prote
26	96.5	11.7	458	2 T29520	hypothetical prote
27	91.5	11.1	576	2 H87414	TPR domain protein
28	91	11.0	835	2 I55603	reduced hepatic gl
29	90	10.9	402	2 A12030	hypothetical prote

30	90	10.9	439	2	F70395	glycine dehydrogen
31	86.5	10.5	311	2	AF2353	hypothetical prote
32	86.5	10.5	398	2	S75202	hypothetical prote
33	86	10.4	290	2	T09363	hypothetical prote
34	82.5	10.0	214	2	F83807	hypothetical prote
35	82.5	10.0	224	2	AH2116	hypothetical prote
36	80	9.7	458	1	A42386	hsp 90-binding pro
37	79	9.6	547	2	AE1884	hypothetical prote
38	78.5	9.5	271	2	E87266	conserved hypotnet
39	78	9.4	422	2	AD2191	hypothetical prote
40	77.5	9.4	371	2	B81985	probable pilus ass
41	76.5	9.3	176	2	H95272	hypothetical prote
42	76.5	9.3	1039	2	T43678	tetratricopeptide
43	76.5	9.3	1039	2	T38447	tetratricopeptide
44	76	9.2	168	2	A05041	hypothetical prote
45	76	9.2	559	1	S55383	peptidylprolyl iso

ALIGNMENTS

RESULT 1

H83432

regulatory protein PirH PA1707 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C:Accession: H83432

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L...

.; Lory, S.; Olson, M.V

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83432

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-167 <STO>

A:Cross-references: UNIPROT:Q9I325; UNIPARC:UPI00000C5455; GB:AE004091; GB:AE004091; N

A:Experimental source: strain PA01

C:Genetics:

A:Gene: pcrH; PA1707

Query Match 66.4%; Score 549; DB 2; Length 167;

Best Local Similarity 64.8%; Pred. No. 1.7e-47;

Matches 103; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MQDTTTLTPEYEAELEAFMADGGTTLAMLQDITSGDTLEQLYALAFSOYQAGKWEADAKTIQ 60

Db 1 MNQPTPSDTQQQALEAFLRDGGGTLLMLRGLSEDTLEQLYALGFNQYQAGKWDQAQKIQ 60

Qy 61 ALCMLDHVEPRYFLGLGACRQAMGEFTAVQSYSGFAMLDLKDPRFPFHAGECRLQOQGL 120

Db 61 ALCMLDHYDARYFLGLGACRQSLGLYEQALQSYSGALMDLINEPRFPFHAECHLQLGLD 120

Qy 121 NGAESGPHSARLLIADTDPPQADLAASAKVMLEAIAIRRD 159

Db 121 DGAESGFYSARALAAQAPAEALAAAGAMLEAVTARKD 159

RESULT 2

C37314

regulatory protein LcrH - Yersinia pseudotuberculosis

C:Species: Yersinia pseudotuberculosis

C:Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 09-Jul-2004

C:Accession: C37314

R:Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.

J. Bacteriol. 173, 1607-1616, 1991

A:Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis:

A:Reference number: A37314; MUID:91154114; PMID:1705541

A:Accession: C37314

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <BER>

A;Cross-references: UNIPROT:P23995; UNIPARC:UPI0000000BC5; GB:M57893; NID:g155456; PIDN:  
C;Superfamily: ippi protein

Query Match 62.5%; Score 517; DB 2; Length 168;  
Best Local Similarity 58.5%; Pred. No. 2.6e-44;  
Matches 93; Conservative 34; Mismatches 32; Indels 0; Gaps 0;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60

DB 1 MQQETTTQEQVLAWESFLKGGGTIAMLNEISSDTLEQLYSLAFNQYQSGKYEDAHKVFQ 60

QY 61 ALCMLDHYEPYRFLGLGACRQAMGEFETAVQVSFGAMLDLKDPRFFPHAGECRLOQGD 120

DB 61 ALCVLDHYDSRFFLGLGACRQAMQYDLAIHSYSYGAIMDIKEPRFFPHAAECLLQKGL 120

QY 121 NGAESGFHSARLLADTPQADLAASAKVMLEAIAIRRD 159

DB 121 AEASGLFLAQELIADKTEPKELSTRVSSMLEAIKLKKE 159

## RESULT 3

C33601 low calcium response protein H - Yersinia pestis plasmid pCD1

C;Species: Yersinia pestis

C;Date: 18-May-1990 #sequence revision 18-May-1990 #text\_change 09-Jul-2004

C;Accession: C33601; T43595; T42890

R;Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C.

J. Bacteriol. 171, 5646-5659, 1989

A;Title: Molecular analysis of lcrGVH, the V antigen operon of Yersinia pestis.

A;Reference number: A33601; MUID:9000806; PMID:2477361

A;Accession: C33601

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-168 <PRI>

A;Cross-references: UNIPROT:P21207; UNIPARC:UPI000012E2B5; GB:M26405; NID:g155448; PIDN:

R;Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Karnes, J.; Kobayashi, A.; Brubaker

J. Bacteriol. 180, 5192-5202, 1998

A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.

A;Reference number: Z22578; MUID:98422474; PMID:9748454

A;Accession: T43595

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-168 <HUP>

A;Cross-references: UNIPARC:UPI000012E2B5; EMBL:AF053946; NID:g2996222; PIDN:AAC62575.1;

A;Experimental source: strain KIM

R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.

Infect. Immun. 66, 4611-4623, 1998

A;Title: DNA sequencing and analysis of the low-Caz+-response plasmid pCD1 of Yersinia P

A;Reference number: Z22273; MUID:98427122; PMID:9746557

A;Accession: T42890

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-168 <PER>

A;Cross-references: UNIPARC:UPI000012E2B5; EMBL:AF074612; NID:g3822037; PIDN:AAC69800.1;

A;Experimental source: strain KIMS

C;Genetics:

A;Gene: lcrH

A;Genome: plasmid

A;Note: plasmid pCD1

C;Superfamily: ippi protein

Query Match 61.5%; Score 509; DB 2; Length 168;

Best Local Similarity 57.9%; Pred. No. 1.7e-43;

Matches 92; Conservative 34; Mismatches 33; Indels 0; Gaps 0;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60

DB 1 MQQETTTQEQVLAWESFLKGGGTIAMLNEISSDTLEQLYSLAFNQYQSGKYEDAHKVFQ 60

QY 61 ALCMLDHYEPYRFLGLGACRQAMGEFETAVQVSFGAMLDLKDPRFFPHAGECRLOQGD 120

DB 61 ALCVLDHYDSRFFLGLGACRQAMQYDLAIHSYSYGAIMDIKEPRFFPHAAECLLQKGL 120

QY 121 NGAESGFHSARLLADTPQADLAASAKVMLEAIAIRRD 159

DB 121 AEASGLFLAQELIADKTEPKELSTRVSSMLEAIKLKKE 159

## RESULT 4

AB0851

hypothetical protein spaT [imported] - Salmonella enterica subsp. enterica serovar Typh

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AB0851

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB0851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-165 <PAR>

A;Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; GB:AL513382; PIDN:CAD05993.1

C;Genetics:

A;Gene: spaT

C;Superfamily: ippi protein

Query Match 20.1%; Score 166.5; DB 2; Length 165;

Best Local Similarity 30.8%; Pred. No. 2.6e-09;

Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKHI 58

DB 1 MDYQNNVSEERVAEMTWDA-VSEGATLKDVHGIPOQMDGLYAHAYEFYVNOGRLDEAETF 59

QY 59 FOALCMLDHYEPYRFLGLGACRQAMGEFETAVQVSFGAMLDLKDPRFFPHAGECRLOQG 118

DB 60 FRPLCIYDFYNDYTWGLAAVQLKQKQACDLYAVFTLLKNDYRPFVFTGCQCQLLMR 119

QY 119 DLNGAESGFHSARLLADTPQADLAASAKVMLEAI 154

DB 120 KAAKARQCFE---LVNTERTEDESLRAKALVLEAL 151

## RESULT 5

S70217

siPE protein - Salmonella typhi

C;Species: Salmonella typhi

C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 09-Jul-2004

C;Accession: S70217

R;Hermant, D.; Menard, R.; Arricau, N.; Parsot, C.; Popoff, M.Y.

Mol. Microbiol. 17, 781-789, 1995

A;Title: Functional conservation of the Salmonella and Shigella effectors of entry into

A;Reference number: S70215; MUID:96111497; PMID:8801431

A;Accession: S70217

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-165 <HER>

A;Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; EMBL:X82670; NID:g1009001; P:

A;Gene: siPE

C;Superfamily: ippi protein

Query Match 20.1%; Score 166.5; DB 2; Length 165;

Best Local Similarity 30.8%; Pred. No. 2.6e-09;

Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKHI 58

DB 1 MDYQNNVSEERVAEMTWDA-VSEGATLKDVHGIPOQMDGLYAHAYEFYVNOGRLDEAETF 59

QY 59 FOALCMLDHYEPYRFLGLGACRQAMGEFETAVQVSFGAMLDLKDPRFFPHAGECRLOQG 118

Db 60 FRFLCIYDFYNDYTMGLAAVQCKQFKACDLYAVAFLLKNDYRVPVFTGQCQLLMR 119  
Qy 119 DLNGAESGFHSGARLLADTDPOQADLAASAKVMLEAI 154  
Db 120 KAAKARQCFFE---LVNERTEDESLRKALVYLEAL 151

RESULT 6  
A57357  
sicA protein - Salmonella typhimurium  
C:Species: Salmonella typhimurium  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: A57357; S37357  
R:Kaniga, K.; Tucker, S.; Trollinger, D.; Galan, J.E.  
J. Bacteriol. 177, 3965-3971, 1995  
A:Title: Homologs of the Shigella IpaB and IpaC invasins are required for Salmonella ty  
A:Reference number: A57357; MUID:95332200; PMID:7608068  
A:Accession: A57357  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-165 <RES>  
A:Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; EMBL:U25631; NID:g975293; PID  
EMBO J. 12, 3779-3787, 1993  
R:Groisman, E.A.; Ochman, H.  
A:Title: Cognate gene clusters govern invasion of host epithelial cells by Salmonella ty  
A:Reference number: S37304; MUID:94008985; PMID:8404849  
A:Accession: S37357  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-32 <GRO>  
A:Cross-references: UNIPARC:UPI00001703EB; EMBL:X73525; NID:g404286; PIDN:CAAS1928.1; PI  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993  
C:Genetics:  
A:Gene: sicA; spat  
C:Superfamily: ippi protein

Query Match 20.1%; Score 166.5; DB 2; Length 165;  
Best Local Similarity 30.8%; Pred. No. 2.6e-09;  
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;  
Qy 1 MQDTTLTPVEYAEI--EAFWADGGTGLAMLDISGDTLEQLYALAFSQYQAGKWEADAKI 58  
Db 1 MDVQNVSERVAEMINDA-VSEGATLKDVHGIQDMMDGLYAHAYFYNQRLDEATFP 59  
Qy 59 FOALCMLDHYEPYFLGLGACRQAMGEFTAVQSYSGFAMLDLKDPRFPFHAGECRLQOG 118  
Db 60 FRFLCIYDFYNDYTMGLAAVCQKQFKACDLYAVAFLLKNDYRVPVFTGQCQLLMR 119  
Qy 119 DLNGAESGFHSGARLLADTDPOQADLAASAKVMLEAI 154  
Db 120 KAAKARQCFFE---LVNERTEDESLRKALVYLEAL 151

RESULT 7  
H91200  
type III secretion system CesD protein [imported] - Escherichia coli (strain O157:H7, su  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: H91200  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gisawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91200  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-151 <HAY>  
A:Cross-references: UNIPROT:O52134; UNIPARC:UPI00000D00B3; GB:BA000007; PIDN:BAE37999.1;  
A:Experimental source: strain O157:H7, substrain RMD 050952  
C:Genetics:  
A:Gene: ECs4576

Query Match 20.0%; Score 165; DB 2; Length 151;  
Best Local Similarity 29.1%; Pred. No. 3.3e-09;  
Matches 39; Conservative 27; Mismatches 68; Indels 0; Gaps 0;  
Qy 18 FMADGGTGLAMLDISGDTLEQLYALAFSQYQAGKWEADAKI FOALCMLDHYEPYFLGLG 77  
Db 14 FYQDGGTGLASLTNLTOQDLNDLHSHYATAYQSGDVITARNLFHLLTYLLEHWNYYDTLSLG 73  
Qy 78 ACROAMGEFTAVQSYSGFAMLDLKDPRFPFHAGECRLQOGDLNGAESGFHSGARLLADTD 137  
Db 74 LCHQRLSNHEDAQLCFARCATLVNQDPFRASYSGISYLLVGNKKWAKKAFACLMWCNEK 133  
Qy 138 PQQADLAASAKVML 151  
Db 134 EKVTYKENIKLL 147

RESULT 8  
D86047  
cesD [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: D86047  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: D86047  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-151 <STO>  
A:Cross-references: UNIPROT:O52134; UNIPARC:UPI00000D00B3; GB:AE005174; NID:g12518467;  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: cesD

Query Match 20.0%; Score 165; DB 2; Length 151;  
Best Local Similarity 29.1%; Pred. No. 3.3e-09;  
Matches 39; Conservative 27; Mismatches 68; Indels 0; Gaps 0;  
Qy 18 FMADGGTGLAMLDISGDTLEQLYALAFSQYQAGKWEADAKI FOALCMLDHYEPYFLGLG 77  
Db 14 FYQDGGTGLASLTNLTOQDLNDLHSHYATAYQSGDVITARNLFHLLTYLLEHWNYYDTLSLG 73  
Qy 78 ACROAMGEFTAVQSYSGFAMLDLKDPRFPFHAGECRLQOGDLNGAESGFHSGARLLADTD 137  
Db 74 LCHQRLSNHEDAQLCFARCATLVNQDPFRASYSGISYLLVGNKKWAKKAFACLMWCNEK 133  
Qy 138 PQQADLAASAKVML 151  
Db 134 EKVTYKENIKLL 147

RESULT 9  
S15576  
ippi protein - Shigella dysenteriae  
C:Species: Shigella dysenteriae  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S15576  
R:Yao, R.; Palchaudhuri, S.  
submitted to the EMBL Data Library, June 1991  
A:Description: Nucleotide sequence of the ipaBCD structure genes of Shigella dysenteria  
A:Reference number: S15575  
A:Accession: S15576  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-155 <YAO>  
A:Cross-references: UNIPROT:P18008; UNIPARC:UPI000012D80A; EMBL:X60777; NID:g46932; PID  
C:Superfamily: ippi protein

Query Match 18.3%; Score 151; DB 2; Length 155;



A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: H85937  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-163 <STO>  
A:Cross-references: UNIPROT:Q8X6H6; UNIPARC:UPI000000D088  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
C:Gene: ygeG  
C:Superfamily: ipbI protein

Query Match	14.0%;	Score 115.5;	DB 2;	Length 163;
Best Local Similarity	22.8%;	Pred. No. 0.00032;		
Matches	31;	Conservative 33;	Mismatches 61;	Indels 11; Gaps 3;
Qy	1	MOTDT- - - - -	TLTPEVEAELEAFMADGGTTLAMLDQISGDTLEQLVALAFSQVQAGKWEDAH	56
Db	1	MDTETIIFNNSDSEAWQLKHALSGENLALHGLTPTDLRIYAYAFDYHEKGNVTDAAE	60	
Qy	57	KIFCALCMLDHYEPRYFGLGACRQAMGEPTAVQ- - - - -	SYSFGAMLDLKDPRFPFHAGE	112
Db	61	IYYKLLCIYAPENHEYLKGFASVCQSKKYQQAADLYKLISNYS- - - - -	PYDDYSVIYRMGQ	117
Qy	113	CRLOQGDNLGAEISGFH	128	
Db	118	COIGAKNIDNMAOCFY	133	

## RESULT 14

D91092  
Hypothetical protein ECs3708 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050952)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: D91092  
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete Genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic  
A:Reference number: A9629; MUID:21156231; PMID:11258796  
A:Accession: D91092  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-163 <HAY>  
A:Cross-references: UNIPROT:Q8X6H6; UNIPARC:UPI00000D0B85; GB:BA000007; PIDN:BA837131.1  
A:Experimental source: strain O157:H7, substrain RIMD 050952  
C:Genetics:  
A:Gene: ECs3708  
C:Superfamily: ipplI protein

Query Match	14.0%;	Score 115.5;	DB 2;	Length 163;
Best Local Similarity	22.8%;	Pred. No. 0.00032;		
Matches	31;	Conservative 33;	Mismatches 61;	Indels 11; Gaps 3;

  

QY	1	MQTDT----	TLTPEYAEAEAF	WADGGT	LAMLDI	SGDTLE	OLYALAF	SQYQAGK	WEDAH	56
				:::		:::		:::		
Db	1	MDTETIEIF	NNSDEW	ANQLKSG	ENLALL	HGLTPT	ILDR	IYAYAF	DYHEKGN	VTDAE
				:::		:::		:::		
QY	57	KIFQALCML	DHYEPR	YFLG	LACRQAM	GEFETA	QVQ----	SYSFG	AMLDL	KDPPFP
				:::		:::		:::		
Db	61	IYVKLLCI	YAFEN	HEYL	KGFASV	CQSKKK	QQAQ	VDLYK	LSYNYS	----
				:::		:::		:::		
QY	113	CRLQOQ	DLNGA	ESGFH	128					
				:::						
Db	118	COIGAK	NIDNAM	OCFY	133					
				:::						

RESULT 15

G75457  
tetraatricopeptide repeat family protein - *Deinococcus radiodurans* (strain R1)  
C:Species: *Deinococcus radiodurans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: G75457  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A|Reference number: A75250; MUID: 20036896; PMID:10567266  
A|Accession: G75457  
A|Status: preliminary  
A|Molecule type: DNA  
A|Residues: 1-596 <WHI>  
A|Cross-references: UNIPROT:Q9RVT5; UNIPARC:UPI000000D3D8B; GB:AE001946; GB:AE000513; NI  
A|Experimental source: strain R1  
C|Genetics:  
A|Gene: DR0937  
A|Map position: 1

	Query Match	13.8%	Score 114;	DB 2;	Length 596;
	Best Local Similarity	26.5%;	Pred. No. 0.0021;		
	Matches	41;	Conservative	26;	Mismatches 72; Indels 16; Gaps 4
Qy	3	TDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEOLYALAFSQVQAGKWEDAHKIFQAL	62		
Db	114	TQTTPTPAGSAPATRPVTVVPLTAEQ-----QQLLQAQAQPAAGRYPOARNEFEAL	166		
Qy	63	CMLDHYEPYFLGLGACQACMGEPETAVQSYSGFAMLDLKDPRF--PFHAGECRLOQGDGL	120		
Db	167	IVRYNNPNPEHFGGLGALYQLGDLRGA--TFEQGFQMFQAPRYEGPNLGVIAIREGY	224		
Qy	121	NGAESGPHSARLLIADTPDQQAADLAASAKVMLEAIA	155		
Db	225	PDALRLYGEALTITQAQAP-----PAARQVLLLRALA	254		

Search completed: June 16, 2006, 19:25:08  
Job time : 17.1585 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 16, 2006, 18:53:15 ; Search time 124.873 Seconds  
(without alignments)  
1177.815 Million cell updates/sec  
Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTTPYEAELEAFMA.....QADLAASAKVMLEAIRRD 159

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827	100.0	167	2	Q70WN6 aeromonas s
2	780	94.3	167	2	Q699Q9 AERHY
3	769	93.0	167	2	Q5XL03 AERHY
4	596	72.1	167	2	Q7N0X2 PHOLL
5	587	71.0	168	2	Q84GV4 PHOLU
6	549	66.4	167	2	Q91325 PSEAE
7	548	66.3	168	2	Q30528 PSEAE
8	537	64.9	165	2	Q6TLM1 AERHY
9	518	62.6	168	2	Q87496 YEREN
10	517	62.5	168	1	LCRH YERPS
11	517	62.5	168	2	Q7BFE3 YEREN
12	517	62.5	168	2	Q84GT6 YEREN
13	509	61.5	168	1	LCRH YERPE
14	390.5	47.2	162	2	Q87P60 VIBPA
15	382	46.2	163	2	Q6QV83 VIBHA
16	247	29.9	186	2	Q2SH37 9GAMM
17	245	29.6	166	2	Q2WT10 DESVH
18	245	29.6	172	2	Q2SC45 9GAMM
19	185	22.4	161	2	Q7NUW9 CHRVO
20	181	21.9	183	2	Q2NVH7 SODGL
21	179	21.6	166	2	Q3JL21 BURPL
22	177	21.4	171	2	Q6K3K3 BURPS
23	175	21.2	190	2	Q6MBE1 PARUM
24	173	20.9	171	2	Q2T712 BURTH
25	172.5	20.9	156	2	Q62B06 BURWA
26	170	20.6	151	2	Q9AJ22 ECOLI
27	168.5	20.4	161	2	Q7WLX5 BORBR
28	167	20.2	161	2	Q84CS6 BORPE
29	167	20.2	167	2	Q7NUS7 CHRVO
30	166.5	20.1	165	1	SICA_SALDU
31	166.5	20.1	165	1	SICA_SALTI

32	166.5	20.1	165	1	SICA_SALTY	P69066 salmonella
33	166.5	20.1	165	2	Q57KN8_SALCH	Q57KN8 salmonella
34	166.5	20.1	165	2	Q5PEB9_SALPA	Q5PEB9 salmonella
35	166	20.1	151	2	Q93FL5_YENTR	Q93FL5 citrobacter
36	165	20.0	151	2	O52134_ECOLI	O52134 escherichia
37	165	20.0	151	2	Q7DB63_ECO57	Q7DB63 escherichia
38	164	19.8	155	2	Q4G4C9_EDWTA	Q4G4C9 edwardsiella
39	163.5	19.8	161	2	Q7W8B7_BORPA	Q7W8B7 bordetella
40	158.5	19.2	163	2	Q3Q839_9GAMM	Q3Q839 shewanella
41	158	19.1	169	2	Q93284_YEREN	Q93284 yersinia en
42	156	18.9	179	2	Q6MB00_PARUM	Q6MB00 parachlamyd
43	151	18.3	130	2	Q45P22_SHIDY	Q45P22 shigella dy
44	151	18.3	155	1	IPGC_SHIDY	P0A2U5 shigella dy
45	151	18.3	155	1	IPGC_SHIFL	P0A2U4 shigella fl

ALIGNMENTS

RESULT 1  
Q70WN6\_AERSA  
ID Q70WN6\_AERSA PRELIMINARY; PRT; 167 AA.  
AC Q70WN6;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE AcRH protein.  
GN Name=acrh;  
OS Aeromonas salmonicida subsp. salmonicida.  
OG Plasmid pASvira.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=29491;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267; PLASMID=pASvira;  
RX MEDLINE=22957181; PubMed=14594831;  
RX DOI=10.1128/JB.185.22.6583-6591.2003;  
RA Burr S.E., Stuber K., Frey J.;  
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";  
RT J. Bacteriol. 185:6583-6591(2003).  
RL [2]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=JF2267;  
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;  
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";  
RL Microbiol. 151:2111-2118(2005).  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AJ516009; CAD56770.1; -; Genomic DNA.  
DR EMBL; AJ616218; CAE83109.1; -; Genomic DNA.  
DR GO; GO:0005488; F.binding; IEA.  
DR GO; GO:0006950; P.response to stress; IEA.  
DR InterPro; IPR005415; SycD chap.  
DR InterPro; IPR011990; TPR\_Ilike\_helical.  
DR InterPro; IPR011716; TPR\_3.  
DR InterPro; IPR013026; TPR\_region.  
DR Pfam; PF07720; TPR\_3; 2.  
DR PRINTS; PR01595; SYCDCHAPRONE.  
DR PROSITE; PS50293; TPR\_REGION; 1.  
KW Plasmid  
SQ SEQUENCE 167 AA; 18566 MW; 569510660770E101 CRC64;

Query Match 100.0%; Score 827; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.3e-78;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MQDTTTPYEAELEAFMADGGTLMLODISDTLEQLYALFASQYQACKWDAHKIFQ 60  
|||||

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Db 1 MQTDTTLTPEYAELEAFNADGGTTLAMLDISGDTLEQLYALAFSQYQAGKVEDAHKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159

RESULT 2
Q699Q9 AERHY
ID Q699Q9 AERHY PRELIMINARY; PRT; 167 AA.
AC Q699Q9;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE AcRH.
GN Name=acrH;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
CC
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CC
DR EMBL; AY763611; AAV30234.1; -; Genomic_DNA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyCD_chap.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR011716; TPR_3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR_3; 2.
DR PRINTS; PR01595; SYCDHAPRONE.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 167 AA; 18533 MW; 18586 MW; 451FCF1DC6ED4211 CRC64;

Query Match 94.3%; Score 780; DB 2; Length 167;
Best Local Similarity 93.1%; Pred. No. 1.le-73;
Matches 148; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MQTDTTLTPEYAELEAFNADGGTTLAMLDISGDTLEQLYALAFSQYQAGKVEDAHKIFQ 60
Db 1 MQTDTTLTPEYAELEAFNADGGTTLAMLDISGDTLEQLYALAFSQYQAGKVEDAHKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159

RESULT 3
Q5XL03 AERHY
ID Q5XL03 AERHY PRELIMINARY; PRT; 167 AA.
AC Q5XL03;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.

DE AcRH.
GN Name=acrH;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Valches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpull G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
CC
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CC
DR EMBL; AY528667; AAS91820.1; -; Genomic_DNA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyCD_chap.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR011716; TPR_3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR_3; 2.
DR PRINTS; PR01595; SYCDHAPRONE.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 167 AA; 18533 MW; C6A9DEBEC335B8DD CRC64;

Query Match 94.3%; Score 780; DB 2; Length 167;
Best Local Similarity 93.1%; Pred. No. 1.le-73;
Matches 148; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Db 1 MQTDTTLTPEYAELEAFNADGGTTLAMLDISGDTLEQLYALAFSQYQAGKVEDAHKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAGGEFETAVQSYSGFAMLDLKDPRPFPHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPDQADLAASAKVWLEAIAIRRD 159

RESULT 4
Q7NOX2 PHOLL
ID Q7NOX2 PHOLL PRELIMINARY; PRT; 167 AA.
AC Q7NOX2;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Similar to low calcium response locus protein H LcrH.
DE OrderedLocusNames=plu3757;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusnok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
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CC EMBL; BX571871; CAE16129.1; -; Genomic_DNA.
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CC DR Photolista; plu3757; -.
CC DR BioCyc; PLUM243265:PLU3757-MONOMER; -.
CC DR GO; GO:0005488; P:binding; IEA.
CC DR GO; GO:0006950; P:response to stress; IEA.
CC DR InterPro; IPR005415; SycD_chap.
CC DR InterPro; IPR011990; TPR-like_helical.
CC DR InterPro; IPR011716; TPR_3.
CC DR InterPro; IPR013026; TPR_region.
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CC Db 124 GAESGFYSAQQLAAALPEQALAAASSAMLEAITIKR 160
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CC DT 07-FEB-2006, entry version 1.
CC DE Lssh.
CC GN Name=Lssh;
CC OS Photorhabdus luminescens (Xenorhabdus luminescens).
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC OC Enterobacteriaceae; Photorhabdus.
CC OX NCBI_TaxID=29488;
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CC RP NUCLEOTIDE SEQUENCE.
CC RC STRAIN=W14;
CC RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
CC RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
CC RT "Genomic islands in Photorhabdus ";
CC RL Trends Microbiol. 10:541-545(2002).
CC
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CC EMBL; AY144116; AA018054.1; -; Genomic_DNA.
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CC DR GO; GO:0006950; P:response to stress; IEA.
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Qy 122 GAESGFHSARLLADTDPQADLAASAKVMLEAIRR 158
Db 124 GAESGFYSAQQLAAALPEQALAAASSAMLEAITIKR 160
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DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, entry version 20.
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GN Name=pcrH; OrderedLocustNames=PA1707;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC
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CC EMBL; AE004597; AA05096.1; -; Genomic_DNA.
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CC DR BioCyc; PAER287:PA1707-MONOMER; -.
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CC DR InterPro; IPR011716; TPR_3.
CC DR InterPro; IPR013026; TPR_region.
CC DR Pfam; PF07720; TPR_3; 1.
CC DR PRINTS; PR01595; SYCDCHAPRONE.
CC DR PROSITE; PS0293; TPR_REGION; 1.
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CC Qy 61 ALCMLDHYEPYRFLGLGACROAMGEFFAVQSYSGAMLDLKDPRFPFHAGECRLOQGDNL 120
CC Db 61 ALCMLDHYDARYFLGLGACROSLGLYEQALQSYSGALMDINEPRFPFHAAECLQLGDL 120
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CC Qy 121 NGAESGFHSARLLADTDPQADLAASAKVMLEAIRR 159
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07-FEB-2006, entry version 10.  
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 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AH-1;  
 RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;  
 RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,  
 RA Leung K.Y.;  
 RT "A type III secretion system is required for *Aeromonas hydrophila* AH-1  
 pathogenesis.";  
 RL Infect. Immun. 72:1248-1256(2004).  
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 QY 67 HYEPYRFLGACRQANGFETAVQSVFGAMLDLKDPRPPFHAGRCRLOQGDNLGAESG 1  
 DB 65 HYEARFFLGLGACRQALGQFLAIDSYSYGAMMDLQBPFRFPFRAAECLQLGLEGAESG 1  
 QY 127 FHSARLLADTDPQOADIAAASKVMLEAIAIRRD 159  
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 DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.  
 DT 01-NOV-1998, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE Chaperone SycD.  
 GN Name=sycD;  
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 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
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 CC NCBI\_TaxID=630;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=W22703;  
 RA Irlarte M., Lambermont I., Kerbourn C., Cornelis G.R.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
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 EMBL; AF102990; AAD16814.1; -; Genomic DNA.

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DR GO:0006950; P:response to stress; IEA.
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DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR011716; TPR 3.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF07720; TPR 3; 2.
DR PRINTS: PR01595; SYCDCHAPRONE.
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Db 121 AEAESGLFLAQELIANKEPFKELSTRVSSMLEAIKLKKE 159

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LCRH YERPS
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AC P23995; Q66310;
DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-1992, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Low calcium response locus protein H.
GN Name=lcRH; OrderedLocusNames=PIV0056;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
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RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakansson S., Forsberg A., Norlander L., Macellaro A.,
RA Baekkan A., Boelin I., Wolf-Watz H.;
RT "Analysis of the v antigen lcrGVH-yopBD operon of Yersinia
pseudotuberculosis: evidence for a regulatory role of LcrH and LcrV.";
RL J. Bacteriol. 173:1607-1616(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP2953 / Serotype I; PLASMID=pYV;
RX PubMed=15358858; DOI=10.1073/pnas.040401201;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Darbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Mediates the negative regulation of the lcrGVH operon by
ATP or calcium. Acts as a modulator of the yop operon expression.
CC -!- SIMILARITY: Belongs to the lcrH/syCD chaparrone family.
CC -----
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CC EMBL: M57893; AAA27646.1; -; Genomic DNA.
CC EMBL: BX936399; CAP25399.1; -; Genomic DNA.
CC DR
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DR PIR: C37314; C37314.
DR PDB: 1OOL; Model; A=32-165.
DR PDB: 1OOS; Model; A=1-168.
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DR InterPro: IPR011716; TPR 3.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF07720; TPR 3; 2.
DR PRINTS: PR01595; SYCDCHAPRONE.
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FT CHAIN 1 168
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FT /FTID=PRO_0000206486.

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DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
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RN [1]
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RC STRAIN=8081;
RX MEDLINE=21295118; PubMed=11402007;
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RX DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popok M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype 0:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
CC -----
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DR EMBL; AF336309; AAK69212.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
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DR InterPro; IPR013026; TPR_region.
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DT 07-FEB-2006, entry version 11.
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90.
RX PubMed=1274790.
RY Foullet B.G.F., Bernard A., Purnelle B., Cornelis G.R.;
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL "Structural organization of virulence-associated plasmids of Yersinia
pestis."
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KIM5 / Biovar Mediaevalis;
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RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
pestis."
RN [3]
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RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
pestis."
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
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KW Plasmid.
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RESULT 13
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AC P21207;
DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1991, sequence version 1.
DT 07-MAR-2006, entry version 48.
DE Low calcium response locus protein H.
GN Name=lcRH; Synonyms=syCD;
GN OrderedLocusNames=YPCD1.30c, y5048, y0051, pCD53;
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OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
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RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=90008906; PubMed=2477361;
RA Price S.B., Leung K.Y., Barve S.S., Straley S.C.;
RT "Molecular analysis of lcRGVH, the V antigen operon of Yersinia
pestis."
RL J. Bacteriol. 171:5646-5653(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
Yersinia pestis KIM5."
RL Infect. Immun. 66:4611-4623(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
pestis."
RL J. Bacteriol. 180:5192-5202(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RT
```

```
RL Nature 413:523-527(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=91001 / Biovar Medaavalis;
RC PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: Mediates the negative regulation of the lcrGVH operon by
CC ATP or calcium. Acts as a modulator of the yop operon expression.
CC -!- SIMILARITY: Belongs to the lcrH/sydc chaperone family.
CC
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CC -----
CC EMBL; M26405; AAA27642.1; -; Genomic_DNA.
CC EMBL; AF074612; AAC69800.1; -; Genomic_DNA.
CC EMBL; AF053946; AAC62575.1; -; Genomic_DNA.
CC EMBL; AL117189; CAB54907.1; -; Genomic_DNA.
CC EMBL; AE017043; AAS58572.1; -; Genomic_DNA.
CC PIR; C33601; C33601..
CC
CC GenomeReviews; AE017043 GR; pCD53.
CC BioCyc; YPES229193:PCD53-MONOMER; -.
CC BioCyc; YPES632:YPCD1_30C-MONOMER; -.
CC InterPro; IPR005415; Sydc chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 2.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS50293; TPR_REGION; 1.
KW Chaperone; Complete proteome; Plasmid.
FT CHAIN 1 168 Low calcium response locus protein H.
FT FTId=PRO_000206485.
FT SEQUENCE 168 AA; 19015 MW; 46206AF240EB0064 CRC64;
Query Match 61.5%; Score 509; DB 1; Length 168;
Best Local Similarity 57.9%; Pred. No. 4e-45;
Matches 92; Conservative 34; Mismatches 33; Indels 0; Gaps 0;
Qy 1 MOTDTLTPEYEA-ELEAFMADGGTGLMQLDISGDTLEQLYALAFSQYQAGKWEDAHKIFQ 60
Db 1 MQQETTTQEQVLAWESFLKGGGTIAMLNELSSDTLEQLSLAFNQSQGYEDAHKVFQ 60
Qy 61 ALCMLDHYEPYRFLGLGACQAMGEFETAVOSYSGFAMLDLKDPRFFPHAGECRLQOQDL 120
Db 61 ALCVLDHYDSRFFLGLGACQAMQYDLAIHYSYGAIMDIKEPRFFPHAAECILQKGL 120
Qy 121 NGAESGFHARLLADTDPQADLAASAKVMLEAIAIRR 159
Db 121 NGAESGFHARLLADTDPQADLAASAKVMLEAIAIRR 159
Qy 121 AEASGLFLAQELIADTKTEFKELSTRVSSMLEAIKLKKE 159
Db 121 AEASGLFLAQELIADTKTEFKELSTRVSSMLEAIKLKKE 159
RESULT 14
Q87P60_VIBPA
ID Q87P60_VIBPA PRELIMINARY; PRT; 162 AA.
AC Q87P60;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Low calcium response locus protein H.
GN OrderedLocNames=VP1658;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP
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RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC
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CC -----
CC EMBL; BA000031; BAC59921.1; -; Genomic_DNA.
CC GO; GO:0005488; P:binding; IEA.
CC GO; GO:0006950; P:response to stress; IEA.
CC InterPro; IPR005415; Sydc chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 2.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 162 AA; 18128 MW; 94FB1967B5C9EC1F CRC64;
Query Match 47.2%; Score 390.5; DB 2; Length 162;
Best Local Similarity 47.5%; Pred. No. 1.2e-32;
Matches 75; Conservative 36; Mismatches 46; Indels 1; Gaps 1;
Qy 2 QTDTTLTPEYEA-ELEAFMADGGTGLMQLDISGDTLEQLYALAFSQYQAGKWEDAHKIFQ 60
Db 3 KTNATDPQMQAABELLSFEEGGTLKMLHDVTSADTIEHIYAVGVYVQSGKLEQAAKVFQ 62
Qy 61 ALCMLDHYEPYRFLGLGACQAMGEFETAVOSYSGFAMLDLKDPRFFPHAGECRLQOQDL 120
Db 63 LLSMLDHYQARFFIGLGAARQELGEYLOAIDAYSAAALVDINPRFFPHAAECHLKLEQL 122
Qy 121 NGAESGFHARLLADTDPQADLAASAKVMLEAIAIRR 158
Db 123 TEAESGFYSAKEMSGAGKSQYADLHQHAGIMLEAVRNKR 160
RESULT 15
Q6QVS3_VIBHA
ID Q6QVS3_VIBHA PRELIMINARY; PRT; 163 AA.
AC Q6QVS3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE VcrH.
GN Names=vcrH;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Henke J.M., Basler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC
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CC -----
CC EMBL; AV524044; AAS13308.1; -; Genomic_DNA.
CC GO; GO:0005488; P:binding; IEA.
CC GO; GO:0006950; P:response to stress; IEA.
CC InterPro; IPR005415; Sydc chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 2.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS50293; TPR_REGION; 1.
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SQ SEQUENCE 163 AA; 18212 MW; A605672027F1252A CRC64;  
Query Match 46.2%; Score 382; DB 2; Length 163;  
Best Local Similarity 49.0%; Pred. No. 9.2e-32;  
Matches 71; Conservative 33; Mismatches 41; Indels 0; Gaps 0;  
Qy 14 ELEAFMADGGT LAMLODISGDTLEQLYALAFSQVQAGKWEDAHKIFQALCMLDHYEPRYF 73  
Db 17 ELLSFLEEGGTLKMLHDVSDTIEHIYAVGVNFFQSGKIEQAAKV FOLL SMLDHYQARFF 76  
Qy 74 LGLGACRQAMGEPETAVQSYSGFAMLDLKDPRFPFHAGECRLOQGD LNGAESGFHSARLL 133  
Db 77 IGLGAARQELGEYLQALDAYSAALVDVNDPRPFHSAECHLKLEQLTEAESGFYSAKEM 136  
Qy 134 ADTDPQADLAASAKVMLEAIRR 158  
Db 137 SAGKSEYADLHQ RAGIMLEAVRNKR 161

Search completed: June 16, 2006, 19:23:00  
Job time : 125.873 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 29.3439 Seconds  
(without alignments)  
474.285 Million cell updates/sec

Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTLTPEYEAELEAFMA.....QADLAASAKVMLEAIRRD 159

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /EMC\_Celerra\_SID3S/protdata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SID3S/protdata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SID3S/protdata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SID3S/protdata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SID3S/protdata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SID3S/protdata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SID3S/protdata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	66.3	239	2	US-09-252-991A-29963 Sequence 29963, A
2	163.5	19.8	182	2	US-09-543-681A-6578 Sequence 6578, A
3	125.5	15.2	157	2	US-09-763-620-19 Sequence 19, Appl
4	121.5	14.7	158	2	US-09-902-540-13633 Sequence 13633, A
5	118	14.3	144	2	US-09-763-620-21 Sequence 21, Appl
6	116.5	14.1	154	2	US-09-902-540-16064 Sequence 16064, A
7	105	12.7	210	2	US-09-198-452A-869 Sequence 869, App
8	105	12.7	242	2	US-09-438-185A-813 Sequence 813, App
9	100	12.1	191	2	US-09-198-452A-1095 Sequence 1095, App
10	100	12.1	191	2	US-09-438-185A-1022 Sequence 1022, App
11	84.5	10.2	1564	2	US-09-976-594-309 Sequence 309, App
12	83	10.0	639	2	US-09-902-540-12091 Sequence 12091, A
13	80	9.7	458	1	US-08-336-618-24 Sequence 24, Appl
14	79	9.6	315	2	US-09-585-645A-42 Sequence 42, Appl
15	79	9.6	667	2	US-09-248-796A-18663 Sequence 18663, A
16	78.5	9.5	380	2	US-09-902-540-12056 Sequence 12056, A
17	78.5	9.5	526	2	US-09-902-540-16327 Sequence 16327, A
18	78.5	9.5	806	2	US-09-328-352-7160 Sequence 7160, App
19	78	9.4	211	2	US-09-205-258-263 Sequence 263, App
20	78	9.4	211	2	US-10-004-860-263 Sequence 263, App
21	78	9.4	261	2	US-09-205-258-505 Sequence 505, App
22	78	9.4	261	2	US-10-004-860-505 Sequence 505, App
23	78	9.4	308	1	US-08-807-050-1 Sequence 1, Appli
24	78	9.4	317	2	US-09-205-258-504 Sequence 504, App
25	78	9.4	317	2	US-10-004-860-504 Sequence 504, App
26	77.5	9.4	322	2	US-09-902-540-11744 Sequence 11744, A

27	77	9.3	1191	2	US-09-921-099A-2 Sequence 2, Appli
28	77	9.3	1191	2	US-09-921-099A-4 Sequence 4, Appli
29	76.5	9.3	528	2	US-09-252-991A-32995 Sequence 32995, A
30	75.5	9.1	1490	2	US-09-252-991A-28442 Sequence 28442, A
31	75	9.1	308	1	US-08-807-050-3 Sequence 3, Appli
32	75	9.1	600	2	US-09-252-991A-31546 Sequence 31546, A
33	75	9.1	981	1	US-08-649-046-2 Sequence 2, Appli
34	74.5	9.0	2472	2	US-09-538-092-1312 Sequence 1312, Ap
35	74	8.9	466	2	US-09-248-796A-19009 Sequence 19009, A
36	74	8.9	1087	2	US-09-252-991A-28584 Sequence 28584, A
37	73.5	8.9	410	2	US-09-248-796A-17607 Sequence 17607, A
38	72.5	8.8	369	2	US-09-902-540-12050 Sequence 12050, A
39	72.5	8.8	479	1	US-08-942-218A-2 Sequence 2, Appli
40	72.5	8.8	499	1	US-08-610-731A-2 Sequence 2, Appli
41	72.5	8.8	499	1	US-09-067-379-2 Sequence 2, Appli
42	72.5	8.8	499	2	US-09-067-506-2 Sequence 2, Appli
43	72.5	8.8	499	2	US-08-951-034B-2 Sequence 2, Appli
44	72.5	8.8	510	2	US-09-252-991A-19584 Sequence 19584, A
45	72.5	8.8	519	2	US-09-786-240-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-252-991A-29963  
; Sequence 29963, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29963  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29963

Query Match	66.3%;	Score 548;	DB 2;	Length 239;
Best Local Similarity	65.2%;	Pred. No. 5.5e-59;		
Matches	103;	Conservative 21;	Mismatches 34;	Indels 0; Gaps 0;
Qy	2	QTDTTLTPEYEAELEAFMADGGTTLMLQDISGDTLEOLYALAFSQYQAGKWEADAKIFQA	61	
Db	74	QQAATPSDTCQQQALEAFRLRGDTLMLRGSEDTLEOLYALGNQYQAGKWDAAQKIFQA	133	
Qy	62	LCMLDHYEPYFGLGACROAMGEFTAVQSYSGAMLDLKDPRFPFHAGECRLQOQDGLN	121	
Db	134	LCMLDHYARYFLGLGACRQSLGLYEQALQSYSGALMINEPRFPFHAAEHLQQLDGLD	193	
Qy	122	GAESGFHSARLLADTPQQADLAASAKVMLEAIRRD	159	
Db	194	GAESGFYSARALAAAPHAHEALAAARAGAMLEAVTARKD	231	

RESULT 2  
US-09-543-681A-6578  
; Sequence 6578, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A





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RESULT 6
US-09-902-540-16064
; Sequence 16064, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15949)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16925
; SEQ ID NO 16064
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16064

Query Match      14.1%; Score 116.5; DB 2; Length 154;
Best Local Similarity 26.9%; Pred. No. 3.7e-06;
Matches 35; Conservative 29; Mismatches 61; Indels 5; Gaps 3;

QY 28 LODISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPYFLGLGACROAMGEFE 87
Db 14 VKPLSGPEMLERATERGENLFQDGRFRESLTLFQSLAMDPTAEYFQTLGACHLALEDLD 73

QY 88 TAVOSYSFGMLDLKDPFRPF--HAGECRLOQGDNLNGAESGFHSARLADTDPOQADLAAS 146
Db 74 LAESYFNRALELDPD--LTFPVNRGEVHLRGKVHEAARDFNHA---VGLDPGEQDPLSA 129

QY 147 AKVMLEIAI 156
Db 130 RARMLAAAL 139

RESULT 7
US-09-198-452A-869
; Sequence 869, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 869
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-869

Query Match      12.7%; Score 105; DB 2; Length 210;
Best Local Similarity 23.4%; Pred. No. 0.00015;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 19 MADGGTTLAQDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPYFLGLGA 78
Db 43 LSNGLDLQQLGLSDYLLEIYTVAYTFYSQGYNEAVGLFQLIAAQAQPNQYKMYLGLSS 102

QY 79 CROAMGEFETAVOSY--SFGAMLDLKDPRFPFHAGE--CRLOQGDNLNGAESGFHSARL-L 133
Db 103 CYHQHLYNEAAGFFLAFAQPD--NPIPPYYIADSLKLQOPE---ESNLFDDVTMDI 157

QY 134 ADTDPQADLAASAKVMLEAI 154
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Db 158 CGNPEFKILKERCQIMKQSI 178

RESULT 8
US-09-438-185A-813
; Sequence 813, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 018941-00041US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 813
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0811
US-09-438-185A-813

Query Match      12.7%; Score 105; DB 2; Length 242;
Best Local Similarity 23.4%; Pred. No. 0.00018;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 19 MADGGTTLAQDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPYFLGLGA 78
Db 75 LSNGLDLQQLGLSDYLLEIYTVAYTFYSQGYNEAVGLFQLIAAQAQPNQYKMYLGLSS 134

QY 79 CROAMGEFETAVOSY--SFGAMLDLKDPRFPFHAGE--CRLOQGDNLNGAESGFHSARL-L 133
Db 135 CYHQHLYNEAAGFFLAFAQPD--NPIPPYYIADSLKLQOPE---ESNLFDDVTMDI 189

QY 134 ADTDPQADLAASAKVMLEAI 154
Db 190 CGNPEFKILKERCQIMKQSI 210

RESULT 9
US-09-198-452A-1095
; Sequence 1095, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1095
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1095

Query Match      12.1%; Score 100; DB 2; Length 191;
Best Local Similarity 22.2%; Pred. No. 0.00054;
Matches 32; Conservative 28; Mismatches 80; Indels 4; Gaps 1;

QY 4 DTTLTPEYEALEAFMADGG----TLAMLQDISGDTLEQLYALAFSQYQAGKWEADAHKIF 59
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APPLICANT: Peattie, Debra A.  
APPLICANT: Harding, Matthew W.  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING  
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN  
TITLE OF INVENTION: CDNA  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336.618  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/963,325  
FILING DATE: 16-OCT-1992  
APPLICATION NUMBER: US 07/777,752  
FILING DATE: 11-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/  
FILING DATE: 09-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: VP191-06A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 458 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-618-24

Query Match 9.7%; Score 80; DB 1; Length 458;  
Best Local Similarity 23.9%; Pred. No. 0.55;  
Matches 38; Conservative 21; Mismatches 76; Indels 24; Gaps 5;

Qy 7 LTPEYAELEAFMADGGTTLMLQDISGDTLQLYALAFSQY-QAGKVEDAHKIF----- 59  
Db 261 MSSEKLEQSAIVKRGTYVF-----KEGKYQALLQYKKIVMLVESSFSSEVQ 312  
Qy 60 --QALCMLDHYEPYFYLGLGACRQAMGEFETAVOSYSGFAMLDLKDPRFPFHAGECKLQ 117  
Db 313 KAQALRLASH-----LNLAMCHLKLOAFSAVESCNAKLELDSNNEKGLFRGGEHLAV 366  
Qy 118 GDINGAEGSFHSA-RLLADTDPQADLAASAQVWLEAIA 155  
Db 367 NDFLARADFOKVLQLYPSNKAQAQLAVCCOORIRKOIA 405

RESULT 14  
US-09-585-645A-42  
Sequence 42, Application US/09585645A  
Patent No. 6838444  
GENERAL INFORMATION:  
APPLICANT: Zoghbi, Huda  
APPLICANT: Bellien, Hugo  
APPLICANT: Bermingham, Nessim  
APPLICANT: Hassan, Bessam  
APPLICANT: Ben-Arie, Nissim

TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associate  
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnormal Cell Proliferation  
FILE REFERENCE: P01899US2  
CURRENT APPLICATION NUMBER: US/09/585,645A  
CURRENT FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: US 60/137,060  
PRIOR FILING DATE: 1999-06-01  
PRIOR APPLICATION NUMBER: US 60/176,993  
PRIOR FILING DATE: 2000-01-19  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 315  
TYPE: PRT  
ORGANISM: FROG  
US-09-585-645A-42

Query Match 9.6%; Score 79; DB 2; Length 315;  
Best Local Similarity 27.2%; Pred. No. 0.43;  
Matches 28; Conservative 11; Mismatches 36; Indels 28; Gaps 4;

Qy 8 TPEYAELEAFMADGGTTLMLQDISGDTLQOLYALAFSQYQAGKVEDAHKIFQALCMLDH 67  
Db 237 TPYEGALTPLSLGIGNFSKQDSSPD-MDKSTAFR-SPYPA----- 276  
Qy 68 YEPYFYLGLGACRQAMGEFETAVOSYSGFAMLDLKDPRFPFPHA 110  
Db 277 -----LGLGSHGHASHFHTSVPRYEL--PIDMAYEPYFPHA 311

RESULT 15  
US-09-248-796A-18663  
Sequence 18663, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 18663  
LENGTH: 667  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-18663

Query Match 9.6%; Score 79; DB 2; Length 667;  
Best Local Similarity 19.7%; Pred. No. 1.3;  
Matches 42; Conservative 34; Mismatches 61; Indels 76; Gaps 10;

Qy 11 YEAELEAFMADGGTTLMLQD--ISGDTLEQLYA-----LAFSQ 46  
Db 160 YEQALNPHVENGETWGLLGHLYMLDNLQRAYAAQYQALFYLENPNVPKLVHGHGILYDR 219  
Qy 47 YQAGKVEDAHKIFQALCMLDHYEPY-----FLGLGACRQAMGEFETAVOSYSGFAMLD 100  
Db 220 Y--GSLEYAEAFVRVLDD---PNFDKANEIVFRLGIYKHQKLOPALECFQY----I 270  
Qy 101 LKDRPFP-----FHAGECRLQOGLNGAESGF-----HSARLL-----ADT 136  
Db 271 LNNPPHPLTQDVMWFQIGSVYEQQKNGAKDAYEKVQLNPHHAKVLQQLGCLYSQAES 330  
Qy 137 DPQ-----QADLAASAQVWLEAIAI 156  
Db 331 NPSTPANGAAPPHKPFQODLTIALKYLKQSLV 363

Search completed: June 16, 2006, 19:28:58  
Job time : 30.3439 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 88.9366 Seconds  
(without alignments)  
828.131 Million cell updates/sec

Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTTLTPEYAELEAFMA.....QADLAASAKVMLEAIAIRRD 159

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA Main.\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pbp.\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pbp.\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pbp.\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pbp.\*
  - 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pbp.\*
  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827	100.0	159	5	US-10-813-908-9
2	549	66.4	167	4	US-10-282-122A-66316
3	214	25.9	179	6	US-11-098-686-11402
4	177	21.4	171	4	US-10-282-122A-50249
5	169.5	20.5	172	4	US-10-282-122A-68873
6	166.5	20.1	165	4	US-10-282-122A-73507
7	166.5	20.1	165	4	US-10-282-122A-76036
8	125.5	15.2	157	4	US-10-282-122A-75323
9	125.5	15.2	157	4	US-10-763-883-19
10	118	14.3	144	4	US-10-763-883-21
11	109	13.2	246	3	US-10-282-122A-55326
12	107.5	13.0	163	3	US-09-741-669-329
13	107.5	13.0	163	4	US-10-282-122A-42727
14	105	12.7	210	4	US-10-289-762-869
15	105	12.7	231	4	US-10-282-122A-54986
16	105	12.5	231	5	US-10-503-135-88
17	103.5	12.5	232	5	US-10-503-135-117
18	100	12.1	172	5	US-10-503-135-91
19	100	12.1	191	4	US-10-289-762-1095
20	90	10.9	304	4	US-10-369-493-18939
21	88.5	10.7	280	4	US-10-369-493-11967
22	84.5	10.2	1564	5	US-10-732-923-17031
23	83	10.0	834	4	US-10-156-761-12909
24	80.5	9.7	562	6	US-11-024-959-422
25	80.5	9.7	579	4	US-10-282-122A-48469
26	80.5	9.7	601	6	US-11-079-463-7428
27	80.5	9.7	676	4	US-10-369-493-3268

28	80	9.7	380	4	US-10-425-115-290062	Sequence 290062,
29	80	9.7	458	5	US-10-732-923-9310	Sequence 9310, Ap
30	80	9.7	482	6	US-11-079-463-6494	Sequence 6494, Ap
31	80	9.7	554	4	US-10-425-115-204269	Sequence 204269,
32	79.5	9.6	225	4	US-10-424-599-260796	Sequence 260796,
33	79	9.6	315	4	US-10-004-717-42	Sequence 42, Appl
34	79	9.6	315	5	US-10-860-373-42	Sequence 42, Appl
35	79	9.6	315	5	US-10-860-724-42	Sequence 11914, A
36	79	9.6	574	6	US-11-024-959-300	Sequence 300, App
37	79	9.6	574	6	US-10-369-493-11914	Sequence 11914, A
38	79	9.6	1080	4	US-10-451-467A-466	Sequence 466, App
39	78.5	9.5	240	5	US-10-732-923-9366	Sequence 9366, Ap
40	78.5	9.5	242	5	US-10-732-923-9367	Sequence 9367, Ap
41	78.5	9.5	292	5	US-10-450-763-50531	Sequence 50531, A
42	78	9.4	193	4	US-10-425-114-62615	Sequence 62615, A
43	78	9.4	211	3	US-09-933-767-263	Sequence 263, App
44	78	9.4	211	4	US-10-004-860-263	Sequence 263, App
45	78	9.4	211	4	US-10-023-282-263	Sequence 263, App

ALIGNMENTS

RESULT 1

US-10-813-908-9  
; Sequence 9, Application US/10813908  
; Publication No. US20050058662A1  
; GENERAL INFORMATION:  
; APPLICANT: Frey, Joachim Stuber  
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and t  
; FILE REFERENCE: MIC01/2315/WO  
; CURRENT APPLICATION NUMBER: US/10/813,908  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US/10/416,902  
; PRIOR FILING DATE: 2003-05-15  
; PRIOR APPLICATION NUMBER: PCT/CA01/01589  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Aeromonas salmonicida  
US-10-813-908-9

Query Match	100.0%;	Score 827;	DB 5;	Length 159;
Best Local Similarity	100.0%;	Pred. No. 6.3e-88;		
Matches	159;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MQDTTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEAHTKIFQ	60	
Db	1	MQDTTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEAHTKIFQ	60	
Qy	61	ALCMLDHYERYFLGLGACQAMGEFETAVQSYSGFAMLDLKDPRFFPHAGECRLQOQDL	120	
Db	61	ALCMLDHYERYFLGLGACQAMGEFETAVQSYSGFAMLDLKDPRFFPHAGECRLQOQDL	120	
Qy	121	NGAESGFHARLLADTDPQADLAASAKVMLEAIAIRRD	159	
Db	121	NGAESGFHARLLADTDPQADLAASAKVMLEAIAIRRD	159	

RESULT 2

US-10-282-122A-66316  
; Sequence 66316, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith





Qy 119 DLNGAESGFHSARLLADTPQADLAASAKVMLEAI 154  
Db 120 KAARQCFE---LVNERTEDSLRAKALVYLEAL 151

## RESULT 7

US-10-282-122A-76036  
; Sequence 76036, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 76036  
; LENGTH: 165  
; TYPE: PRT  
; ORGANISM: Salmonella typhi

US-10-282-122A-76036

Query Match 20.1%; Score 166.5; DB 4; Length 165;  
Best Local Similarity 30.8%; Pred. No. 7.7e-11;  
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;  
Qy 1 MOTDTTLTPEYAEAL--EAFMADGGTLAMLQDISGDTLEQLYALAFSQQAGKWEADAKI 58  
Db 1 MDYQNVSEERVAEMTWDA-VSEGATLKDVGIPQDMMDGLYAHAYEFYNOGRLEDAET 59  
Qy 59 EQALCMLDHYEPRYFLGLCACROAMGEFETAVQSISFGAMLDLKDPRFPFHAGECRLOOG 118  
Db 60 FRFLCIYDFYNDYTNGLAAVQLKKQOKACDLVAFVTLKNDYRPVFTGQCQLMR 119

Qy 119 DLNGAESGFHSARLLADTPQADLAASAKVMLEAI 154  
Db 120 KAARQCFE---LVNERTEDSLRAKALVYLEAL 151

## RESULT 8

US-10-282-122A-75323  
; Sequence 75323, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 75323  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Salmonella typhimurium

US-10-282-122A-75323

Query Match 15.2%; Score 125.5; DB 4; Length 157;  
Best Local Similarity 27.0%; Pred. No. 4.4e-06;  
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;  
Qy 1 MOTDTTLTPEYAEALAFMADGGTLAM-LQDISGDTLEQLYALAFSQQAGKWEADAKIF 59  
Db 1 MKKDFTLQAHDT--MRFFRGSLRMLDDDDVTQPLNTLYRYATQLMVEKFAAGARLF 58  
Qy 60 QALCMLDHYEPRYFLGLCACROAMGEFETAVQSISFGAMLDLKDPRFPFHAGECRLOOG 119  
Db 59 QULLTYDAMSFDYWFRLGECQCAQKHGGEAIYAYGAAQIKIDAPQAPWAAAECYLACDN 118  
Qy 120 LNGAESGFHS-ARLLADTPQADLAASAKVMLEAI 157  
Db 119 VCYATKALKAVVVICGVSEHQLRQRAEKMLQQLSDR 156  
RESULT 9  
US-10-763-883-19  
; Sequence 19, Application US/10763883  
; Publication No. US20040203039A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Hensel  
; APPLICANT: David William Holden





```

; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Alllyn
; APPLICANT: Ohlssen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; TITLE OF INVENTION: proliferation of E. coli
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-329

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Query Match	13.0%;	Score 107.5;	DB 3;	Length 163;
Best Local Similarity	22.3%;	Pred. No. 0.00058;		
Matches	31;	Conservative 30;	Mismatches 61;	Indels 17; Gaps 3

  

Qy	1	WOTDT----	TLTPEYAELEAFMADGGTGLAMLQDISGDTLLEQLYALAFSQYQAGKWEDAH	56
			: : : :         : : : :	
Db	1	MSTEIETIFNNSDWMANQLKHALSKGENLALLHGLTPTDLIRIYAYAFDYHEKGNITDAE	60	
			: : : :         : : : :	
Qy	57	KIFQALCMLDHYEPYFLGLGACQAMGEFETAVQSYSGFAMDLKDPPFP-----FH	109	
			: : : :         : : : :	
Db	61	IYYKELCIYAPENHEYLKDFASVCQPKKKYQQAYDLYK-----LSYNYFPDDYSVIYR	114	
			: : : :         : : : :	
Qy	110	AGECRLOQGDNLNGAESGFH	128	
			: : : :         : : : :	
Db	115	MGOCOIGAKNIDNMAQCFY	133	
			: : : :         : : : :	

RESULT 13  
US-10-282-122A-42727  
; Sequence 42727, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

```

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42727
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-42727

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Query Match	13.0%;	Score 107.5;	DB 4;	Length 163;
Best Local Similarity	22.3%;	Pred. No. 0.00058;		
Matches 31; Conservative	30;	Mismatches 61;	Indels 17;	Gaps 3
Qy	1	MQTDT---	TITPEYAELEAFMADGGTTLAMLDQISGDTLEQLVALAFSQVQAGKWEADH	56
Db	1	MSTETIIFNNSDEWANQLKHALSKGENLALHGLTTPDLRIIYAYAFDYHEKGNITDAE		60
Qy	57	KIFQALCMLDHYEPFYPLGLGACRQAMGEFETAVQSYSGFAMGLDLKDPFRP-		109
Db	61	IYYKFLCIYAFENHEYLKDFASVCQPKKYYQAYDLK----	LSYNYFPDYDYSVIVR	114
Qy	110	AGECRLOQGDNLNGAESGFH		128
Db	115	MGQCQIGAKNIDNAMQCIFY		133

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RESULT 14
US-10-289-762-869
; Sequence 869, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifats, R.
; TITLE OF INVENTION: Chlamydia pneumoniae
; TITLE OF INVENTION: thereof and uses thereof
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 869
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-869

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	Query Match	12.7%	Score 105;	DB 4;	Length 210;
	Best Local Similarity	23.4%	Pred. No. 0.0016;		
	Matches	33;	Conservative	34;	Mismatches 64;
					Indels 10;
					Gaps 5
Qy	19	MADGGTLLAMLDISGDTLEQLYALAFSQYQAGKWEDAHKIFQALCMLDHYSPRYFLGGA	78		
Db	43	LSNGLDLQQILGSLDYLLEETVYATFYSGKKNEAVGLFQLLAAAQPNYKYMGLGSS	102		
Qy	79	CRQAMGFEFATAVSQY--SFGAMLDLKDPRFPFFHAGE--CRLQQGDNLNGAESGFHSARL-L	133		
Db	103	CYHQLHLYNEAAGCFFLAFDAQPD--NPIPPYYTADSLLLKQQPE---ESNFLDVTWDI	157		
Qy	134	ADTDPQQADLAASAKVMLEAI	154		
Db	158	CGNPFKILKERCOIMKQSI	178		

RESULT 15  
US-10-282-122A-54986  
; Sequence 54986, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos

```

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA. 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54986
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54986
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Query Match      12.7%; Score 105; DB 4; Length 231;
Best Local Similarity 23.4%; Pred. No. 0.0018;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

Qy      19  MADGGTAMQLQDISGDTLEQLYALAFSQYQAGKWDHAKIFQALCMLDHYEPRYFLGLGA 78
Db      64  LSNGLDLQQILGLSDYLEEITYVATFYSGQKYNEAVGLFQLLAAAQPNKYKMYLGLSS 123

Qy      79  CRQAMGFEFATAVQSY--SFGAMLDLKDPRFPFHAGE--CRLQQGDLNGAESGFHSARL-L 133
Db     124  CYHQHLHYNEAAGFFLAFAQPD--NPIPPYYIADSLKLOQPE---ESNNFLDVTMDI 178

Qy     134  ADTDPQQAADLAASAKVMLEAI 154
Db     179  CGNNPEFKILKERCQIMKQSI 199
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Search completed: June 16, 2006, 20:24:57  
Job time : 89.9366 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 6.85122 Seconds  
(without alignments)  
523.484 Million cell updates/sec

Title: US-10-813-908A-9  
Perfect score: 827  
Sequence: 1 MQDTTITPEYEAEAFMA.....QADLAASAKVMLEIAIRRD 159

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB.pap:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pap:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pap:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pap:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pap:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pap:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pap:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	10.2	330	6	US-10-449-902-39402
2	80	9.7	183	6	Sequence 39402, A
3	80	9.7	255	6	Sequence 20069, A
4	80	9.7	671	6	US-10-953-349-20068
5	76.5	9.3	220	6	US-10-449-902-48030
6	76.5	9.3	250	6	Sequence 48030, A
7	76.5	9.3	365	6	US-10-953-349-1110
8	74.5	9.0	403	6	Sequence 1110, Ap
9	71	8.6	638	7	US-10-953-349-1108
10	70.5	8.5	269	6	Sequence 1108, Ap
11	68.5	8.3	344	6	US-10-449-902-48463
12	68	8.2	580	6	US-10-471-571A-5142
13	67	8.1	357	6	US-10-449-902-47938
14	67	8.1	375	6	Sequence 20, Appl
15	67	8.1	483	6	Sequence 47938, A
16	67	8.1	483	6	Sequence 5142, Ap
17	67	8.1	655	7	US-10-449-902-56054
18	67	8.1	726	6	Sequence 56054, A
19	66.5	8.0	270	7	US-10-953-349-13122
20	66.5	8.0	304	7	Sequence 13122, A
21	66.5	8.0	575	6	US-10-953-349-13121
22	66.5	8.0	643	6	Sequence 13121, A
23	66.5	8.0	847	6	US-10-449-902-54809
24	66.5	8.0	1196	6	Sequence 54809, A
25	66	8.0	485	6	US-10-449-902-55852

26	66	8.0	847	6	US-10-449-902-42616	Sequence 42616, A
27	66	8.0	927	6	US-10-449-902-43750	Sequence 43750, A
28	66	8.0	972	6	US-10-449-902-41420	Sequence 41420, A
29	65.5	7.9	315	6	US-10-449-902-39948	Sequence 39948, A
30	65.5	7.9	338	6	US-10-449-902-40923	Sequence 40923, A
31	65.5	7.9	450	6	US-10-449-902-45860	Sequence 45860, A
32	65.5	7.9	541	6	US-10-449-902-55288	Sequence 55288, A
33	65.5	7.9	727	6	US-10-449-902-42699	Sequence 42699, A
34	65	7.9	428	6	US-10-953-349-27904	Sequence 27904, A
35	65	7.9	441	6	US-10-953-349-27903	Sequence 27903, A
36	65	7.9	477	6	US-10-953-349-27902	Sequence 27902, A
37	65	7.9	710	6	US-10-449-902-46982	Sequence 46982, A
38	64.5	7.8	147	6	US-10-953-349-21775	Sequence 21775, A
39	64.5	7.8	279	6	US-10-953-349-23178	Sequence 23178, A
40	64.5	7.8	307	6	US-10-953-349-23177	Sequence 23177, A
41	64.5	7.8	341	6	US-10-953-349-23176	Sequence 23176, A
42	64	7.7	255	6	US-10-953-349-27760	Sequence 27760, A
43	64	7.7	271	6	US-10-953-349-27759	Sequence 27759, A
44	64	7.7	313	6	US-10-953-349-27758	Sequence 27758, A
45	64	7.7	439	6	US-10-953-349-11386	Sequence 11386, A

## ALIGNMENTS

## RESULT 1

US-10-449-902-39402  
; Sequence 39402, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39402  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-39402

Query Match 10.2%; Score 84.5; DB 6; Length 330;  
Best Local Similarity 25.2%; Pred. No. 0.12;  
Matches 32; Conservative 15; Mismatches 61; Indels 19; Gaps 3;  
Qy 36 LEQYIALAFS-----QYQAGKWDHAKI FOALCMLDHYEPYFLGLGACRQAMGEFTAV 90  
Db 118 LDRLYTLSSVRARPDPASHPEWRRESLVTSLAADLAHR-----EFDVAL 164  
Qy 91 QSYSFQAMLDKDPFPFHAGECRLQOGLNGAESGHSARLLADTDPOQADLAASAKVM 150  
Db 165 ALLASVAALDPGNPVLISRLGYAHLQIGNLAAAAAAPHVESVAGGDPFAHSLARNRA - 223  
Qy 151 LEAIAIR 157  
Db 224 LECVAK 230

## RESULT 2

US-10-953-349-20069  
; Sequence 20069, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.

```
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20069
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20069

Query Match          9.7%; Score 80; DB 6; Length 183;
Best Local Similarity 23.2%; Pred. No. 0.18; Indels 36; Gaps 3;
Matches 33; Conservative 15; Mismatches 58; Indels 36; Gaps 3;

QY 36 LEQYALAFSQYQAGKWEDAHKIFQALCMLDHYEPRYFLGLGACRQAMGEFETAVQSY-- 93
Db 38 VEVHGLANLYSSLSYWRDAEICLQAKALKTYSATTLHVGNKHELHEKIQDAVAAYFN 97
QY 94 -----SFGAMLDLKDPRF-----P-----FHAGECRLOQGD 119
Db 98 AISMEVEHVPSKYSIGALLSKQGPFLPVARCFLSDALRLIPTNRMWAFYLGVEVHKQDGR 157
QY 120 LNAESGFHSARLLADTDPOQA 141
Db 158 LADAADCFQAASMLESDPVES 179

RESULT 3
US-10-953-349-20068
; Sequence 20068, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20068
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20068

Query Match          9.7%; Score 80; DB 6; Length 255;
Best Local Similarity 23.2%; Pred. No. 0.27; Indels 36; Gaps 3;
Matches 33; Conservative 15; Mismatches 58; Indels 36; Gaps 3;

QY 36 LEQYALAFSQYQAGKWEDAHKIFQALCMLDHYEPRYFLGLGACRQAMGEFETAVQSY-- 93
Db 110 VEVHGLANLYSSLSYWRDAEICLQAKALKTYSATTLHVGNKHELHEKIQDAVAAYFN 169
QY 94 -----SFGAMLDLKDPRF-----P-----FHAGECRLOQGD 119
Db 170 AISMEVEHVPSKYSIGALLSKQGPFLPVARCFLSDALRLIPTNRMWAFYLGVEVHKQDGR 229
QY 120 LNAESGFHSARLLADTDPOQA 141
Db 230 LADAADCFQAASMLESDPVES 251

RESULT 4
US-10-449-902-48030
; Sequence 48030, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
```

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; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205YI-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48030
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48030

Query Match          9.7%; Score 80; DB 6; Length 671;
Best Local Similarity 21.2%; Pred. No. 0.89; Indels 44; Gaps 5;
Matches 38; Conservative 23; Mismatches 74; Indels 44; Gaps 5;

QY 1 MOTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLLEQYALAFSQYQAGKWEDAHKIFQ 60
Db 491 VETYTQLLAVIQLRTKSFNAGISVLKSGSKDDRSLEIETWYDLVLLYIRMSQWRDAELIS 550
QY 61 ALCMLDHYEPRYFLGLGACRQAMGEFETAVQSYSGAMLDLKDPRF----- 106
Db 551 KIKATSPYSALAFHATGKLHEAKGFLKALRAYS--TALDL-EPHVPSPSLIATAIVLRL 607
QY 107 ---PFHAGECRL-----QQDGLNGAESG--FHSARLLADTD 138
Db 608 GERPLPVCFLTDALQDLDRTNHIANLGLLYEDEGSSALEAACFCFTAALLEETNP 666

RESULT 5
US-10-953-349-1110
; Sequence 1110, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1110
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1110

Query Match          9.3%; Score 76.5; DB 6; Length 220;
Best Local Similarity 20.7%; Pred. No. 0.54; Indels 47; Gaps 5;
Matches 31; Conservative 23; Mismatches 49; Indels 47; Gaps 5;

QY 10 EYEAELEAFMADGGTTLAMLDISGDTLLEQYALAFSQYQAGKWEDAHKIFQALCMLDHYE 69
Db 56 QYEMAI-AYMGD-----DFMFQLY-----GKYQDMALAVQNP----- 87
QY 70 PRYFLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFPFHAGECRLOQDGLNGAESGFHS 129
Db 88 ----HLNTIAACLLIKLRYDEAIGHCHNIVLTEENKPKALFRGKAKAELQOMDSARDDFRK 144
QY 130 ARLLADTDPPQADLAASAKWMLAIAIRRD 159
Db 145 AQKYAPDDK-----AIRRE 158

RESULT 6
US-10-953-349-1109
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; Sequence 1109, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1109
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1109

Query Match          9.3%; Score 76.5; DB 6; Length 250;
Best Local Similarity 20.7%; Pred. No. 0.63;
Matches 31; Conservative 23; Mismatches 49; Indels 47; Gaps 5;

Qy 10 EYEAELEAFMADGGTGLAMLQDISGDTLEQLYALAFSQYQAGKWDHAHKIFQALCMLDHYE 69
Db 86 QYEMAI-AYMGD-----DFMFQLY-----GKYQDMALAVKNPC----- 117

Qy 70 PRYFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDLNGAESGFHS 129
Db 118 ---HLNTAAACLIKLRYDEAIGHCNIVLTBEKNPKALFRGKAKAELGQMSARDDFRK 174

Qy 130 ARLLADTDPQOADLAASAKVMLEAIAIRRD 159
Db 175 AQYAPDDK-----AIRRE 188

RESULT 7
US-10-953-349-1108
; Sequence 1108, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1108
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1108

Query Match          9.3%; Score 76.5; DB 6; Length 365;
Best Local Similarity 20.7%; Pred. No. 1;
Matches 31; Conservative 23; Mismatches 49; Indels 47; Gaps 5;

Qy 10 EYEAELEAFMADGGTGLAMLQDISGDTLEQLYALAFSQYQAGKWDHAHKIFQALCMLDHYE 69
Db 201 QYEMAI-AYMGD-----DFMFQLY-----GKYQDMALAVKNPC----- 232

Qy 70 PRYFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDLNGAESGFHS 129
Db 233 ---HLNTAAACLIKLRYDEAIGHCNIVLTBEKNPKALFRGKAKAELGQMSARDDFRK 289

Qy 130 ARLLADTDPQOADLAASAKVMLEAIAIRRD 159
Db 290 AQYAPDDK-----AIRRE 303

RESULT 8
US-10-449-902-48463
; Sequence 48463, Application US/10449902
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48463
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48463

Query Match          9.0%; Score 74.5; DB 6; Length 403;
Best Local Similarity 27.7%; Pred. No. 1.8;
Matches 23; Conservative 17; Mismatches 38; Indels 5; Gaps 2;

Qy 78 ACQAMGEFTAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDLNGAESGF-HSARLLADT 136
Db 301 ACKLGLDGLGALLDADFALREGEENPKAFFRQOARIALNDIDAAVESFKHALQLEPND 360

Qy 137 DPOQADLAASAKVMLEAIAIRRD 159
Db 361 GGIKRELAARK---KIADRRD 379

RESULT 9
US-11-116-142B-20
; Sequence 20, Application US/11116142B
; Publication No. US20060115482A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Wisconsin Alumni Research Foundation
; APPLICANT: Sauer, Frank
; APPLICANT: Wasserman, David A
; APPLICANT: Maile, Tobias
; TITLE OF INVENTION: MODIFICATIONS OF HISTONE PROTEINS AS INDICATORS OF CELL
; TITLE OF INVENTION: PROLIFERATION AND DIFFERENTIATION
; FILE REFERENCE: 407E-001130US
; CURRENT APPLICATION NUMBER: US/11/116,142B
; CURRENT FILING DATE: 2005-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-11-116-142B-20

Query Match          8.6%; Score 71; DB 7; Length 638;
Best Local Similarity 22.9%; Pred. No. 7.5;
Matches 36; Conservative 25; Mismatches 52; Indels 44; Gaps 7;

Qy 1 MQDTTTLTPEYAELEAFMADGGTGLA-----MLQDISGDTLEQLYALAFSQYQAGKWDHAH 56
Db 399 IKTDLLLSAGEDAEEDAGSDSDGDAEAAVQLSGVG-----YYAQDSVSGGVD--- 449

Qy 57 KIFQALCMLDHPYRFLGLGACRQAMGEFETAVQSYSGFAMLDL-KDPRFPFHAGECRL 115
Db 450 -----PNYDPSDFLAMHKQRSIGE-----NSSLDMGAEISFLSH----- 484

Qy 116 QOQDLNGAESGFHSARLLADTDPQOADLAASAKVMLE 152
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